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OM protein - protein search, using sw model

Run on: September 11, 2002, 08:58:47 : Search time 75.59 Seconds
(without alignments)
17.633 Million cell updates/sec

Title: US-09-884-696-6
Perfect score: 57
Sequence: 1 FLSLNKLEAE 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	57	100.0	927	22	AA62110	M. bovis Dalton 2d
2	43	75.4	450	22	AAE04637	Pasteurella haemol
3	43	75.4	608	22	AAE04636	Pasteurella haemol
4	43	75.4	924	12	AA10889	Leukotoxin 352 enc
5	43	75.4	924	14	AA42385	Recombinant leukot
6	43	75.4	924	14	AA42380	Recombinant leukot
7	43	75.4	924	14	AA42378	Recombinant leukot
8	43	75.4	926	12	AA14482	LKT352. Pasteurel
9	43	75.4	926	14	AA43458	Leukotoxin 352 pro
10	43	75.4	926	15	AA50291	Recombinant leukot
11	43	75.4	926	17	AAW03945	P. haemolytica tru

12	43	75.4	926	19	AAW79568	Leukotoxin 352 pol
13	43	75.4	936	14	AA34547	GnRH-Leukotoxin ge
14	43	75.4	943	14	AA34546	Somatostatin-Leuko
15	43	75.4	951	14	AA34548	Rotavirus VP4-Leuk
16	43	75.4	953	11	AA407167	105KD PTX protein
17	43	75.4	953	12	AA415159	Leukotoxin from P.
18	43	75.4	953	14	AA43865	Leukotoxin protein
19	43	75.4	953	15	AA460072	PTXA protein of Pa
20	43	75.4	953	22	AAE04638	Pasteurella haemol
21	43	75.4	956	12	AA412561	APPA haemolysin an
22	43	75.4	956	18	AAW22156	Aprtic protein. A
23	43	75.4	956	21	AAV51410	A. pleuropneumonia
24	43	75.4	977	17	AAW03942	LKT-GnRH protein f
25	43	75.4	977	19	AAW79569	LKT-GnRH chimeric
26	43	75.4	1069	15	AA452748	Bovine IFNgamma/LK
27	43	75.4	1069	18	AAW13867	Chimeric protein #
28	43	75.4	1069	21	AA421074	Bovine gamma-IFN/P
29	43	75.4	1098	13	AA422103	Bovine IL-2 - LKT
30	43	75.4	1098	15	AA452747	Bovine IL-2/LKT ch
31	43	75.4	1098	18	AAW13866	Chimeric protein #
32	43	75.4	1098	21	AA421073	Bovine IL-2/Pasteu
33	41	71.9	28	20	AAV31518	Exendin agonist pe
34	41	71.9	28	20	AAV24822	Exendin agonist pe
35	41	71.9	28	20	AAV17577	Exendin agonist pe
36	41	71.9	28	21	AA411144	Exendin agonist pe
37	41	71.9	28	21	AA411234	Exendin agonist pe
38	41	71.9	28	21	AA452903	Exendin agonist pe
39	41	71.9	28	21	AA453000	Exendin agonist c
40	41	71.9	28	21	AAV94057	Amino acid sequenc
41	41	71.9	28	21	AAV94155	Exendin agonist pe
42	41	71.9	28	22	AAE08396	Exendin agonist pe
43	41	71.9	28	22	AAE08486	Exendin agonist pe
44	41	71.9	28	22	AA464232	Exendin agonist, S
45	41	71.9	28	22	AA464322	Exendin agonist, S

ALIGNMENTS

RESULT 1	
AA62110	standard; Protein; 927 AA.
ID	AA62110
AC	AA62110;
XX	
DT	29-MAY-2001 (first entry)
XX	
DE	M. bovis Dalton 2d RTX toxin A subunit.
XX	
KW	Moraxella; antigen; Immune response; Infection; RTX toxin; vaccine;
KM	antibacterial; A subunit.
XX	
OS	Moraxella bovis.
XX	
PN	MO200116172-A1.
XX	
PD	08-MAR-2001.
XX	
PF	31-AUG-2000; 2000MO-AU01048.
XX	
PR	31-AUG-1999; 99AU-0002571.
XX	
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.
PA	(UYME) UNIV MELBOURNE.
XX	
PI	Farn J, Strugnell R, Tennent J;
XX	
DR	WPI: 2001-235092/24.
XX	
PT	N-PSDB; AAF57290.
XX	
PT	Novel Moraxella bovis antigen useful in compositions for raising immune
XX	response in an animal, has protease, lipase or hemolysin activity

PS Claim 26; Fig 5; 60pp; English.
XX
CC The invention relates to new Moraxella bovis antigens and nucleic acid
CC sequences encoding these antigenic polypeptides. The antigenic
CC polypeptides and polynucleotides are useful for raising an immune
CC response in an animal directed against Moraxella, preferably against
CC M. bovis or M. catarrhalis, and for treating Moraxella infections. The
CC present sequence represents the amino acid sequence of the A subunit of
CC the RTX toxin from M. bovis Dalton 2d.
XX
SQ Sequence 927 AA;

Query Match 100.0%; Score 57; DB 22; Length 927;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FLSEINKELAE 12
Db 433 flseinkelae 444

RESULT 2
AAE04637
ID AAE04637 standard; Protein; 450 AA.
XX
AC AAE04637;
XX
DT 10-SEP-2001 (first entry)
XX
DE Pasteurella haemolytica modified leukotoxin 50 (Lkt50) protein.
XX
KW Leukotoxin 50; Lkt50; respiratory disease; infection; therapy;
KW Immunostimulant; antibacterial; vaccine; transgenic plant;
KW animal feed; mutant; mutain.
XX
OS Pasteurella haemolytica.
OS Synthetic.
XX
FN WO200144289-A2.
XX
PI 21-JUN-2001.
XX
PD 15-DEC-2000; 2000WO-CA01498.
XX
PE 17-DEC-1999; 99US-0172148.
XX
PR 17-DEC-1999; 99US-0172148.
XX
PA (UYGU-) UNIV GUELPH OFFICE.
XX
PI Lo RYC, Shewen PE, Lee RWH, Hodgins D, Strommer JN;
XX
DR WPI: 2001-408470/43.
DR N-PSDB: AAD08976.
XX
PT Modified leukotoxin polypeptide is useful in a vaccine to prevent or
PT treat Mannheimia (Pasteurella) infection (particularly M. haemolytica
PT infection), and disease associated with a leukotoxin, e.g., respiratory
PT disease -
XX
PS Claim 4; Fig 12; 70pp; English.
XX
CC The present sequence is Pasteurella (Mannheimia) haemolytica
CC modified leukotoxin-50 (Lkt50) protein. The modification comprises
CC the removal of amino acids within the hydrophobic transmembrane
CC domain of a full length leukotoxin protein. Modified leukotoxin
CC sequences are used in vaccines to treat or prevent diseases associated
CC with leukotoxin, e.g., respiratory disease, and Mannheimia infection
CC (particularly M. haemolytica infection). In addition, the vaccine
CC is used to prepare a medicament. Furthermore, the plant transformed
CC with modified leukotoxin sequences is fed to an animal such as a
CC ruminant, to prevent or treat respiratory diseases.
XX
SQ Sequence 450 AA;

Query Match 75.4%; Score 43; DB 22; Length 450;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSEINKELAE 12
Db 1 flnlnkelgae 12

RESULT 3
AAE04636
ID AAE04636 standard; Protein; 608 AA.
XX
AC AAE04636;
XX
DT 10-SEP-2001 (first entry)
XX
DE Pasteurella haemolytica modified leukotoxin 66 (Lkt66) protein.
XX
KW Leukotoxin 66; Lkt66; respiratory disease; infection; therapy;
KW Immunostimulant; antibacterial; vaccine; transgenic plant;
KW animal feed; mutant; mutain.
XX
OS Pasteurella haemolytica.
OS Synthetic.
XX
FN WO200144289-A2.
XX
PI 21-JUN-2001.
XX
PD 15-DEC-2000; 2000WO-CA01498.
XX
PE 17-DEC-1999; 99US-0172148.
XX
PR 17-DEC-1999; 99US-0172148.
XX
PA (UYGU-) UNIV GUELPH OFFICE.
XX
PI Lo RYC, Shewen PE, Lee RWH, Hodgins D, Strommer JN;
XX
DR WPI: 2001-408470/43.
DR N-PSDB: AAD08975.
XX
PT Modified leukotoxin polypeptide is useful in a vaccine to prevent or
PT treat Mannheimia (Pasteurella) infection (particularly M. haemolytica
PT infection), and disease associated with a leukotoxin, e.g., respiratory
PT disease -
XX
PS Claim 2; Fig 2; 70pp; English.
XX
CC The present sequence is Pasteurella (Mannheimia) haemolytica
CC modified leukotoxin-66 (Lkt66) protein. The modification comprises
CC the removal of amino acids within the hydrophobic transmembrane
CC domain of a full length leukotoxin protein. Modified leukotoxin
CC sequences are used in vaccines to treat or prevent diseases associated
CC with leukotoxin, e.g., respiratory disease, and Mannheimia infection
CC (particularly M. haemolytica infection). In addition, the vaccine
CC is used to prepare a medicament. Furthermore, the plant transformed
CC with modified leukotoxin sequences is fed to an animal such as a
CC ruminant, to prevent or treat respiratory diseases.
XX
SQ Sequence 608 AA;

Query Match 75.4%; Score 43; DB 22; Length 608;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSEINKELAE 12
Db 106 flnlnkelgae 117

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RESULT 4
ID AAR10889 standard; Protein: 924 AA.
XX
AC AAR10889;
XX
DT 11-APR-1991 (first entry)
XX
DE Leukotoxin 352 encoded by plasmid pAA352.
XX
KM LKT; vaccine: antigen; respiratory disease; shipping fever pneumonia.
XX
OS Pasteurella haemolytica A1 strain B122.
XX
PN CA2014033-A.
XX
PD 07-OCT-1990.
XX
PF 06-APR-1990; 90CA-2014033.
XX
PR 07-APR-1989; 89US-0335018.
XX
PA (UYSA-) UNIV SASKATCHEWAN.
XX
PI Acres SD, Babluk LA, Potter AA, Lawman MJP;
XX
DR WPI; 1991-000097/01.
XX
DR N-PSDB; AAQ10272.
XX
PT Pasteurella haemolytica proteins and genes - used for producing
PT vaccines to protect animals esp. cattle from respiratory diseases
PT e.g. pneumonia.
XX
PS Claim 13; Fig 5; 87pp; English.
XX
CC Plasmid pAA352 is derived from pAA114, a clone isolated from a
CC genomic library of P. haemolytica. The protein, designated "new
CC leukotoxin" or "LKT 352" is 98% homologous to authentic leukotoxin.
CC LKT 352 and pref. antigenic fragments of it, can be used in
CC vaccines to protect cattle from respiratory diseases. They can also
CC be used to produce antibodies for immunoinfinity purification.
CC further proteins. [Fig. contg. sequence v. poor].
CC See also AAR10890, AAR10909, AAR10910 and AAQ10783.
XX
SQ Sequence 924 AA;

Query Match 75.4%; Score 43; DB 12; Length 924;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKLEAE 12
   ||| ||| ||| |||
Db 422 FLNlnkElgae 433

RESULT 5
ID AAR42385 standard; Protein: 924 AA.
XX
AC AAR42385;
XX
DT 19-APR-1994 (first entry)
XX
DE Recombinant leukotoxin peptide from plasmid PCR28.
XX
KM Haemophilus somnus; immunogenic; haemolysin; lppB; lppC;
KM thromboembolic meningococcal septicemia; arthritis;
KM pneumonia; lktA gene; haemin-binding protein; fusion protein.
XX
OS Pasteurella haemolytica.
XX
PN WO9321323-A.

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XX
PD 28-OCT-1993.
XX
PF 05-APR-1993; 93WO-CA00135.
XX
PR 09-APR-1992; 92US-0865050.
PR 04-JUN-1992; 92US-0893424.
PR 04-JUN-1992; 92US-0893426.
PR 29-MAR-1993; 93US-0038287.
PR 29-MAR-1993; 93US-0038288.
PR 29-MAR-1993; 93US-0038719.
XX
PA (UYSA-) UNIV SASKATCHEWAN.
XX
PI Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
PI Rioux C, Theisen M;
XX
DR WPI; 1993-351733/44.
XX
DR N-PSDB; AAQ51086.
XX
PT Haemophilus somnus immunogenic proteins used in vaccines -
PT selected from haemin-binding protein, haemolysin, lppB and lppC,
PT and corresp. DNA
XX
PS Disclosure; Fig 11; 119pp; English.
XX
CC The lppB gene protein was expressed in E. coli as a fusion to the
CC Pasteurella haemolytica leukotoxin gene lktA coded for by plasmid
CC pAA352. The lppB gene fragment was taken from pMS11. lppB can be
CC used in vaccines for preventing or treating H. somnus infections,
CC which cause thromboembolic meningococcal septicemia, arthritis
CC and pneumonia in vertebrates.
XX
SQ Sequence 924 AA;

Query Match 75.4%; Score 43; DB 14; Length 924;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKLEAE 12
   ||| ||| ||| |||
Db 424 FLNlnkElgae 435

RESULT 6
ID AAR42380 standard; Protein: 924 AA.
XX
AC AAR42380;
XX
DT 19-APR-1994 (first entry)
XX
DE Recombinant leukotoxin peptide (split) from plasmid pGCH4.
XX
KM Haemophilus somnus; immunogenic; haemolysin; lppB; lppC;
KM thromboembolic meningococcal septicemia; arthritis;
KM pneumonia; lktA gene; haemin-binding protein; fusion protein.
XX
OS Pasteurella haemolytica.
XX
PN WO9321323-A.
XX
PD 28-OCT-1993.
XX
PF 05-APR-1993; 93WO-CA00135.
PR 09-APR-1992; 92US-0865050.
PR 04-JUN-1992; 92US-0893424.
PR 04-JUN-1992; 92US-0893426.
PR 29-MAR-1993; 93US-0038287.
PR 29-MAR-1993; 93US-0038288.

```

PR 29-MAR-1993; 93US-0038719.
 XX
 PA (UYSA-) UNIV SASKATCHEWAN.
 PI Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
 PI Rioux C, Theisen M;
 XX
 DR WPI; 1993-351733/44.
 DR N-PSDB; AAQ51082.
 XX
 XX Haemophilus somnus immunogenic proteins used in vaccines -
 PT selected from haemin-binding protein, haemolysin, lppb and lppc,
 PT and corresp. DNA
 XX
 PS Disclosure; Fig 6; 11ppp; English.
 CC
 CC The hmb gene encoding the haemin-binding protein was expressed in
 CC E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene
 CC lktA coded for by plasmid pAA352. The hmb gene fragment was taken
 CC from PRAP504 and starts at the codon for the 33 rd amino acid residue
 CC of ORF1. The haemin binding protein can be used in vaccines for
 CC preventing or treating H. somnus infections, which cause thromboembolic
 CC meningo-encephalitis, septicemia, arthritis and pneumonia in
 CC vertebrates.
 CC See also AAR42370-86.
 CC
 XX
 SQ Sequence 924 AA;

 Query Match 75.4%; Score 43; DB 14; Length 924;
 Best Local Similarity 75.0%; Pred. No. 52;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FLSLNKELEAE 12
 || |||||:
 Db 424 fllnlknlqae 435

 RESULT 7
 AAR42378
 ID AAR42378 standard; Protein; 924 AA.
 AC AAR42378;
 XX
 DT 19-APR-1994 (first entry)
 XX
 DE Recombinant leukotoxin peptide (SPLT) from plasmid pGCH5.
 XX
 KW Haemophilus somnus; immunogenic; haemolysin; lppb; lppc;
 KW thromboembolic meningoencephalitis; septicemia; arthritis;
 KW pneumonia; lktA gene; haemin-binding protein; fusion protein.
 XX
 OS Pasteurella haemolytica.
 XX
 FM W09321323-A.
 XX
 PD 28-OCT-1993.
 XX
 PF 05-APR-1993; 93WO-CA00135.
 XX
 PR 09-APR-1992; 92US-0865050.
 PR 04-JUN-1992; 92US-0893424.
 PR 04-JUN-1992; 92US-0893426.
 PR 29-MAR-1993; 93US-0038287.
 PR 29-MAR-1993; 93US-0038288.
 PR 29-MAR-1993; 93US-0038719.
 XX
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
 PI Rioux C, Theisen M;
 XX
 DR WPI; 1993-351733/44.

DR N-PSDB; AAQ51081.
 XX
 PT Haemophilus somnus immunogenic proteins used in vaccines -
 PT selected from haemin-binding protein, haemolysin, lppb and lppc,
 PT and corresp. DNA
 XX
 PS Disclosure; Fig 5; 11ppp; English.
 CC
 CC The hmb gene encoding the haemin-binding protein was expressed in
 CC E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene
 CC lktA coded for by plasmid pAA352. The hmb gene fragment was taken
 CC from PRAP501 and starts at the codon for the third amino acid residue
 CC of ORF1. The haemin binding protein can be used in vaccines for
 CC preventing or treating H. somnus infections, which cause thromboembolic
 CC meningo-encephalitis, septicemia, arthritis and pneumonia in
 CC vertebrates.
 CC See also AAR42370-86.
 CC
 XX
 SQ Sequence 924 AA;

 Query Match 75.4%; Score 43; DB 14; Length 924;
 Best Local Similarity 75.0%; Pred. No. 52;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FLSLNKELEAE 12
 || |||||:
 Db 424 fllnlknlqae 435

 RESULT 8
 AAR14482
 ID AAR14482 standard; Protein; 926 AA.
 AC AAR14482;
 XX
 DT 15-JAN-1992 (first entry)
 XX
 DE LKT352.
 XX
 KW Antigen; leukotoxin; vaccine; lktA.
 XX
 OS Pasteurella haemolytica.
 XX
 FM W09115237-A.
 XX
 PD 17-OCT-1991.
 XX
 PF 17-OCT-1991; 91WO-CA00170.
 XX
 PR 05-APR-1990; 90US-0504850.
 XX
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Acres SD, Bariuk LA, Potter AA, Lawman MJP;
 XX
 DR WPI; 1991-324967/44.
 XX
 PT Vaccines for Pasteurella haemolytica infection in cattle -
 PT comprise sub-unit antigens from p haemolytica fimbrial protein,
 PT plasmid receptor, 50 K outer membrane protein and leukotoxin.
 XX
 PS Disclosure; Fig 5; 92pp; English.
 CC
 CC LKT352 is 98% homologous with authentic leukotoxin and migrates
 CC to the same position on gels.
 CC The LKT352 gene was prep'd. as follows: lktA, an MaeI fragment
 CC contg. the gene was ligated into the SmaI site of pUC13 to form
 CC pAA11/9. From this, two constructs were made in the pTac-based
 CC vector, pGH432:lact digested with SmaI. One, pAA342, consisted of
 CC the 5' Ahairi fragment from lktA while the other, pAA345, contained
 CC the entire MaeI fragment. Clone pAA342 expressed a truncated
 CC leukotoxin peptide at high levels while pAA345 expressed full

CC length leukotoxin at very low levels. The 3' end of the lktA gene
 CC of pAA345 was therefore ligated to StyI/BamHI digested pAA342 to
 CC yield pAA352 contg. the lkt352 sequence. The protein expressed
 CC from the vector can be used to prepare a subunit vaccine with
 CC other P. haemolytica antigens, e.g. fibrinolytic protein, plasmin
 CC receptor or 50K outer membrane protein. The vaccines can be used
 CC to protect cattle from respiratory diseases such as pneumonia, esp.
 CC shipping fever pneumonia.
 CC See also AAR14481, 83,84 and 85.
 XX
 SQ Sequence 926 AA;

Query Match 75.4%; Score 43; DB 12; Length 926;
 Best Local Similarity 75.0%; Pred. No. 52;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
 || |||||:
 Db 424 flnlInkElgae 435

RESULT 9

AAR34545
 ID AAR34545 standard; Protein: 926 AA.
 XX
 AC AAR34545;

XX 23-AUG-1993 (first entry)

XX Leukotoxin 352 produced from pAA352.

XX Vector: LKT 352; flanking; recombinant; antigen; somatostatin;
 KM gonadotropin releasing hormone; rotavirus viral protein 4;
 KM carrier protein; lactation; reproduction.
 XX
 OS Pasteurella haemolytica.

XX MO9308290-A.

XX 29-APR-1993.

XX 15-OCT-1992; 92MO-CA00449.

XX 16-OCT-1991; 91US-0779171.

XX 14-OCT-1992; 92US-0960932.

XX (UYSA-) UNIV SASKATCHEWAN.

XX Hughes HPA, Potter AA, Redmond MJ;

XX WPI; 1993-152482/18.

XX N-PSDB; AAO41317.

PT Immunological carrier system with enhanced immunogenicity -
 PT comprises chimeric protein comprising leuco:toxin peptide or
 PT homologous protein fused to antigen esp. somatostatin or
 PT gonadotropin releasing hormone
 XX
 XX Disclosure; Fig 3; 95pp; English.

XX Gene libraries of P. haemolytica A1 (strain B122) were constructed
 CC in lambda gIII and pUC13. Resulting clones were used to transform E.
 CC coli and individual colonies were pooled and screened for reaction
 CC with serum from a calf which had survived a P. haemolytica infection
 CC and that had been boosted with a conc. culture supernatant of P.
 CC haemolytica to increase anti-leukotoxin antibody levels. Positive
 CC colonies were screened for their ability to produce leukotoxin by
 CC incubating cell lysates with bovine neutrophils and measuring the
 CC release of lactate dehydrogenase from the neutrophils. A 4kb
 CC fragment was obtd. Progressively larger clones were isolated by
 CC chromosome walking to isolate full length recombinants of ca. 8kb.
 CC In pAA114. The clone was subjected to restriction enzyme digestion

CC to yield two clones, one expressing truncated leukotoxin peptide at
 CC high levels and the other expressing the full length leukotoxin at
 CC low levels. The 3' end of the lktA gene from the full length clone
 CC was ligated to the truncated gene clone to yield plasmid pAA352. The
 CC clone was used to produce chimeric proteins by gene fusion with an
 CC antigen coding sequence, e.g. the coding sequence of somatostatin,
 CC gonadotropin releasing hormone or rotavirus viral protein 4, i.e.
 CC leukotoxin works as a carrier protein to bring about a larger
 CC immune response than the antigen alone. Immunisation with these
 CC antigens can regulate growth rate, lactation and reproductive
 CC efficiency. See also AAR34546-8.
 XX
 SQ Sequence 926 AA;

Query Match 75.4%; Score 43; DB 14; Length 926;
 Best Local Similarity 75.0%; Pred. No. 52;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
 || |||||:
 Db 424 flnlInkElgae 435

RESULT 10

AAR50291
 ID AAR50291 standard; Protein: 926 AA.

XX AAR50291;

XX 06-OCT-1994 (first entry)

XX Recombinant leukotoxin from plasmid pAA352.

XX Vaccine; outer membrane protein; OMP; Haemophilus somnus;

KM iron regulated protein; leukotoxin; Pasteurella haemolytica;

KM LKT352.

XX Pasteurella haemolytica A1 (strain B122).

XX CA2099707-A.

XX 03-JAN-1994.

XX 29-JUN-1993; 93CA-2099707.

XX 02-JUL-1992; 92US-0908253.

XX (UYSA-) UNIV SASKATCHEWAN.

XX Harland RJ, Potter AA;

XX WPI; 1994-092909/12.

XX N-PSDB; AAO44760.

PT Haemophilus somnus outer membrane protein extract -
 PT enriched with iron-regulated proteins, opt. contg.
 PT leuco:toxin antigens, for use as vaccine
 XX
 XX Claim 5; Fig 5; 78pp; English.

XX A vaccine comprising an outer membrane protein (OMP) extract of
 CC Haemophilus somnus enriched with iron regulated proteins is new.
 CC The vaccine pref. further comprises an immunogenic leukotoxin
 CC polypeptide, esp. an immunogenic Pasteurella haemolytica leukotoxin
 CC homologous to LKT352. Example 1.2 describes the prodn. of
 CC P. haemolytica recombinant leukotoxin from pAA352.
 CC Two expression constructs were made. One, pAA342, contained the
 CC 5'-AhaII fragment of the lktA gene, while the other, pAA345,
 CC contained the entire lktA gene. pAA342 expressed a truncated
 CC leukotoxin peptide at high levels, while pAA345 expressed full
 CC length leukotoxin at very low levels. Therefore, the 3' end
 CC of the lktA gene was ligated into pAA342, yielding plasmid pAA352.

CC LKT352 or new leukotoxin is 98% homologous to authentic
 CC leukotoxin.
 CC NB: the protein sequence in Fig 5 comprises 926 amino acids,
 CC however this protein is described in the text as having
 CC 931 amino acids.
 XX
 SQ Sequence 926 AA;

Query Match 75.4%; Score 43; DB 15; Length 926;
 Best Local Similarity 75.0%; Pred. No. 52;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
 DB 424 flnlInkElgae 435

RESULT 11

AAW03945
 ID AAW03945 standard; Protein; 926 AA.

AC AAW03945;

DE 20-NOV-1996 (first entry)

P. haemolytica truncated leukotoxin (LKT352).

Leukotoxin; LKT; gonadotropin-releasing hormone; GnRH;
 fusion protein; immunogen; vaccine; fertility control;
 contraceptive; sterilisation; plasmid pAA352.

Pasteurella haemolytica A1 strain B122.

WO9624675-A1.

15-AUG-1996.

24-JAN-1996; 96WO-CA00049.

10-FEB-1995; 95US-0387156.

(UYSA-) UNIV SASKATCHEWAN.

Manns JG, Potter AA;

WPI; 1996-384447/38.

N-PSDB; AAT37179.

Gonadotropin-releasing hormone multimer fusion proteins - with
 leukotoxin polypeptide for increased immunogenicity, useful in
 antiferility vaccine prodn.

Example 1; Fig 3A-3I; 87pp; English.

A truncated leukotoxin (AAW03945). LKT 352, lacks the cytotoxic
 portion of the native protein from Pasteurella haemolytica. It is
 the product of plasmid pAA352 which carries a truncated lktA gene
 (AAT37179). A fusion protein (AAW03942) between LKT352 and a
 gonadotropin releasing hormone tetramer can be expressed in
 Escherichia coli. This is useful as a vaccine for fertility
 control, paric. immunological sterilisation of domestic or
 farm animals.

Sequence 926 AA;

Query Match 75.4%; Score 43; DB 17; Length 926;

Best Local Similarity 75.0%; Pred. No. 52;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
 DB 424 flnlInkElgae 435

DB 424 flnlInkElgae 435

RESULT 12

AAW79568
 ID AAW79568 standard; Protein; 926 AA.

AC AAW79568;

DE 24-DEC-1998 (first entry)

Leukotoxin 352 polypeptide.

Gonadotropin releasing hormone; GnRH; chimera; leukotoxin polypeptide;
 multimer; vaccine; tumour; Leukotoxin 352; LKT 352; lktA; plasmid pAA352;
 cytotoxic.

Synthetic.

Key Location/Qualifiers

Misc_feature 11.924
 /note="Recombinant leukotoxin peptide"

WO9806848-A1.

19-FEB-1998.

08-AUG-1997; 97WO-CA00559.

09-AUG-1996; 96US-0694865.

(UYSA-) UNIV SASKATCHEWAN.

Manns JG, Potter AA;

WPI; 1998-159540/14.

N-PSDB; AAV61530.

Chimeric protein of leukotoxin and gonadotropin releasing hormone -
 useful for, e.g. preparation of vaccines for reduction of incidence
 of mammary tumours in mammals

Claim 7; Figure 3.1-9; 118pp; English.

The present sequence represents a recombinantly produced or chemically
 synthesised leukotoxin 352 (LKT 352) polypeptide, derived from the lktA
 gene that is present in the plasmid pAA352. This gene produces a
 truncated protein that has an estimated molecular weight of about 99 kDa
 and lacks the cytotoxic portion of the molecule. Thus this gene has a
 higher expression level than that of the full-length molecule. This can
 be used in the construction of a chimeric protein that comprises a
 leukotoxin polypeptide, several multimers, and a GnRH sequence. The
 chimeric protein can be used as a vaccine to help reduce the incidence of
 mammary tumours in a mammalian individual.

Sequence 926 AA;

Query Match 75.4%; Score 43; DB 19; Length 926;

Best Local Similarity 75.0%; Pred. No. 52;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
 DB 424 flnlInkElgae 435

RESULT 13

AAAR34547

ID AAR34547 standard; Protein; 936 AA.

AC AAR34547;

XX

DT 23-AUG-1993 (first entry)
 XX
 DE GNRH-leukotoxin gene fusion prod.
 XX
 KM Vector; LKT 352; flanking; recombinant; antigen; somatostatin;
 KM gonadotropin releasing hormone; rotavirus viral protein 4;
 KM carrier protein; lactation; reproduction; SRIF.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..926
 FT /note="recombinant leukotoxin protein"
 FT Peptide 927..936
 FT /note="GNRH"
 XX
 FT
 XX
 PN MO9308290-A.
 XX
 PD 29-APR-1993.
 XX
 PF 15-OCT-1992; 92WO-CA00449.
 XX
 PR 16-OCT-1991; 91US-0779171.
 PR 14-OCT-1992; 92US-0960932.
 XX
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Hughes HPA, Potter AA, Redmond MJ;
 PI N-PSDB; AAQ41321.
 DR WPI: 1993-152482/18.
 DR N-PSDB; AAQ41322.
 XX
 PT Immunological carrier system with enhanced immunogenicity -
 PT comprises chimeric protein comprising leuco:toxin peptide or
 PT homologous protein fused to antigen esp. somatostatin or
 PT gonadotropin releasing hormone
 XX
 PS Example 2; Fig 8; 95pp; English.
 XX
 CC Oligonucleotides contg. sequences from bovine gonadotropin
 CC releasing hormone (GNRH) gene were constructed on a Pharmacia Gene
 CC Assembler using standard phosphoramidite chemistry. The oligo-
 CC nucleotides were annealed and ligated into vector PAA352 (contg.
 CC the Pateurella haemolytica leuko-toxin gene) which had been digested
 CC with BamHI. The ligated DNA was used to transform E. coli strain
 CC MH3000. Transformants contg. the oligonucleotide inserts were
 CC identified by restriction endonuclease mapping and the recombinant
 CC plasmid designated PAA502. The chimeric protein produced from the
 CC plasmid works to bring about a larger immune response than the antigen
 CC alone, i.e. the leukotoxin works as a carrier protein.
 CC See also AAR34545-8.
 CC
 XX
 SQ Sequence 936 AA;
 XX

Query Match 75.4%; Score 43; DB 14; Length 936;
 Best Local Similarity 75.0%; Pred. No. 52;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FLSLNKLEAE 12
 II |||||:II
 DB 424 fllnlkqlgae 435

RESULT 14
 AAR34546
 ID AAR34546 standard; Protein; 943 AA.
 XX
 AC AAR34546;
 XX
 DT 23-AUG-1993 (first entry)
 XX
 DE Somatostatin-leukotoxin gene fusion prod.

XX
 KM Vector; LKT 352; flanking; recombinant; antigen; somatostatin;
 KM gonadotropin releasing hormone; rotavirus viral protein 4;
 KM carrier protein; lactation; reproduction; SRIF.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..929
 FT /note="recombinant leukotoxin protein"
 FT Peptide 930..943
 FT /note="SRIF"
 XX
 PN MO9308290-A.
 XX
 PD 29-APR-1993.
 XX
 PF 15-OCT-1992; 92WO-CA00449.
 XX
 PR 16-OCT-1991; 91US-0779171.
 PR 14-OCT-1992; 92US-0960932.
 XX
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Hughes HPA, Potter AA, Redmond MJ;
 PI N-PSDB; AAQ41321.
 DR WPI: 1993-152482/18.
 DR N-PSDB; AAQ41321.
 XX
 PT Immunological carrier system with enhanced immunogenicity -
 PT comprises chimeric protein comprising leuco:toxin peptide or
 PT homologous protein fused to antigen esp. somatostatin or
 PT gonadotropin releasing hormone
 XX
 PS Example 2; Fig 6; 95pp; English.
 XX
 CC Oligonucleotides contg. sequences from bovine somatostatin (SRIF)
 CC gene were constructed on a Pharmacia Gene Assembler using standard
 CC phosphoramidite chemistry. The oligonucleotides were annealed and
 CC ligated into vector PAA352 (contg. the Pateurella haemolytica leuko-
 CC toxin gene) which had been digested with BamHI. The ligated DNA was
 CC used to transform E. coli strain JM105. Transformants contg. the
 CC oligonucleotide inserts were identified by restriction endonuclease
 CC mapping and the recombinant plasmid designated PAA496. The
 CC chimeric protein produced from the plasmid works to bring about a
 CC larger immune response than the antigen alone, i.e. the leukotoxin
 CC works as a carrier protein.
 CC See also AAR34545-8.
 CC
 XX
 SQ Sequence 943 AA;
 XX

Query Match 75.4%; Score 43; DB 14; Length 943;
 Best Local Similarity 75.0%; Pred. No. 53;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FLSLNKLEAE 12
 II |||||:II
 DB 424 fllnlkqlgae 435

RESULT 15
 AAR34548
 ID AAR34548 standard; Protein; 951 AA.
 XX
 AC AAR34548;
 XX
 DT 23-AUG-1993 (first entry)
 XX
 DE Rotavirus VP4-leukotoxin gene fusion prod.
 XX
 KM Vector; LKT 352; flanking; recombinant; antigen; somatostatin;
 KM gonadotropin releasing hormone; rotavirus viral protein 4;

carrier protein; lactation; reproduction; SRIF
synthetic.

Synthetic.

FH	Key	Location/Qualifiers
FM	Distances	1000

Protein

1..926

ET
ET
post-ide

/note="recombinant leukotoxin protein"
037 051

FT	Peptide	927..951
FT		/5040 = "

927.:.951

	/note= "Rotavirus VP-4"
FT	
VV	

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/note= "Rotavirus VP-4"
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PN W09308290-A.

PD 29-APR-1993.

AA 15-OCT-1992: 92WO-CA00449
PF

XX
XX
C
E
T
C
T
T
T

PR 14-OCT-1992; 92US-0960932.

PA (UYSA-) UNIV SASKATCHEWAN.

xx Hughes HPA. Potter AA. Redmond MT
PT

[illegible]

DR N-PSDB; AAQ41322.

PT gonadotropin releasing hormone

PS Example 2; Fig 8; 95pp; English.

CC oligonucleotides conty. sequences from bovine Rotavirus viral
CC protein 4 (VP-4) gene were constructed on a Pharmacia Gene
CC Assembler using standard phosphoramidite chemistry. The oligo-
CC nucleotides were annealed and ligated into vector pAA352 (conty.
CC the *Pateurella hemolytica* leuko-toxin gene) which had been digested
CC with BamHI. The ligated DNA was used to transform *E. coli* strain
CC MH3000. Transformants conty. the oligonucleotide inserts were
CC identified by restriction endonuclease mapping and the recombinant
CC plasmid designated pAA501. The chimeric protein produced from the
CC plasmid works to bring about a larger immune response than the antigen
CC alone, i.e. the leukotoxin works as a carrier protein.
CC See also AAR34545-7.

Sequence 951 AA;

Query Match 75.4%; Score 43; DB 14; Length 951;

Best Local Similarity 75.0%; Pred. No. 53;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY      1 FLSLNKLEAE 12
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Db 424 flinInkelgae 435

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Search completed: September 11, 2002, 08:58:48
Job time: 192 sec
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Result No.	Score	Query Match	length	DB	ID	Description
1	2325	50.0	953	1	B30169	leukotoxin A - Pass
2	2240.5	48.2	956	1	B33389	toxoin II - Actinob
3	2236	48.1	955	1	A35254	leukotoxin A - Pass
4	2209.5	47.6	956	1	A43834	toxoin II - Actinob
5	1959.5	42.2	1052	1	B49119	toxoin III - Actino
6	1928	41.5	1049	1	S51784	toxoin III - Actino
7	1851.5	39.9	1024	1	S10056	hemolysin A - Esch
8	1849	39.8	1023	1	LEECA	hemolysin A - Esch
9	1820	39.2	1055	1	A37205	leukotoxin A - Act
10	1767.5	38.0	1022	1	I39643	RTX-toxin I - Acti
11	1752	37.7	998	2	T00227	hemolysin A toxin
12	1733	37.3	998	2	I41078	hemolysin - Esche
13	809.5	17.4	1705	2	S51672	adenylate cyclase
14	806	17.3	1766	1	OYBRC	cyclolysin - Borda
15	434	9.3	1829	2	S35027	cytotoxin RTX hom
16	432.5	9.3	1829	2	E81086	iron-regulated pro
17	416	9.0	1302	2	C81182	iron-regulated pro
18	411	8.8	1208	2	C82779	hemolysin-Lyph cal
19	410	8.8	1636	2	B82736	hemolysin-Lyph cal
20	403.5	8.7	1115	2	A47058	Fe-regulated RTX c
21	391	8.4	2064	2	G82652	bacteriocin XF2407
22	383	8.2	208	2	S34238	leukotoxin A - Pas
23	365	7.9	687	2	F81856	probable RTX-famil
24	343	7.4	4536	2	AH2515	hypothetical prote
25	332.5	7.2	1944	2	AH3098	rhiboblocin/RTX t
26	332.5	7.2	1990	2	A96188	probable phosphoe
27	328.5	7.1	1296	2	C82521	hemolysin-Lyph ca
28	305.5	6.6	993	2	AE1905	outer membrane se
29	304.5	6.6	1072	2	G95851	probable hemolysin

30	287.5	6.2	306.3	2	AD2493	hypothetical prote
31	287	6.2	1417	2	AC3137	hypothetical prote
32	280	6.0	643	2	T03518	hypothetical prote
33	280	6.0	900	2	AC1852	hypothetical prote
34	276	5.9	650	2	CG5752	calcium-binding pr
35	269.5	5.8	1112	2	H95964	probable outer mem
36	268	5.8	539	2	CG5405	hypothetical prote
37	267.5	5.8	387	2	E95995	hypothetical calci
38	266.5	5.7	589	2	AD2263	hypothetical prote
39	266	5.7	2348	2	AD1841	hypothetical prote
40	263.5	5.7	387	2	E95933	probable calcium-b
41	262.5	5.7	1741	2	S74910	hemolysin - synec
42	262.5	5.7	3262	2	AH2137	hypothetical prote
43	261.5	5.6	1839	2	S77626	mannuron C-5-epi
44	260	5.6	1038	2	T03516	probable outer mem
45	259.5	5.6	219	2	B95953	probable secreted

ALIGNMENTS

```

RESULT      1
B30169
leukotoxin A - Pasteurella haemolytica (serotype 1)
N:Alternate names: Ikta protein
C:Species: Pasteurella haemolytica
C>Date: 12-Oct-1999 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999
C:Accession: B30169; C32051; S29516
R:Higlander, S.K.; Chidambaram, M.; Engler, M.J.; Weinstock, G.M.
DNA 8, 15-28, 1989
A>Title: DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster.
A:Reference number: A30169; MUID:89210283
A:Accession: B30169
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-953 <HTG>
R:Strathdee, C.A.; Lo, R.Y.C.
J:Bacteriol. 171, 916-928, 1989
A>Title: Cloning, nucleotide sequence, and characterization of genes encoding the se...
A:Reference number: A32051; MUID:89123172
A:Accession: C32051
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 947-953 <STR>
R:Lo, R.Y.C.; Strathdee, C.A.; Shewen, P.E.
Infect. Immun. 55, 1987-1996, 1987
A>Title: Nucleotide sequence of the leukotoxin genes of Pasteurella haemolytica A1.
A:Reference number: S29515; MUID:87306837
A:Accession: S29516
A:Molecule type: DNA
A:Residues: 1-741,'D',743-953 <LOR>
A:Cross-references: EMBL:M20730; NID:g150492; PIDN:AAA25529.1; PID:g150494
C:Comment: This organism causes bovine pneumonic pasteurellosis (shipping fever).
C:Genetics:
A:Gene: lkta
C:Function:
A>Description: lyses leukocytes
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytotoxic; exotoxin, hemolysins; lipoprotein; tandem rep
E:238-784/Domain: hemolysin A homology <HYA>
F:716-807/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIRF]-X)
F:554/Binding site: palmitate (lys) (covalent) #status predicted

50.0%; Score 2325; DB 1; Length 953;
Best Local Similarity 49.9%; Pred.No.1.6e+11;
Matches 464; Conservative 175; Mismatches 264; Indels 26; Gaps 13;

QY      8 KSNIQAGINSTKSGIKNLVLAIPKD--YDPQKGGLANDFIKADELGIARLAEEPNNHET 65
       :| | | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db      28 QSLTQAG-SSLKTGAKKITILIVTPQNYGYDTDEGGNGLDPLVKAAEEELGIEVGOREERNINAT 86
Yy      66 AKKSVDIYNQGLSLTQTGTIAISATKLEKFLOKHSTNKKLAKGLDSVENIDRKLGKASNVL 125

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Db      87 AQTSGTGTATAGLTERGIVISAPQIDKLQK--TKAQALGASAESIVONANKAKTVLS 143
      126 TLSSFLTALAGIELDSITKKGADPADLAKASIDLINEITIGLSQOTTEAFASQALAK 185
      144 GIGSTLSGLVLAQMDLDEL--QNSNMQHLAKRAGELTSLINELINSKYTTIDEFEQISQ 202
      186 LGSTISQAKGFSNIGNKQLONT--NFSKTNLGEIITGLLSGASGALADKNASTGKYAA 244
      203 FGSKLQNIKIGLGTLDCKLKNIGGDKAGLGLDIVISGLSGATMALVLDKNASTAKKVA 262
      245 GPELSNOYIGVNTKATISSVLAQRYAAGLSTTGANAALITSSIMLAISPLAFMAADKFN 304
      263 GPELANOVGNITKAVSSYLLAQRYAAGLSTGPAALIASVSLAISPLAFAGIADKFN 322
      305 HANALDEFKOPRKFGYGDHLLAEYRGVGTIEASTITSTALGASAGVSAVAAYAV 364
      323 HAKLSLEYAERFKKIGYGDNLAEYRGVGTIDASVTAINTALAIAGVSAVAAYAV 382
      365 GAPIALLVAGYTGILSIGILEASQAMFESSVANRLOGKILLEMKGNGGQYEDKGYDRA 424
      383 ASPIALLVSGITGVSTILQYSKQAMFHVANKIHNKIVEMKNNHKNYFENGYDARYL 442
      425 AYLANNKELSELNKELEAEVIAATQORNNITGELAGITRKGRITSGRAYADAFEDG 484
      443 ANLDONMKFLLNLNKELOAEVIAATQOQNNIGDLAGISLGRVLSGAYADAFEEG 502
      485 KKEVAGSNITLDAKTGIDISNSNGKTOALHTFSPLLTACGESRRLTNGKYSYINKLK 544
      503 KHIRADKLVOGLDSANGITIDVNSGKAKTOHLFRPLPLTPGHEHERQOTGKYETITKLN 562
      545 FGRYKMNQVOTGEASSKIDFSKVIOYV-----AETGTEDEGLIVAKAGNDIEFGQ 597
      563 INRVDSMKITLGAASSTFDTLNVVQRIEILDNAGNVTKETKTIIAKIGEGDDNVFVS 622
      598 GKMNIDGGDGDHRYFYSGDGFNGITVDGTSTAEAGSTTVARKVAKGDIYHEVYKQETK 657
      623 GTTELIDGEGEDRYAHSR--GNGALTLDATKETEGETSVNFEYTGALHEVSTHTAL 681
      658 VGRKTEITQYRDYELRKAGYQSTDNLSVEEVIGSOFNVFSGKNDIFHSGEGDDL 717
      682 VGNNEEKLEYR--HSMNQNHAGYTKDLKAVEIIGTSHNDIFKSKNDADFNGSDGYDT 740
      718 LDGAGADDRLFGKGNDRILSGDEGDDLLDGGSGDDVNLGAGANDYIFRKGDDNDTLVG 777
      741 IYGNMGNDRLFGKGGDDLLDGGNGDDFDIDGGKNDLHFGKGGDDIFVHRKGGNDIITDS 800
      778 TGNKLAFAADNIDGIMIERKKEGLIVAKNDHSGSINIPRY-----ITSNLQNYOSKNTD 833
      801 DGNKLSFSDSNLKDLEFEKVKHNLVLT--TNSKKEKVTIOMNFEADFAKEVPANRATK-D 858
      834 HKIEDLIGKDSYITSDQIDKILQDKDGVITTSQELKRLADENKSKLSASDIASSLAK 893
      859 EKIEELIQONERITRSKQVDDLI--AKNGKITDQELSKVVDNVELLKH--KNVTNSLDK 915
      894 LVGSMALFEGTANSVSSNALQPIOTPOGI 922
      916 LISSVAFSTSSNDSRNVLVAPTSMIDQL 944

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RESULT 2
 B33389
 toxin II - Actinobacillus pleuropneumoniae
 N:Alternate names: cytotoxin II; RTX-toxin II (ApxII)
 C:Species: Actinobacillus pleuropneumoniae
 C>Date: 09-Mar-1990 #sequence_revision 01-Nov-1996 #text-change 18-Jun-1999
 C:Accession: B33389; S18853; B43599
 R:Chang, Y.F.; Young, R.; Struck, D.K.
 DNA 8, 635-647, 1989
 A:Title: Cloning and characterization of a hemolysin gene from Actinobacillus (Haemophilus) pleuropneumoniae
 A:Reference number: A33389; MUID:90126233
 A:Accession: B33389
 A:Molecule type: DNA

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A:Residues: 1-956 <CHA>
A:Cross-references: GB:M30602; NID:g141823; PIDN:AAA87232.1; PID:g141825
A:Experimental source: serotype 5
R:Smith, M.A.; Briatore, J.; Jansen, R.; Smith, H.E.; Kamp, E.M.; Gielkens, A.L.J.
submitted to the EMBL Data Library, July 1991
A:Description: Cytolysins of Actinobacillus pleuropneumoniae serotype 9.
A:Reference number: S18852
A:Accession: S18853
A:Molecule type: DNA
A:Residues: 1-956 <SMT>
A:Cross-references: EMBL:X61111; NID:g38939; PIDN:CAA43423.1; PID:g38941
R:Smith, M.A.; Briatore, J.; Jansen, R.; Smith, H.E.; Kamp, E.M.; Gielkens, A.L.J.
Infect. Immun. 59, 4497-4504, 1991
A:Title: Cytolysins of Actinobacillus pleuropneumoniae serotype 9.
A:Reference number: A43599; MUID:92040145
A:Accession: B43599
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-27; 948-956 <SMT>
A:Cross-references: GB:X61111; NID:g38939
C:Comment: This organism causes porcine pleuropneumonia.
C:Genetics:
A:Gene: apxIIA; apxII; clyIIA
C:Function:
A:Description: attacks blood cell membranes and causes cell lysis
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytolysin; exotoxin; hemolysin; lipoprotein; tandem repeat; 243-787/Domain: hemolysin A homology <HYA>
F:243-787/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVYIF]-X)
F:557/Binding site: palmitate (lys) (covalent) #status predicted

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Query Match 48.2%; Score 2240.5; DB 1; Length 956;
 Best Local Similarity 47.8%; Pred. No. 3,4e-107;
 Matches 454; Conservative 188; Mismatches 254; Indels 53; Gaps 15;

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      1 MSNINW--TKSNIOAGL-----NSTKSGKLNLYLAIPKDYDPO 36
      1 MSKITLSLKSLSLQGLKNGKNKLNQAGTTLKNGLTGHSILQNGAKKLIITYIPGYDSG 60
      37 KGGTINDITKADDELGIARLAEERPHHTETAKSVTVNOFLSLTQGTALISTKIEKRLQ 96
      61 QGNGVQDLVKAAANDGIEVWRERNSNDIARTSFPTTKILGFTDRGIVLAPOLDNLK 120
      97 KHSYTKLAKGDSYVNIIDRLGKASNVLTSLSSFLGTALAGTEIDSLYKGDPAADALAK 156
      121 KNP--KIGNTGLSASISQIGNKANTVYLGIDISLGSVNLNELLQNDPNQLELAK 178
      157 ASIDLINEIIGNLSQSTQTEAFSSQALAKLSTTSIQAKGFSNIGKQLONT--NFSKTNLGL 215
      179 AGLELTNELVGNIASSVQTVDAFAQISKLSHLQNLQNGLGLSKNLQNLPLDGRKASIGL 238
      216 EITGILSGISAGFPLADKNASTGKRYAAGFELSNOVIGNVTKAISSVYLAQRYAAGLST 275
      239 DIISGLISGASAGLILAKKEASTERKKAAGVFAQIIGNTVKAASSYTLAQRYAAGLST 298
      276 TGAVALITSSIMLAISPLAFMAADKFNHANALDEFKOPRKFCYGDCHLLAEYRGVGV 335
      299 TGPVALILASTYVALAVSPLFLNADKQKQADLISYSERQKLGDDDRLLADHRETG 358
      336 TTEASLTTISTALGAVSAGVAAVAGVAPIALLVAGYTGILSIGILEASQAMFESSVA 395
      359 TIDASVTTINTALAAISGCVGAASGLVGAIPVALLVAGYGLTITILEYSKQAMFEHVA 418
      396 NRLQGLILEMKGNGQVYFPDKGDSRYAATLANLKLSELNKELEAEVIAATQOQWMD 455
      419 NKVHRIIVEMEKH--NKNYFEGYDSDRHLADLDONMKELINLNKELOAEVIAATQOQWMD 477
      456 NNIGELIITLGERIKSGRAYADAFEDGKKEVAGSNITLDAKTGIDISNSNGKTOAL 515
      478 NOIGDLAISTRTDKITSSGKAYVDAFEQGQSDSSVQDLNKKIINISNTN--RTIOSV 536
      516 HTSPLLTACGESRRLTNGRYSYINKLKFGRYKMNQVTTDEASSKIDFSKVIOYVA--- 572

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Db 537 LEFTPLLTPEENRERIOEGKNSYITKLHIOFVDSWTVTDGDASSSYDFTNVQRIAVKF 596
QY 573 -----EFGTDEIGLIYNAAKAGNDIFYGCKMINDGGDHDREYFKSDGFGNTIYD 625
Db 597 DDAGNIIESDYK---IINALGAGNDNVFSGSFTYVIDGGDGHDRHYSR-GEYGAIVD 652
QY 626 GTATAGSYTYVNRKVARCGDIYHEVVKROETKYGKRTETIYRDYELRKGYGYQSTDL 685
Db 653 ATAFETKGSYVKRYVGDSCALHETIATNOTNGNREKEIYR-REDDRHHTGYTIDSL 711
QY 686 KSYEEVIGSQFNDYFKSGKENDIFHSGEEDLLDGGAGDDRLFGKGNDRLSGDEGDDL 745
Db 712 KSYEEIISQFNDIFKSGQDVDFHCGNGVDITIDGNDGDHDLFGAGADDYIDGCGNMF 771
QY 746 DGGSGDDVLNGAGNDYIFRKDGDNTLYDGTGNDKLAADANISDIEMERKEGIYK 805
Db 772 VGGTGDIIISGKNDIYHKTGDBDSDITDSCGDKLAFSDVNLKDLFFKKYDSSLEI- 830
QY 806 RNHSSSINIPRWY----ITSNLQNYQSNKTDHRIEOLIGKDGSYITSDIDKTLQDKD 861
Db 831 INKGEKVRIGNMFLEDDLASTYANKAT-NDRKIEIIEIKGGERITSEYDKLI--KEG 887
QY 862 GTVITSQELKKLADENKSKORLSASDIASSLNLKLVGSMALFGTANSVSN 910
Db 888 NNOISAEALSKVNDYNTSK-DRONVNSNLAKLISSVGSFTSSSDFRN 935
RESULT 3
A35254
Leukotoxin A - Pasteurella haemolytica (serotype T10)
N:Alternate names: Ikta protein
C:Species: Pasteurella haemolytica
C:Date: 10-Aug-1990 A:sequence, revision 15-Nov-1996 #text-change 18-Jun-1999
C:Accession: S37145; A35254; S34237; S34235
R:Lalison, A.F.; Alchison, K.; Donachie, W.
submitted to the EMBL Data Library, September 1993
A:Description: DNA sequence of the leukotoxin A gene from P. haemolytica T10 serotype.
A:Reference number: S37145
A:Accession: S37145
A:Molecule type: DNA
A:Residues: 1-955 <LA1>
A:Cross-references: EMBL:226247; NID:9400424; PIDN:CAA81206.1; PID:9400425
R:Highlander, S.K.; Engler, M.J.; Weinstein, G.M.
J. Bacteriol. 172, 2343-2350, 1990
A:Title: Secretion and expression of the Pasteurella haemolytica leukotoxin.
A:Reference number: A35254; M0ID:90236868.
A:Accession: A35254
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 950-955 <HTG>
A:Cross-references: GB:M24197; GB:M34943; GB:M34944
R:Lalison, A.F.; Alchison, K.D.; Donachie, W.
submitted to the EMBL Data Library, June 1993
A:Description: DNA sequence of the carboxy terminal end of leukotoxin A from the T3 sero
A:Reference number: S34235
A:Accession: S34237
A:Molecule type: DNA
A:Residues: 745-955 <LA2>
A:Cross-references: EMBL:222864; NID:9311828; PIDN:CAA80498.1; PID:9311829
A:Experimental source: serotype T3
A:Accession: S34235
A:Molecule type: DNA
A:Residues: 723-955 <LA3>
A:Cross-references: EMBL:222867; NID:9311824; PIDN:CAA80501.1; PID:9311825
A:Experimental source: serotype T10
C:Function:
A:Description: attacks cell membranes and causes cell lysis
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytotoxins; exotoxin; hemolysis; lipoprotein; tandem repeat;
F:240-786/Domain: hemolysin A homology <HLA>
F:718-809/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIF]-X)
F:718-726/Region: repeat

F:727-735/Region: repeat
F:736-744/Region: repeat
F:745-753/Region: repeat
F:754-762/Region: repeat
F:763-771/Region: repeat
F:772-780/Region: repeat
F:781-789/Region: repeat
F:792-800/Region: repeat
F:801-809/Region: repeat
F:556/Binding site: palmitate (lys) (covalent) #status predicted
Query Match 48.1%; Score 2236; DB 1; Length 955;
Best local Similarity 48.2%; Pred. No. 5,9e-107;
Matches 458; Conservative 178; Mismatches 271; Indels 44; Gaps 17;
QY 5 NTKSNIAQ---GLN-----STKSGKLNLYATPKD--YDPOKGTLLDFFKAA 48
Db 12 NGIRSTLTATRGGINRAGSLTQAGTLPKNGAKKIILYIPKDYKSGSGNGLDLVKAA 71
QY 49 DELGIARLAEPPHNTETAKKSYDPTVNOFLSTQTGTAISATKLEKFLQKSTNKLAGLD 108
Db 72 EELGIEYQKEEGNDIAKQTSLSLTIONVLGTERGIVLSAPQDLQK--NKVGALG 128
QY 109 SVENIDRKLGKASNVLTSSFLGTALAGIELDLSLIRKGDAAADALAKASIDLINEIGN 168
Db 129 SSESQTQNFQOAKTYLSGVGNGSRITYLAGMDLEAL-QNESDQLTAKAGLELNSLIEN 187
QY 169 LSQSTQTIKFAFSSQLAKGSTISQAGFSNIGKNLQNL-NFSKTNLGLEIITGLSISA 227
Db 188 IANSVQTLDAFSEQISQFCGKLNQVKGALGALCKLKNIGLDLRAGLDLVKSRLSGATA 247
QY 228 GFALADKNASTGKVVAGFELSNQVGNVTKATISSYVLAQVAAAGSTGAVALLTSSI 287
Db 248 ALVLDADASTAKKVGFPFLANQVGNITKAVSSYVLAQVAAAGSTGAVALLTSSI 307
QY 288 MLASPLAFMAADKFNHANAALDEFKQFRKFGYDGDHLAEYORGCTIEASTITISTA 347
Db 308 AVAISPLSFAGIADKFPRAKSLNVAERFKKLGEGSLLAEVGHGCTIDASTALNTA 367
QY 348 LGAVSAGVSAAVGSAVADPALLVAGVTGLISGLEPASKQAMFESYANRLQKILEMEK 407
Db 368 LAAIAGVSAAAGSVASPLALLVSIGTIVSTILOYSKQAMEHVAANKIHNVEMEK 427
QY 408 QNGQNYFEDKGYDSRYAAYLANNLKELSELKELAEARVYALIQQRDNNTIGELATKL 467
Db 428 NNGKNTFENGVDARYLANLDNNKFTLLNKLKELAEARVYALIQQRDNNTIGELATKL 487
QY 468 GERIKSGKAYADAFEDSKKYEAGSNITLDKKTGIIDISNSNGKKTQALHFTSPLTAGTE 527
Db 488 GEKVLSCGKAVDAFEEGCHLAKOKLVQDSAKGIIDVTNNGEAKTOHILFRTPLLTGTTE 547
QY 528 SRERLNGKSYLNKLKFGVKKMQVTDGEASKLDFSKYIQVA-----ELEGDEI 580
Db 548 KREVRQYKGEYITKLHINIVDSQIKDGAASFDTLTNNVORIGVELDAENVIKTKET 607
QY 581 GLIYNKAGNDIIFYGCKMNIOSGDGHDREYFKSDGFGIITDGSATPAGSYTYNRK 640
Db 608 KIVATLGDGDNVFGVGTTEIIDGEGYDRVHNSR-GNYGALLTDAKTEQGGSYTYNR 666
QY 641 VARGDIYHEVVKROETVYKRTETIYRDYELRKVGYGYSTQDLKSYEEVIGSQFNDV 700
Db 667 VESGKALHEGSTHTYFALVGNREKEIYR-HSNQNHAGYTTKQDLKAVEELIGSHNDIF 725
QY 701 KGSKFNDIFHSGEEDLLDGGAGDDRLFGKGNDRLSGDEGDDLDDGSGDDVLNGAGN 760
Db 726 KGSKFNDAFNGCGDVDTIDGNDGDRFLFGGKGGDIIDGNGDDPDIIDGKGNLHLHGKGD 785
QY 761 DVIYIFKGGDNDLYDGTGNDKLAFAADANISDIEMERKEGIYKRDHSGSINIPRWY- 819
Db 786 DIFVHRQNDNDISTESEGDKLSFSDSNKLDTFFEKVGNHLLVLT-TTKQEKVYIQMFR 844
QY 820 ---ITSNLQNYQSNKTDHRIEOLIGKDGSYITSDIDKTLQDKKGTVITSQELKLAD 876

Qy	8	KSNIQAGLNSRKSGLK-----NLTLAIKPYDYPQKGGTLDNFI	45
Db	19	KRAQAKGIDVYTKNGLQYGVSOAKLQALAAKAVOKYGNKLVLPYRKEDSDVSGVGFEDLV	78
Qy	46	KAADGLGATRLAEERNHETAKKSVDPVNVQFLSTGTGIAISATKLEKFLQKHSTNKLAK	105
Db	79	KAABELGQVYVARNNELEVAHKSLGTAADGLGTEGTLTFAQDQFLQKHSTINNV	138
Qy	106	GLDSVENIDRKLGASVNLSTLSSFLGTAQGLDLSLKKGAAPALAKASIDLINFI	165
Db	139	GSSTGDDAVS--KLAKSQTIIISGIVSLGTVLGIMLNIAIISGSGELE-LAEAGVSLASEL	196
Qy	166	IGNLSQSTQTEARSSOLAKGSTITISQAKKSGNSGNKLQNN--FECTNLGTEITIGL	222
Db	197	VSNIAKGTITIDAEFTTQIQNFQNGKILENNKGLGVGRQIQNNISGALSLSKTLGLDIISSLL	256
Qy	223	SGISAGPALADKNASTGCKKVAAGELSSNOVIGNYTKAISSVYLQRYAAGLSTTGAAVAL	282
Db	257	SGVTASFALANKNASTPKVAAGELSSNOVIGITKAVSSYTLIAQRLAAGLSTTGPAAL	316
Qy	283	ITSSIMLAISPLAAMNAADKRNHNAALDEPAKQKRRKGYDGDHLAEYQKGVGTIESLT	342
Db	317	IASSISLAISELAEPLVADNERNKEKEIGEFAERKKLGYDDDKLLSEFHEAGTIDASIT	376
Qy	343	TIITALGAVSGASAAVAGSVAPILLLVAGVLTGSLGILEAKSGMFESVAVARLQKI	402
Db	377	TIITALSIAAGTAAASAGALVGPITLLVYGTIGLISGIIIEFSKQPMLDIVASKIGNKI	436
Qy	403	LEMEKONGONGYFPDKGYDSRYAAVLAANLKLSELNKELEAEVRYAITAQRMNDNIGELA	462
Db	437	DEMEKK--GKNYFENGZYDARHKAFLEDSFLLSSFNQYETERAVILLTQOMDEYIGELA	496
Qy	463	GITLGERIKSGKAYADAPEDEGKVEAG----SNITTDARKGITDINSNCKKTQALHFT	518
Db	496	GITKKGDLSSGKAYVDYFQEGKLEKKPDDFSKRVDPDKTGELDISNS--QTSTLLKFV	553
Qy	519	SPLLTAGESREERTLNKYYSYINKLFGRYVNMQVOTG--EASSKLPFSKYIQR-----	570
Db	554	TPLLTPGESNERKQYOTKYEITYTLVYKGRKW--VYVNGYDKGAVYDTNLQIAHAISSS	612
Qy	571	VAETEGHDEIGLLYNAKAGNDLIFVGQKMNIDGGDGHRYEYSKDGSGFNITVDTSAT	636
Db	613	VARGEEYREVLVSHLGNNDKVFLLAGSABIIHAGEGHVYUYDKT--DTGLLVIDGTKAT	672
Qy	631	EAGSTVARKAARG--DIYHEVVKROETKVKGRFETIQYRVELKRYG--YGVQSTDLNLSV	688
Db	672	EQGRSVYTRELSGATKILREYIKKOKSAVGRRETFLEYRDELTLQSGNSLNKADELHSHV	733
Qy	689	BEVIGSOFNDVFKSKSFNDIFHSEGGDILLDGGAGDDRLEFGKGNDRSLSGEGD-----	742
Db	732	EEIIGSNQRFDEKSKPRDFIHGADGDDLNGNNGDOLLVQDKKNDELGRGNMGNDQLYGG	799
Qy	743	-----DLDDGSGDDV	755
Db	792	EGNDKLLGNGNNNLSGDDGDNDELQVLGNGFNVLRGKGDDKTLGSSGSGDILLDGGEGNDY	851
Qy	754	LNGAGGNDVYLFRRKGDDGNDTLYD---GTGNDKLAFADANISDIMEIERTKEIIYKRRDHS	810
Db	852	LEGGGSGSFYRYRSTSGNHTTYIDGOKSSDDLKTLSDSFEDRLIVERKYDNLVLRSSNS	911
Qy	811	---GSINIPRYITSNLQNYOSNTDRIIEOLICKDGSYITSDIDKTIIDKKKGYVITS	866
Db	912	HNNGVLTIKDMF-----KCGKNYNNKHIEDIYVKNKGKRLTAENLGYTFKNAAPRADMLN	966
Qy	868	QELKKLADENKSQKLSASDIASSLNKLGVSGNALFGTA	904
Db	965	YATKE--DONES---NLSLSTELSKITTNAGNCGVA	996

N:Alternate names: RTX-toxin IIIA (ApxIII)
C:Species: *Actinobacillus pleuropneumoniae*
C:Date: 14-Jul-1995 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999
C:Accession: S51784
R:Change, Y.F.: Shi, J.; Ma, D.P.; Shin, S.J.; Iain, D.H.
DNA Cell Biol. 12, 351-362, 1993
A:Title: Molecular analysis of the *Actinobacillus pleuropneumoniae* RTX toxin-III gene
A:Reference number: S51783; MUID:93263992
A:Accession: S51784
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 11049 <CHA>
A:Cross-references: EMBL:L12145; NID:9349605; PIDN:AAA21924.1; PID:9470685
C:Comment: This organism causes porcine pleuropneumonia.
C:Genetics:
A:Gene: apxIIIa
C:Function:
A:Description: Lyses lung macrophages
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytotoxins; exotoxin; lipoprotein; tandem repeat; thiolases
F:253-803/Domain: hemolysin A homology <HLHA>
F:753-861/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVYF]-X)
F:571,702/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match	41.5%;	Score 1928;	DB 1;	length 1049;
Best Local Similarity	43.1%;	Pred. No. 4.1e-91;		
Matches 429;	Conservative 152;	Mismatches 295;	Indels 120;	Gaps 21

0Y	8	KSNIQAGJNSRKSIGK-----NLYAIAPKPYDDQOKGLUNDFI	45
0Y	19	KROYKKGIQVTKRNLQYVSQAKIQLAAGKAVOKYGNKLVLPKPKDQSVGNPFVDV	78
0Y	46	KADELGIARLAEENHETAKKSVDPVNOFLSJTOGIAISATKLEFLQKHSTNKLAK	105
Db	79	KADELGIQVYVNRNNELEVAHKSIGTAGDEFLGTERGTLFAPOLDQFLOKHSKISNV	138
0Y	106	GUDSVENIDRKLKASANVLSLTSFLGTALAGIELDLSYIKKQDAAPDALAKASIDLNEI	165
Db	139	GSSTQDAVS-KLAASQTTISIGISVLCTVLAGINLNEAIIISGSELE-LAEAGVSLASEL	196
0Y	166	IGNLSQSTQYIEAFSSQAKIGSTISQACFSNIGNKLQNLN--FSKTNIGLEIITGL	222
Db	197	VSNIAKGTTITDAFTTQIQNNGKLAENAKKIGGVGRQLONSGALSALSKTGIGDIISLL	256
0Y	223	SGISAGPALADKNASTGKKVAAGELSNQYIGNVTKAISSTVYLQRYAAGLSTGGAVAL	282
Db	257	SGVTSFSPALRRKNASTSKYVAGELSNQYIGGITKAVSSITLQORLAGESTTGPAVAL	316
0Y	283	ITSSIMLAIISPLAPMNADKRFNHNALDEFKQKRKGYOGDHLAEYOGGVIEAST	342
Db	317	IASSISLAIISPLAFRAVDNFRNSKEITGEFERKKKLGIDODKLSEFYIEAGTIDISIT	376
0Y	343	TISTALGVASAGVSAAGVANGAPIALVAGVTGLISGLEASKQAFESVANRLQKI	402
Db	377	TISTALAIAGTAAASAGALVGAPITLVLGTIGTISGLEFSKQEMLDHVASKIGNI	436
0Y	403	LEMEKONGGQNYFDKQYDSIRAAATLANNLKFLSELKLELAEKRYIATIQORMDNNGELA	462
Db	437	DEMEKKY-GKNYFENGZYDARKAELEDEFSLSLSEFNNOYETERAVALLTQORMDXEIOLA	495
0Y	463	GITTKGERIKSGKAVADAFEDGKKVYVAG---SNITLDARKGIIDISNSNGKQVALHFT	518
Db	496	GITTKGDLSSGKAVVDYFQCGKLEKKPPDFSKVYVDPPTKGELDISNS--QTSYLLKFV	553
0Y	519	SPLLTAGTESREBRLTNGKYYSYINKLFGKRYKNMWQYTDG--EASSKLDFSKVIOR-----	570
Db	554	TPLLTPGESREBROTQKYEYITFLVYKQKDM-VVNGVYDKGCAVYDYTNLIIQHATISS	612
0Y	571	VAETGDETEIGLYNARAGNDIIVGQGNMIDGQDGHDRVFSKDGQFENITVDTGSAT	630
Db	613	VARGEYREVLVYSHLGNQDKVPLAAGSAEIIHAGEBHDVVYDKT--DTGLVLVDGKAT	671

R:Haertlein, M.; Schlessl, S.; Wagner, W.; Rdest, U.; Krefl, J.; Goebel, M.
 J. Cell Biol. 22, 87-97, 1983
 A>Title: Transport of hemolysin by *Escherichia coli*.
 A:Reference number: 141280
 A:Accession: 141280
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1, 'P', 3, 'V', 5, 'T', 7-44 <RES>
 A:Cross-references: GB:M29173; NID:9146337; PIDN:AAA23957.1; PID:9146338
 C:Genetics:
 A:Gene: hlyA
 C:Function:
 A:Description: attacks blood cell membranes and causes cell lysis
 C:Superfamily: hemolysin A; hemolysin A homology
 C:Keywords: calcium binding; cytotoxic; exotoxin; hemolysis; lipoprotein; tandem repeat;
 F:246-791/Domain: hemolysin A homology <HLA>
 F:723-851/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIF]-X)
 F:563,689/Binding site: palmitate (lys) (covalent) #status experimental

Query Match 39.8%; Score 1849; DB 1; Length 1023;
 Best Local Similarity 41.7%; Pred. No. 4, 5e-87;
 Matches 429; Conservative 154; Mismatches 306; Indels 140; Gaps 25;

7 IKSNIOAGL-----NSTKSGLK-----NLVLAIPKDYDPKGTLDNF 44
 9 IKSTLDSAKOSANKLHSGOSTKDALKAEOETRNAAGNLLILIKRDYGO GSSINDL 67
 45 IKADELGIARLAEENHETAKSVYDNOFLSTQGTIAISATKLEFLQKH--STNK 102
 68 VRADELGEIVQYDEKNKGTAITKQVETAKELGLTERGVITAPOLDKLQKQKAGNK 127
 103 LANGLDSEVIDRKLCKASNVSTLSSFLGTALAGLELDSLIK----GPAADALAKAS 158
 128 LG---GSAENIGDNLGKAGVSTFQNLGTALSSMKIDELIKQKSGVSSSELSAKAS 184
 159 IDLINEIGLSTOTIEFSSOLAKGSTIOAKGFSNIGKLNOL--NFSNTNGLLET 217
 185 TELINOLV-DTASLNNVNSFSQOLNKLGSVLSNTRKHLNNGVGNKLQNLPHLDNIGAGLDT 243
 218 ITGLSGISAGFALDNASTGKVAAGFELSNQVIGNTVTKAISVYLAQRAVAGLSTTG 277
 244 VSGILSISASFLISNADATGTAKAAGVELTKVLGNVKGISQYIIAARAQGLSTSA 303
 278 AVALITSSIMLAISPLAFNMAADKEFNHANALEDFAKQFKEGVDGHLAEQKGVGT 337
 304 AAGGLIASVVTALISPLSFLSIADKFRANKIEYSQRFKFLGYDGSLLAAFRHKGTAI 363
 338 EASLITSTALGAVSAGVSAAGVAVGAPIALVAGVTGLISGILEASKQAFESVAVNR 397
 364 DASLITRISTYLASVSSGISAATTSLVGAPVSLVGAVTGIIISILEASKQAFENYASK 423
 398 LQKRIEWEKONGQNYFDKYSRYAAYLANNLKFLSELNKELEAEKRVIAITQQRDNN 457
 424 MADVIAMEKKH-GKNYFENGUYDARHAAFLIEDNFKILSYQNKESYRSVRLITQOHWDTL 482
 458 IGLAGITTKIGERIKSKATAADAFEDCKKYEAG-----SNTLLDAKTIIDISNCKKQ 513
 483 IGLAGITRNGDKTLCKSYIDYEEGKRLEKRPDEFQKQVFPPLKNDILDSK--KST 540
 514 ALHPTSLFLAGTESRRLNGKYSYINKLFGKRVKMMQVTD--GEASSKIDFSVIVORVA 572
 541 LKLFVPLPLTPEGEIERRROSGKYEITTELLVGVGDKMTYKGVQDKSGVYDYSNLIOHAS 600
 573 ETEGT-DEIGLIVNARAGNDIFVGGOKMINDGGDHDRAVYSK-DGFGNITVDTSAT 630
 601 VGNNOYREIRIESHLGGDDKVLFLASGASANIYAGKGDVYVYKDTDGY--LTLDGKAT 658
 631 EASSTYVNRKVAAGD--IYHEVVKROFTKYGKRTETIQTQYDELKRVK-GYGYOSTDLKAS 687
 659 EAGNTVYTR-VLGGDVKVLQVEVKEQEVSGKRTKTYSTEFTHINGKLNLETDLKYS 717
 688 VEREIVSQFNDVFKSGFNDFIHSGECDLDDGACGDDRLF----- 728

DB 718 VEELIGTRADKRFPGSKFADIFHGACDDHIEGNDGNDRLYCGKNDTLSCGNGDDOLY 777
 729 -----GGKGNDRLSGDCDDLLGCGSG 750
 DB 778 GDCNDKILGAGANNYINGGDDDELQVQNSLAKNVLSCGKNDKLYSGSGALLDGC 837
 751 DQVLNGAGNDVYIFRKGDDNPLLYDQGT-NDKLAFADANISDIEMTEGIIYVRND- 808
 DB 838 NDLLKGGYGNIDYRLSGYGHIIIDDDGKDDKLSLADIDFQVAFPRREGNDLIMYKAE 897
 809 -----HSGSINIPRWYTSNLYQNSKTDHKEQLIGDGSYTSQIDKILQDK-- 860
 DB 898 NVLSIGHKNQITFRKNMF-----EKESGDISNHQIEQIFDQGRVITPDSLKALYQOSN 952
 861 -----DGYVITSG-----ELKRLADEKSKLSASDASSLKNLVGSMALFQT 903
 DB 953 NKASVYGNDAALAVSGGNLPLNELISKTIISAGNVDKREERAAASLLQSGNASDFSY 1012
 904 A-NSVSSNA 911
 DB 1013 GRNSITLTA 1021

RESULT 9
 A37205
 Leukotoxin A - *Actinobacillus actinomycetemcomitans*
 C:Species: *Actinobacillus actinomycetemcomitans*
 C:Date: 16-Sep-1992 #sequence, revision 01-Nov-1996 #extl, change 31-Mar-2000
 C:Accession: A37205; A60768; B34345; A32276; PH0267; PH0266; S17284
 R:Kraib, E.; Dailey, T.; Kolodrubetz, D.
 Infect. Immun. 58, 920-929, 1990
 A>Title: Nucleotide sequence of the leukotoxin gene from *Actinobacillus actinomycetemcomitans*
 A:Reference number: A37205; M0ID:90202154
 A:Accession: A37205
 A:Molecule type: DNA
 A:Residues: 1-1055 <KRA>
 A:Cross-references: GB:X16829; NID:938643; PIDN:CAA34731.1; PID:938645
 A>Note: The authors present evidence that the nucleotide sequence is correct in the
 sng nucleotide
 R:Kolodrubetz, D.; Dailey, T.; Ebersole, J.; Kraib, E.
 Infect. Immun. 57, 1465-1469, 1989
 A>Title: Cloning and expression of the leukotoxin gene from *Actinobacillus actinomycetemcomitans*
 A:Reference number: A60768; M0ID:89212893
 A:Accession: A60768
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 297-309, 'Y', 311-364, 434-440, 'KC', 443-474, 'H', 476-489, 'S', 491-493, 'VUK', 495-500, 'E', 501-502, 'S', 503-504, 'S', 505-506, 'S', 507-508, 'S', 509-510, 'S', 511-512, 'S', 513-514, 'S', 515-516, 'S', 517-518, 'S', 519-520, 'S', 521-522, 'S', 523-524, 'S', 525-526, 'S', 527-528, 'S', 529-530, 'S', 531-532, 'S', 533-534, 'S', 535-536, 'S', 537-538, 'S', 539-540, 'S', 541-542, 'S', 543-544, 'S', 545-546, 'S', 547-548, 'S', 549-550, 'S', 551-552, 'S', 553-554, 'S', 555-556, 'S', 557-558, 'S', 559-560, 'S', 561-562, 'S', 563-564, 'S', 565-566, 'S', 567-568, 'S', 569-570, 'S', 571-572, 'S', 573-574, 'S', 575-576, 'S', 577-578, 'S', 579-580, 'S', 581-582, 'S', 583-584, 'S', 585-586, 'S', 587-588, 'S', 589-590, 'S', 591-592, 'S', 593-594, 'S', 595-596, 'S', 597-598, 'S', 599-600, 'S', 601-602, 'S', 603-604, 'S', 605-606, 'S', 607-608, 'S', 609-610, 'S', 611-612, 'S', 613-614, 'S', 615-616, 'S', 617-618, 'S', 619-620, 'S', 621-622, 'S', 623-624, 'S', 625-626, 'S', 627-628, 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A:Residues: 17-42 <OH>
 A:Experimental source: strain 301-b
 A:Accession: PH0266
 A:Molecule type: protein
 A:Residues: 2-6, 'L', 8-26 <OH>
 C:Genetics:
 A:Gene: ltxA
 C:Function:
 A:Description: lyses human polymorphonuclear lymphocytes and monocytes
 C:Superfamily: hemolysin A; hemolysin A homology
 C:Keywords: cytolysis; hemolysis; lipoprotein; periplasmic space; tandem repeat; thioles
 F:245-790/Domain: hemolysin A homology <HLYA>
 F:731-847/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIVF]-X)
 F:562,687/Binding site: palmitate (lys) (covalent) #status predicted

Query Match 39.2%; Score 1820; DB 1; Length 1055;
 Best Local Similarity 40.3%; Pred. No. 1,4e-85;
 Matches 414; Conservative 185; Mismatches 298; Indels 130; Gaps 23;

QY 3 NINIVKSNQAGLNSTKSLKLNLYAIPKQDPOKGGTLINDFIKADELGIARLAEPNH 62
 DB 27 NIDAAEQLOKALDKLGTGKRLTYIPKNY--KKGNGLTALIKAAQKIGIEVHEGKDG 84
 QY 63 TETAKSVDPVNOFLSTPOTGIAISATKLEFLQ--KHSNKLAGLGSVENIDKRLGA 120
 DB 85 PALTNGILNTGKKLGLTFRGLTPAPELDMKIOGNKHLNSVG---STGMLTFAIDV 140
 QY 121 SNVLSTLSFLGTALAGLDSLIK--KGAAPDA-TAKASIDLINELIIGMISOSTOTI 176
 DB 141 QSVLTLOAFMLTAFSGMDLALIKARONGKNVTVQALAKSLINELIGTISSTNNV 200
 QY 177 EAFSSQALAKGSTISOAKFESNIGKLOL---NEKTNLGLIITIGLSISGFLA 232
 DB 201 DFFSQKLKLGALQVHKFGSGKLNKPKLNGK---GLGALSGVLSAISALLA 257
 QY 233 DKNASTGKVAAGFELSNQVIGNVTKAISVYLAQVAVAGVAAVALLTSIMLAIS 292
 DB 238 NKDAOTAKAAAAAEELTKVGNIGKAITQYLIQAARAAAGLSTTPVAGLIASVLAIS 317
 QY 293 PLAFNNADKPFHANAADFEAKQFKEGYDGHLLAEYQVGTIEASLTITSTALGAVS 352
 DB 318 PLSEFLGAKOPDRAHMEYSRFRKFGYNDSLGQFYKNTGIADAAITINVLISAIA 377
 QY 353 AGVSAAGVAVGAPIALVAVGTGLISGLEASQKAMEESVAVNLOCKITLMEWONGQ 412
 DB 378 AGVGAASAGSLVGAPITGLVSAITSLISGLDASKQAVFEHIANOLADKIAMENKY-GK 436
 QY 413 NYFDKGYSTRYAATLANNKFLSELNKELEARYAIAITQQRWNNIGELAGITKIGERIK 472
 DB 437 NYFENGYPARHSAFLEDSLKLFNELREKYTENILSTIQQGMORIGELAGITNGDKIQ 496
 QY 473 SGKAVADAFEDGKVEYAGSN---ITLDAKGIIIDISNCKKQALHFTSPLLTAGTES 528
 DB 497 SGKAVVDLAKGEEELAKHSDKFTQIOLDPKINGNIDLSGKIST--LTFLMLPTAGKEE 554
 QY 529 RERLTNGKYSTYNLKEFGRVKNQVOTDEASSKL-DESKVIOR-VAETEGDEGLIYNA 586
 DB 555 RKTROSGKEFETTELKXKGRIDMKVKGPNNSGYDSENLIQHAVTRDNKYLEARLANL 614
 QY 587 KAGMDLIFVGGKMNIDGGGHDHREYFSKDGFGNITVDTSATSEAGSYTVNRKVARGI 646
 DB 615 GAKDDYFVFGSGSTIVNAGDGYDVADYSK--GRTGALFTIDGRNATKAGQYVERDLSGIV 673
 QY 647 YHEVYKROETVVGKRTETIOYRDYEL--RKVGYGYOSTDNLSKVEEYVIGSOFNDVEGSK 704
 DB 674 LQETVSKQETKRGKAVYTDLELRYNKLDYYTYTNKGFKAHDELINSVEELTIGLDRKFGYSK 733
 QY 705 FNDIFHSGEGDDL-----LDGAGGDRLEF----- 728
 DB 734 FNDVFHGDGDDLTYGYDGDRLGCGNGDEIHGGCGNDKLYGAGAGNDRLFGEGYGNYYLD 793
 QY 729 -----GGKGNDRLSGDEGDDLIDGGSGDDVYLVNGAGANDVYIFRKGDG 770

DB 794 GGGGDHLEGGNGSDILKRGSGNDKLFENQGGDDLDDGGEGDQLAGGEGNDIYVRKEYG 853
 QY 771 NDTLYDGTGN-DKLAEPADANISDIMIERTKEGIYVRNDSGSINIPRYITSN-----LQ 825
 DB 854 HHTTEHSGDKDKLSLANINLAKDVSPERNQNDLLKTNRT-AVTFKMFSPNSAGID 912
 QY 826 NYO-----SNKTDHKIEOLIGKDGSYITSDQIDKTIIDK 859
 DB 913 ETQRKILEYAPKDRARLRKQPELORGKVDKSLNKNKVEIIGKDEGERTISODIDNLFPSK 972
 QY 860 KDGTVITSQELKRL-ADENKSQKLSASDIAS-----LMLKVGSMALFETA-NS 906
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 DB 1033 LSASPLQ 1039

RESULT 10 139643

RXN-toxin I - Actinobacillus pleuropneumoniae

N:Alternate names: hemolysin Apxi

C:Species: Actinobacillus pleuropneumoniae

C:Date: 19-Jul-1996 #sequence revision 08-Nov-1996 #text_change 18-Jun-1999

C:Accession: I39643; S18769; I39645; S60732; S35781

R:Jansen, R.; Bialtre, J.; Kamp, E.M.; Gielkens, A.L.; Smits, M.A.

Infect. Immun. 61, 3688-3695, 1993

A:Title: Structural analysis of the Actinobacillus pleuropneumoniae-RXN-toxin I (Apxi

A:Reference number: I39641; MUID:9336425

A:Accession: I39643

A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/

A:Molecule type: DNA

A:Residues: 1-1022 <RES>

A:Cross-references: EMBL:X73117; NID:g312897; PIDN:CAA51548.1; PID:g312899

R:Freij, J.; Meier, R.; Gygis, D.; Nicolet, J.

Infect. Immun. 59, 3026-3032, 1991

A:Title: Nucleotide sequence of the hemolysin I gene from Actinobacillus pleuropneumo

A:Reference number: S18769; MUID:91348845

A:Accession: S18769

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-209, 'AMPYTLA', 218-373, 'R', 375-561, 'Q', 563-686, 'TC', 688-1022 <PRE>

A:Cross-references: EMBL:X52899; NID:g38949; PIDN:CAA37081.1; PID:g38950

R:Freij, J.; Heldmann, A.; Nicolet, J.; Boffin, A.; Prentki, P.

Gene 142, 97-102, 1994

A:Title: Sequence analysis and transcription of the apxi operon (hemolysin I) from Ac

A:Reference number: I39644; MUID:94237497

A:Accession: I39645

A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/

A:Molecule type: DNA

A:Residues: 1-209, 'AMPYTLA', 218-373, 'R', 375-561, 'Q', 563-686, 'TC', 688-1022 <RE2>

A:Cross-references: EMBL:X68595; NID:g505568; PIDN:CAA46886.1; PID:g505570

R:Tacon, R.I.; Vazquez-Boland, A.; Gutierrez-Martin, C.B.; Rodriguez-Barbosa, I.;

MOL. Microbiol. 14, 207-210, 1994

A:Title: The RTX haemolysins Apxi and ApxiI are major virulence factors of the swine

A:Reference number: S60731; MUID:95131743

A:Accession: S60732

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 604-685 <TAS>

C:Comment: This organism causes porcine pleuropneumonia.

C:Genetics:

A:Gene: apxiA

C:Function:

A:Description: attacks blood cell membranes and causes cell lysis

C:Superfamily: hemolysin A; hemolysin A homology

C:Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repe

F:243-789/Domain: hemolysin A homology <HLYA>

F:721-847/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIVF]-X)

F:560,686/Binding site: palmitate (lys) (covalent) #status predicted

Query Match 38.0%; Score 1767.5; DB 1; Length 1022;
 Best Local Similarity 40.1%; Pred. No. 6,8e-83; Indels 109; Gaps 26;
 Matches 401; Conservative 181; Mismatches 308;

8 KSNIOAGLNTSTKSGL-----KNLYLAIPKDYDPQKGTGTLNFIKADELGIARLAEEP 60
 21 KSAKAGACALKNKGLQOVQAKGKLLIYIPKQVASTGSLNLYVAAELGIEVHRSEK 80
 61 NHTETKASVDYVNOFLSTLQTGIAISAVKLEFLQKHSTNKLAKGL-DSVENIDRKLGK 119
 81 NGTALAKLEFGTTEKLIGFSEGCIALFAPQFDKLKMN--QKLSKSLGSSSEALGOLNK 138
 120 ASNVLTSLSLCTALAGIELDLIK-----GGAAPDALAKASIDLINELIGLMSOSTOT 175
 139 TOTALALOSFLCTAIGMDLRLRRRNGEVSSELAAGVDLAADLVDAIASATGT 198
 176 IEAFSSOLAKLGSTISOAKFSGNIGNKLNQ--NFSKTNLGLTITGLSGISAGFALADK 234
 199 VDAFAQLGLKGNALSNTR-LSGLASKNLNPLSLAGPFDVSGILSVSASFILSNK 257
 235 NASTGKVAAGFELSNQVIGNVTKAISVYLAQVAAAGLSTTGAVAAALITSSIMLAISPL 294
 258 DADAGTKAAAGIEISKILGNIKAVSQYIIAQVAAAGLSTTAATGGLIGSVVALAISPL 317
 295 AFNNADKFNHAAALDEFAPQFPGYDGHLLAEYQRCVGTIEASTITSTALGAVSAG 354
 318 SFLNVADKFERAKOLEQYSERFKFEGSGSLASFYREGALAEALTTINVSLSAASAG 377
 355 VSAAGAAGAPIALLVAGTGLISGLEPASKQAFESVANRLOGKILEMEKONGCONY 414
 378 VGAALGSLVAGAVAAVVAITGIIISGILDASKAIFERATLANLANKIDMEKKH-GKNY 456
 415 EDKQYSRAAYVLANNLKFLSELNKELEAERVIAITQQRMDNNGELAGITTKLGERIKSG 474
 437 FENGQYARHSAFLIEDTFELLISQYNEKESYERVAITQQRMDVNIIGELAGITRKGSPTKSG 496
 475 KAAVADPEOCKYKAG-----SNITLDAKGIIDISNSNGKQALHTPSLTLGAPESRE 530
 497 KAVVDFEELKEBERDFKVPFLEKIDLSIN--KTYLLKLVTVTFVFAAGEIRRE 554
 531 RLNGKSYINKLFGVKNMAYTDEBASSKL-DEFSKIORVATEEGTDEIGLIVNAKAG 589
 555 RKOTGKEYTELFPVKGKEMVYTVGOSHAIYDITMLIDLADKK--EKROYTIESHLG 613
 590 --NDJFVGGKMNIDGGDGHDRVYSK-DGFGNITVDGTSATEAGSYTVNKKV-ARGD 645
 614 EKMDRIYLSGSSIVYAGNHDVAAYDKTDGY--LTFDQSAQKAGEYIVTKELKADVK 671
 646 IYHEVYKROETKYKRFETIQQYRDYELR--KVGYGVSOTNMLKSVERTISQFNDPVKGS 703
 672 VLEEVYKTOOISVKKSEKLEYRDYELSPRELNGIRAKELHSVEETISSNRKKDFGS 731
 704 KFNDFHSGGD-----DLLDGAGDRLFGKGNDRLSGDEGDDL 745
 732 RFDIFIGAAGDEIYGNODHDLIGDDGNDVYHGGGNDHIVGNGNDLIGSKGNFL 791
 746 DGGSGD-----VLNGAGNDY-----IFRKDGDNTLYDTGND----- 781
 792 NGGCGDELOVFEQYVNLVLLGAGANDILYSGDGTNLFEDGVGNDKIYGGKGLDIYRSKE 851
 782 -----KLAFADANI-----SDIMEERKEGIIVVRNHSQ-SINIPR 817
 852 YGRHIIIEKGGDDTLTLLSDFRDFGFIIGDOLLVNNKIGGLLYLHEBYNGALATKD 911
 818 WYITSNLQYNSKTDKHIKIDOLIGKDSYITSDQIDKILDDKDGVTYSQELKLADEN 877
 912 WF--KEKEGQNN--KIKIYDKGAGAYVLSQYLFELFAPGRGINFNGLEEKLYYEGG 965
 878 KSKRLASDIASSLNLKLVGSMALF-GTANSYSSNALOPT 915
 966 YN--ALPOLRKDIEQIISSTGAFTGDHGRVSVSGSGL 1001

RESULT 11

T00227

hemolysin A toxin protein - Escherichia coli plasmid p0157

C:Species: Escherichia coli

C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000

C:Accession: T00227; T42148

R:Makino, K.; Ishii, K.; Yasunaga, T.; Hattori, M.; Yokoyama, K.; Yatsudo, H.C.; Kube

S.; Shinagawa, H.

DNA Res. 5, 1-9, 1998

A>Title: Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an enterohemor

A:Reference number: 214127; M0ID:98290540

A:Accession: T00227

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-998 <MAY>

A:Cross-references: EMBL:AB011549; NID:94589740; PIDN:BA031774.1; PID:93337015

A:Experimental source: strain EHEC O157:H7, substrain RIMD 0509952

R:Burland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.

Nucleic Acids Res. 26, 4196-4204, 1998

A>Title: The complete DNA sequence and analysis of the large virulence plasmid of Es

A:Reference number: 222068; M0ID:98391744

A:Accession: T42148

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-998 <MAY>

A:Cross-references: EMBL:AF074613; PIDN:AC070116.1

A:Experimental source: strain EDJ933; serotype O157:H7

C:Genetics:

A:Gene: hlyA

A:Genome: plasmid p0157

C:Superfamily: hemolysin A; hemolysin A homology

C:Keywords: cytotoxins; hemolysins; lipoprotein; toxin

F:233-776/Domain: hemolysin A homology <HLYA>

F:550,675/Binding site: palmitate (lys) (covalent) #status predicted

Query Match 37.7%; Score 1752; DB 2; Length 998;
 Best Local Similarity 40.1%; Pred. No. 4.1e-82;
 Matches 392; Conservative 177; Mismatches 307; Indels 102; Gaps 21;

8 KSNIOAGLNTSTKSGLKNLYLAIPKDYDPQKGTGTLNFIKADELGIARLAEPNHTETAK 67
 18 KSAFNATSSSVRSRSGKLLILIPNEYAQ--GVGINELVKADELGIEIHRERDFTALN 76
 68 KSDVTVNOFLSLTQGTIAISATKLEFLQKHSTNKLAKGL-DSVENIDRKLGKSNVLS 126
 77 QFEGAERKVVGLTERGVAIFAPQLDKLQY--QKVSIGTGAENGNMNGKAGTVLSA 134
 127 LSSFLGTALAGIELDLSLKK-----GDAAPDALAKASIDLINELIGNLSQSTQTEAFSSQ 182
 135 LQNTGTALSGMALDELIRKOREGEDISQNDIASSSTELNQVLVDVYSSITVSDFSSQ 194
 183 LAKLGSTISOAKFGSNIGNKLNQ--NFSKTNLGLTITGLSGISAGFALADKNASTGK 241
 195 LQNGSLSSKSPRLSSVSGKQNLNPLDGLPLGDGVVSGILSAVSASPIILGNSDAHGTG 254
 242 VAAGFELSNQYIGNVTAISVYLAQRYAAGLSTTGAVAAALITSSIMLAISPLAFMNAAD 301
 255 AAAGIELTVOYLVGNVGAVSQYIIAQRMAOGLSTTAASAGITSAVMALAIPLSFLAAD 314
 302 KFNHANLDEFAPQFKEFGYDGHLLAEYQRCVGTIEASTITSTALGAVSAGVSAAYG 361
 315 KFERAKOLESTSERFKLNTNEGDLALFAFKETAIDALTTINTVSSVAGVSAASSA 374
 362 SAVGAPIALLVAGYTGILSGILBASQAFESVANRLOGKILEMEKONGCONYEDKGYDS 421
 375 SLIGAPISMLVSAITGTLISGLEASQAMFEVBAKEFAARINWEKEH-GKNYFENGYDA 433
 422 RYAAYVLANNLKFLSELNKELEAERVIAITQQRMDNNGELAGITTKLGERIKSGAYDAF 481
 434 RHAFLIEDSLTLADFSRQAHVRAVAITQQRMDHMEKIGELAGITRMDRSQSKRAYINYL 493

C:Superfamily: cyclolysin; calmodulin-sensitive adenylate cyclase catalytic domain homol
 C:Keywords: tandem repeat
 F:15-338/Domain: calmodulin-sensitive adenylate cyclase catalytic domain homology <ADB>
 F:543-1084/Domain: hemolysin A homology <HLTA>

Query Match 17.4%; Score 809.5; DB 2; Length 1705;
 Best Local Similarity 27.8%; Pred. No. 1.9e-33;
 Matches 255; Conservative 137; Mismatches 333; Indels 193; Gaps 28;

QY 106 GLDSVENIDRLKASNVLTSLSEFLGTALAGIELDLSL-----KKGDAP-----151
 D 403 GYSLDGV-----GSRFSLGEVSDMAAVEAELEMTROVLHAGARODAEVGSASAHW 458
 QY 152 -----DALAKASIDLNEIIGLSO-----STQT-TEAFSSQAKIG-----STI 190
 D 459 GORALOGAQAQVAAQRLVHAIALMTQFGKAGSTNTPQEAASLSAAVFGLEASSAVAEV 518
 QY 191 S-----OAKGFSNIGKNLQNLNFSKTLNLEITGLLSGTSAGFALADKNASTGKV 242
 D 519 SGFFRRSSRNAGRGVAG-----GAMALGGIGAGVAGMSLTD-DAPAGOKA 564
 QY 243 AAGFELSNOVIGNTAKAISVYL-----AQRVAGLSTTGAVAAITSSIMLAISPLAFMN 298
 D 565 AAGAEIALQLTGTVELASSIALALAAARGVSGIQVAGSAGAAALAAALPMEIYG 624
 QY 299 AADKFNANMLDEFKPKFRFGYGDHLLAEYQGVGTIESLTTISTALGAVSAGVSA 358
 D 625 LVQOSHADLDLKAQESSAAYEGEDALLAQVLRDKTAABEAGAVASAVLSTVAAASIA 684
 QY 359 AVGSANGAPIALALVAGYTGILGILEASQAMFESVANRLQGLLEWEKONGCONYFDKG 418
 D 685 AASVYCAPAAVAVYSLTGLANGILRGVQPIIEKLANDYARKI---DELGGPAYEYK 741
 QY 419 YDSRYAAYLANN---LKFSELNKELEAERYIAITQGRWNNIGELAGTYKGRISGK 475
 D 742 LQARH--QLANSDGLRKMLADLQAGMNASVYIGVQTEISKAELAITGNAANLKSAD 800
 QY 476 AYDAFEDGKRVKESNITLDAKTIIDISNKGKTKQALHFTSLTAGHESREPLNG 535
 D 801 VFDRLFGQERK-AGQPVLDVAAGIDIASRKGR-PALFTPLAPAGEQRRKRTKG 858
 QY 536 KYSYINKLKF-GRVKNQVTDGEASRLDFSKVIQRYAEETEGT--DEIGLIVNKAAGND 592
 D 859 KSEFTTVEIVGKODRRIRIDGADTTIDLAKVSQLVANGVLKHSIKLEIVGGDDDV 918
 QY 593 IFWGQGMNIDGDDHDFVFSKDGFGENTVDGTSATEAGSYTVNKKVARGDIYHEVYK 652
 D 919 VLNASRIHYDGAGTWTVSAAALGRDSDITV---SADGERFNVKQLNANNAYREGVA 974
 QY 653 ROETKVKKRTETIOYRDYELRKVGYGOSTDNLKSVEEVIGSOFNDVFKSGKFNDFHSG 712
 D 975 TOKAYGKRENVQYRVEELARVGO-LVEYDTLEHVOHIIIGAGNDSTIGHAHNPLAGG 1033
 QY 713 EGDLDLGGAGDDDLFGKGNDRLSGDEGDDL-----DDGSG-----750
 D 1034 AGDRLDGGAGNDLTVGGBEGHNTVVGAGDDVFLQDLGCVMSNOJDDGGAGVDTYKYNVQ 1093
 QY 751 -----751
 D 1094 SEERLEKMGDTGIHADLOKGTVEKWPALNLFSDVHKNIENHGLSSLNDSTIAGDDRDEL 1153
 QY 755 NGAGANDVYIFRKGD-----GNDTLYDGTGNDKLAFAADANISDIM-----IERTEGI 802
 D 1154 WGHGNDPTIHRRDDDLRGGLDPTLYGEDGNDIFLQDDTVSDDDIDGAGLDTVDYAA 1213
 QY 803 IVKRNDSGSINIPRWY---ITSNLQANYQSKTDHK-----IEOLIG---KDGSSY 846
 D 1214 MI-----HAGNIVARHVEYFGLEADLSBGMVAKARRGHDYDVSRYSENVNIGTSMKD-VL 1268
 QY 847 ITSQIDIKLIQDKKQGV 864
 D 1269 IGDQANTLTMGGGDDTV 1286

RESULT 14
 OYBC
 C:Superfamily: Bordetella pertussis
 N:Alternate names: adenylate cyclase precursor; calmodulin-sensitive adenylate cyclase
 N:Contents: adenylate cyclase (EC 4.6.1.1), calmodulin-sensitive; hemolysin
 C:Species: Bordetella pertussis
 C:Date: 31-Dec-1990 #sequence,revision 31-Dec-1990 #text,change 16-Jul-1999
 C:Accession: S00893; S14100; S02389
 R:Glaser, P.; Ladant, D.; Sezer, O.; Pichot, F.; Ullmann, A.; Danchin, A.
 Mol. Microbiol. 2, 19-30, 1988
 A:Title: The calmodulin-sensitive adenylate cyclase of Bordetella pertussis: cloning
 A:Reference number: S00893; MUID:88216178
 A:Accession: S00893
 A:Molecule type: DNA
 A:Residues: 1-1706 <GLA>
 A:Cross-references: EMBL:Y00545; NID:g396665; PIDN:CAA68613.1; PID:g396666
 R:Glaser, P.; Sakamoto, H.; Bellalou, J.; Ullmann, A.; Danchin, A.
 EMBO J. 7, 3997-4004, 1988
 A:Title: Secretion of cyclolysin, the calmodulin-sensitive adenylate cyclase--haemo-
 A:Reference number: S02386; MUID:99091151
 A:Contents: annotation: Identification of adenylate cyclase--hemolysin bifunctional
 R:Manier, H.; Gilles, A.M.; Glaser, P.; Krin, E.; Danchin, A.; Sartati, R.; Barzu, O
 Eur. J. Biochem. 196, 469-474, 1991
 A:Title: Isolation and characterization of catalytic and calmodulin-binding domains
 A:Reference number: S14100; MUID:91177021
 A:Accession: S14100
 A:Molecule type: protein
 A:Residues: 1-78, 'M', 80, 'M', 82-97, 'M', 99-139, 'M', 141-178, 'M', 180-399 <MUN>
 R:Hackett, M.; Guo, L.; Shabanowitz, J.; Hunt, D.F.; Hewlett, E.L.
 Science 266, 433-435, 1994
 A:Title: Internal lysine palmitoylation in adenylate cyclase toxin from Bordetella p
 A:Reference number: A55167; MUID:95025937
 A:Contents: annotation: lysine palmitoylation
 A:Comment: B. pertussis, the etiological agent of whooping cough, disrupts mammalian
 action by host cell calmodulin of the adenylate cyclase activity of bacterial cyclo-
 C:Comment: Adenylate cyclase activity is activated upon binding of calmodulin in the
 C:Genetics:
 A:Gene: cyaA; cya
 C:Superfamily: cyclolysin; calmodulin-sensitive adenylate cyclase catalytic domain h
 C:Keywords: calcium binding; calmodulin binding; cAMP biosynthesis; carbon-oxygen ly
 F:15-338/Domain: calmodulin-sensitive adenylate cyclase catalytic domain homology <N
 F:25-35/Region: calmodulin binding #status predicted
 F:59-66/Region: nucleotide binding #status predicted
 F:544-1085/Domain: hemolysin A homology <HLTA>
 F:1033-1041,1042-1050,1174-1182,1289-1297,1298-1308,1316-1324,1430-1438,1556-1564/Re
 F:983/Binding site: palmitate (Lys) (covalent) #status experimental

Query Match 17.3%; Score 806; DB 1; Length 1706;
 Best Local Similarity 27.2%; Pred. No. 2.8e-33;
 Matches 247; Conservative 142; Mismatches 346; Indels 174; Gaps 26;

QY 106 GLDSVENIDRLKASNVLTSLSEFLGTALAGIELDLSL-----KKGDAP-----151
 D 403 GYSLDGV-----GSRFSLGEVSDMAAVEAELEMTROVLHAGARODAEVGSASAHW 458
 QY 152 -----DALAKA-----SIDLINEI-----IGNLSQTYTEAFSSQLAKGTSIO-A 193
 D 459 GORALOGAQAQVAAQRLVHAIALMTQFGKAGSTNTPQEAASLSAAVFGLEASSAVAEV 518
 QY 194 KGFNSIGKNLQNLNFSKTLNLEITGLLSGTSAGFALADKNASTGKVVAGFELSNOVI 253
 D 519 SGFFR-GSSRNAGRGVAGGAMALGGGTAAVAGAKMSLTD-DAPAGQAAAAGAEIALDUT 576
 QY 254 GNTVKAISVYL-----AQRVAGLSTTGAVAAITSSIMLAISPLAFNNAADKFNHANAL 309
 D 577 GGYVELASSIALALAAAGVTSGLQVAGASAGAAAGALAAALSPMEIYGLVQSHYADQL 636
 QY 310 DEFAKQFRKFGYDGDHLLAEYQGVGTIEASLTTISTALGAVSAGVSAVAGSAGVAP 369
 D 637 DLAQESSAYVEGDALLAQVLRDKTAABEAGAVASAVLSTVGAIVSIAAASVAGAV 696

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OM protein - protein search, using sw model

Run on: September 11, 2002, 08:58:48 : Search time 75.59 seconds
(without alignments)
20.572 Million cell updates/sec

Title: US-09-884-696-13

Perfect score: 77

Sequence: 1 FNDIFHSGEDDL 14

Scoring table:

BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

A.Geneseq_032802:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	927	22	AA62110 M. bovis Dalton 2d
2	58	75.3	1049	18	AAW2159 ApxIIIB protein.
3	58	75.3	1049	21	AA51412 A. pleuropneumonia
4	58	75.3	1244	15	AA54781 Leukotoxin A protein
5	52	67.5	758	17	AA86998 Enterohaemorrhagic
6	49	63.6	127	16	AA76990 Actinobacillus ant
7	49	63.6	450	22	AA60437 Pasteurella haemol
8	49	63.6	608	22	AA60436 Pasteurella haemol
9	49	63.6	924	12	AA10889 Leukotoxin 352 enc
10	49	63.6	924	14	AA42385 Recombinant leukot
11	49	63.6	924	14	AA42380 Recombinant leukot

12	49	63.6	924	14	AA42378 Recombinant leukot
13	49	63.6	926	12	AA14482 LKT352. Pasteurel
14	49	63.6	926	14	AA34545 Leukotoxin 352 pro
15	49	63.6	926	15	AA50291 Recombinant leukot
16	49	63.6	926	17	AAW03945 P. haemolytica tru
17	49	63.6	926	19	AAW79568 Leukotoxin 352 pol
18	49	63.6	936	14	AA34547 GHR1-leukotoxin ge
19	49	63.6	943	14	AA34546 Somatostatin-leuko
20	49	63.6	951	14	AA34548 Rotavirus VP4-leuk
21	49	63.6	953	11	AA607167 105SD PRX protein
22	49	63.6	953	12	AA15159 Leukotoxin from P.
23	49	63.6	953	14	AA43865 Leukotoxin protein
24	49	63.6	953	15	AA60072 Ptx protein of Pa
25	49	63.6	953	22	AA60438 Pasteurella haemol
26	49	63.6	977	17	AAW03942 LKT-GHR protein f
27	49	63.6	977	19	AAW79569 LKT-GHR chimeric
28	49	63.6	1022	18	AAW22152 ApxIIA protein. Ac
29	49	63.6	1022	21	AA51406 A. pleuropneumonia
30	49	63.6	1023	16	AA76991 LhaA (low homology
31	49	63.6	1059	15	AA52748 Bovine IFNgamma/LK
32	49	63.6	1059	18	AAW13867 Chimeric protein #
33	49	63.6	1059	21	AAW21074 Bovine gamma-IFN/P
34	49	63.6	1058	13	AAW22103 Bovine IL-2 - LKT
35	49	63.6	1058	15	AA52747 Bovine IL-2/LKT ch
36	49	63.6	1058	18	AAW13866 Chimeric protein #
37	49	63.6	1058	21	AAW21073 Bovine IL-2/Pasteu
38	49	63.6	1059	12	AAW12561 ApxII protein. A
39	49	63.6	1059	18	AAW22156 A. pleuropneumonia
40	49	63.6	1059	21	AAW51410 A. suis leukotoxin
41	49	63.6	1059	17	AAW07637 pseudomonas fluore
42	49	63.6	1059	18	AAW27448 Staphylococcus aur
43	49	63.6	1059	22	AAW37416 Haemolysin C-termi
44	49	63.6	1059	8	AAW70435 Staphylococcus aur
45	49	63.6	1059	22	AAW34347

ALIGNMENTS

RESULT 1	
AA62110	standard; Protein; 927 AA.
XX	
XX	
AC	AA62110:
XX	
DT	29-MAR-2001 (first entry)
XX	
DE	M. bovis Dalton 2d RTX toxin A subunit.
XX	
KW	Moraxella: antigen; Immune response; Infection; RTX toxin; vaccine;
KW	antibacterial; A subunit.
XX	
OS	Moraxella bovis.
XX	
PN	WO200116172-A1.
XX	
PD	08-MAR-2001.
XX	
XX	
PF	31-AUG-2000; 2000MO-AU01048.
XX	
PR	31-AUG-1999; 99AU-0002571.
XX	
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.
PA	(UYME) UNIV MELBOURNE.
PI	Farn J, Strugnell R, Tennent J;
XX	
DR	WPI: 2001-235092/24.
XX	
DR	N-PSDB; AAF57290.
XX	
PT	Novel Moraxella bovis antigen useful in compositions for raising immune
XX	response in an animal, has protease, lipase or hemolysin activity

PS Claim 26; Fig 5; 60pp; English.

CC The invention relates to new Moraxella bovis antigens and nucleic acid
CC sequences encoding these antigenic polypeptides. The antigenic
CC polypeptides and polynucleotides are useful for raising an immune
CC response in an animal directed against Moraxella, preferably against
CC M. bovis or M. catarrhalis, and for treating Moraxella infections. The
CC present sequence represents the amino acid sequence of the A subunit of
CC the RTX toxin from M. bovis Dalton 2d.

XX Sequence 927 AA;

Query Match

Best Local Similarity 100.0%; Score 77; DB 22; Length 927;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 FNDIFHSGEGDDL 14
Db 705 fndifhsgeddl 718

RESULT 2

AAW22159 ID AAW22159 standard; Protein; 1049 AA.

XX AAW22159;

DT 16-FEB-1998 (first entry)

DE AprXIIIB protein.

KW RTX toxin; aprXICA gene; aprXIBD gene; aprXIIABCD gene;
KW repeat in toxins toxin; cell-associated RTX toxin; vaccine production;
KW therapy; A. pleuropneumoniae infection; swine pleuropneumonia.

XX Actinobacillus pleuropneumoniae.

XX CA2170839-A.

XX 02-SEP-1996.

XX 01-MAR-1996; 96CA-2170839.

XX 01-MAR-1995; 95US-0396244.

XX (UYGU-) UNIV GUELPH.

PI MacInnes J, Mallard B, Ricciatti P, Rosendal S;

WPI; 1997-245536/23.

DR N-PSDB; AAT73220.

PT Preparations of microorganisms producing cell-associated RTX toxins
PT -especially for production of vaccines against swine
PT pleuro-pneumonia

PS Disclosure; Pages 107-110; 151pp; English.

XX AAW22151-W22161 represent A. pleuropneumoniae RTX (repeat in toxins)
CC toxins. These sequence are encoded by the aprXICA, aprXIB, aprXIIAB, C, and
CC aprXIIABCD genes (see AAT73217-773220), and can be expressed by
CC microorganisms used in the preparations of the invention. The
CC preparations are bacterial preparations comprising one or more isolated
CC and purified strains of a microorganism that produces one or more RTX
CC toxins, where the strains have at least one cell-associated RTX toxin.
CC The preparations are used for production of vaccines for the prophylaxis
CC and treatment of infectious diseases caused by microorganisms that
CC produce RTX toxins, where the strains have been attenuated or
CC inactivated. The vaccines are preferably against Actinobacillus
CC pleuropneumoniae infection (swine pleuropneumonia). It has been found
CC that A. pleuropneumonia produces significant quantities of
CC cell-associated RTX toxins when cultured under certain conditions, and

CC that the whole-cell protein composition of the cultures corresponds to
CC the whole-cell protein profiles obtained from cells recovered at
CC necropsy from the pleural fluid of infected swine. Vaccination with a
CC bacterin prepared from heat-inactivated cultures having significant
CC quantities of cell-associated RTX toxins give significant protection of
CC swine against challenge with homologous strains.

XX Sequence 1049 AA;

Query Match

Best Local Similarity 75.3%; Score 58; DB 18; Length 1049;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGEGDDL 14
Db 747 fndifhsgeddl 760

RESULT 3

AAV51412 ID AAV51412 standard; protein; 1049 AA.

XX AAV51412;

DT 05-MAY-2000 (first entry)

DE A. pleuropneumoniae aprXIIIA protein.

KW RTX toxin; vaccine; Repeats in Toxins; immunostimulatory; antimicrobial;
KW antiinflammatory; antiarthritic; antiabortive; treatment; pneumonia;
KW pleuropneumonia; septicemia; nephritis; arthritis; endocarditis;
KW shipping fever; abortion; whooping cough; sleepy foal disease; joint ill;
KW urinary infection; peritonitis; meningitis; gastroenteritis;
KW passive immunization; aprXIIIA.

XX Actinobacillus pleuropneumoniae.

XX US6019984-A.

XX 01-FEB-2000.

XX 23-DEC-1996; 96US-0772270.

XX 01-MAR-1995; 95US-0396244.

XX (UYGU-) UNIV GUELPH.

PI Mallard B, Rosendal S, MacInnes J, Ricciatti P;

WPI; 2000-146864/13.

DR N-PSDB; AAZ88587.

PT Bacterial preparation comprising microorganisms which produce a member
PT of the Repeats in Toxins (RTX) family, useful for treating swine
PT pleuropneumonia, arthritis in swine, shipping fever and abortion in
PT cattle, and sleepy foal disease -

PS Disclosure; Column 77-84; 96pp; English.

XX This invention describes a novel bacterial preparation (I) which
CC comprises one or more isolated and purified strain(s) of a microorganism,
CC cultured in tryptone yeast extract (TYE) broth, which produces one or
CC more RTX toxins (belonging to the family of toxins referred to as Repeats
CC in Toxins), where the strain(s) have at least one RTX toxin which is
CC cell-associated. The products of the invention have immunostimulatory,
CC antitumor, antiinflammatory, antiarthritic and antiabortive activity.
CC The bacterial preparation may be used as vaccines and for the prophylaxis and
CC treatment of infectious diseases caused by strains of microorganisms
CC which produce one or more RTX toxins. The infectious diseases are swine
CC pleuropneumonia, pneumonia, septicemia, nephritis and arthritis in swine;
CC septicemia, nephritis, endocarditis and arthritis in piglets; shipping
CC fever and abortion in cattle; whooping cough, sleepy foal disease or

CC joint ill (purulent nephritis, arthritis) in foals; septicemia,
CC polyarthritis and abortion in horses; and urinary infections,
CC peritonitis, meningitis, and gastroenteritis. The bacterial preparations
CC may also be used to prepare antibodies which may be used as a means of
CC passive immunization. This sequence represents the *Actinobacillus*
CC *pleuropneumoniae* *aprilia* protein described in the method of the
CC invention.

XX
SQ Sequence 1049 AA:

Query Match

Best Local Similarity 75.3%; Score 58; DB 21; Length 1049;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGEGDDL 14
Db 747 frdIfhgadgddl 760

RESULT 4

AA854781
ID AAR54781 standard; Protein; 1244 AA.

XX
AC AAR54781:

DT 15-OCT-1994 (first entry)

XX
DE Leukotoxin Aprilia.

XX
KM Leukotoxin; Aprilia; pleuropneumonia; vaccine; diagnostic.

OS *Actinobacillus pleuropneumoniae*.

XX
FH Key Location/Qualifiers

FT Domain 327..345

FT Domain /label= transmembrane domain

FT Domain 488..503

FT Domain /label= transmembrane domain

FT Domain 570..587

FT Domain /label= transmembrane domain

XX
PN MO9409821-A.

XX
PD 11-MAY-1994.

XX
PF 04-NOV-1993; 93MO-US10500.

XX
PR 05-NOV-1992; 92US-0972229.

XX
PR 03-JUN-1993; 93US-0072285.

XX
PA (CORR) CORNELL RES FOUND INC.

XX
PI Chang Y;

XX
DR WPI: 1994-167130/20.

XX
DR N-PSDB; AA064827.

XX
PT DNA encoding *Actinobacillus pleuropneumoniae* leukotoxin - used to
XX
PT prepare prods. for use in vaccines for porcine pleuropneumonia
XX
PS and as diagnostic reagents

XX
PS Disclosure: Fig 3; 65pp; English.

XX
CC The Aprilia gene having the sequence given in AA064827 was isolated
XX
CC from phage lambda clones yfc 26-28 and yfc 31-32 of a genomic
XX
CC library of *A. pleuropneumoniae* ser. 2. The gene encodes a novel
XX
CC leukotoxin (sequence AAR54781).

XX
SQ Sequence 1244 AA:

Best Local Similarity 71.4%; Pred. No. 0.21;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGEGDDL 14
Db 920 frdIfhgadgddl 933

RESULT 5

AA86998
ID AAR86998 standard; Protein; 758 AA.

XX
AC AAR86998:

DT 04-JUL-1996 (first entry)

XX
DE Enterohaemorrhagic *E. coli* hlyA gene product.

XX
KM Enterohaemorrhagic *Escherichia coli*; virulent; EHEC; O157:H7 serotype;
XX
KM detection; probe; primer: hlyA gene; enterohaemorrhagic colitis;
XX
KW haemolytic uremic syndrome; mesenteric adenitis.

XX
OS *Escherichia coli* (enterohaemorrhagic).

XX
PN US5475098-A.

XX
PD 12-DEC-1995.

XX
PF 14-JUN-1994; 94US-0258188.

XX
PR 14-JUN-1994; 94US-0258188.

XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
PI Hall RH, Xu JG;

XX
DR WPI: 1996-048546/05.

XX
DR N-PSDB; AAT08098.

XX
PT Enterohaemorrhagic *E. coli* (EHEC) nucleic acid sequences - useful
XX
PT for probe and primer design for sensitive and specific detection of
XX
PT EHEC

XX
PS Claim 1; Columns 37-42; 32pp; English.

XX
CC Enterohaemorrhagic *E. coli* (EHEC) associated with enterohaemorrhagic
XX
CC colitis, haemolytic uremic syndrome and mesenteric adenitis have
XX
CC been found to carry a hlyA gene and a hlyB gene, separated by an
XX
CC intergenic region. The hly genes and the intergenic region are
XX
CC absent from bacteria not associated with these diseases and so
XX
CC provide a useful target for detecting EHEC pathogens, esp. O157:H7
XX
CC serotype *E. coli*. The present sequence is that of the protein
XX
CC encoded by the EHEC hlyA gene.

XX
SQ Sequence 758 AA:

XX
PT Query Match

XX
PT Best Local Similarity 67.5%; Score 52; DB 17; Length 758;
XX
PT Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGEGDDL 14
Db 480 frdIfhgadgndyl 493

RESULT 6

AA876990
ID AAR76990 standard; Protein; 127 AA.

XX
AC AAR76990:

XX
DT 13-MAR-1996 (first entry)

XX Actinobacillus antigenic toxin repeat (RTX) region.
DE RTX; repeat; vaccine; antigenic; immunisation; pneumonia;
XX APl disease.
KW Actinobacillus pleuropneumoniae.
XX OS
XX Key Location/Qualifiers
FH Region 1..127
FT /label= repeat region
FT /note= "tandem repeat units of 9 amino acids"
XX JF07138185-A.
PN 30-MAY-1995.
XX 23-JUN-1993; 93JP-0152264.
XX 23-JUN-1993; 93JP-0152264.
XX (NISK) NIPPON SEIBUTSU KAGAKU KENKYUSHO ZH.
XX WPI; 1995-228639/30.
XX A vaccine contg. a product of the lhaa gene as the active ingredient
PT - for prophylaxis of Actinobacillus (Haemophilus) pleuropneumoniae
PT infectious diseases.
XX Claim 1; Page 8; 15pp; Japanese.
XX AAR76990 represents a repeat region of the lhaa (low homology to appa)
CC gene product which is a toxin component. The repeat region and full
CC gene product are useful as the active ingredient in vaccines for the
CC prophylaxis of Actinobacillus (Haemophilus) pleuropneumoniae
CC infectious (Apl) diseases.
XX Sequence 127 AA;
SQ

Query Match 63.6%; Score 49; DB 16; Length 127;
Best Local Similarity 66.7%; Pred. No. 0.62;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGEGDD 12
| | | | | : | | | |
Db 15 ftdlthgkqgd 26

RESULT 7
AAE04637
ID AAE04637 standard; Protein; 450 AA.
XX
AC AAE04637;
XX
DT 10-SEP-2001 (first entry)
XX
DE Pasteurella haemolytica modified leukotoxin 50 (lkt50) protein.
XX
KW Leukotoxin 50; lkt50; respiratory disease; infection; therapy;
KW immunostimulant; antibacterial; vaccine; transgenic plant;
KW animal feed; mutant; muten.
XX
XX Pasteurella haemolytica.
OS Synthetic.
OS
PN WO200144289-A2.
XX
PD 21-JUN-2001.
XX
PF 15-DEC-2000; 2000WO-CA01498.
XX
PR 17-DEC-1999; 99US-0172148.

XX (UYGU-) UNIV GUELPH OFFICE.
PA
XX Lo RYC, Shewen PE, Lee RWH, Hodgins D, Strommer JN;
PI WPI; 2001-408470/43.
XX N-PSDB; AAD08976.
DR
DR Modified leukotoxin polypeptide is useful in a vaccine to prevent or
PT treat Mannheimia (Pasteurella) infection (particularly M. haemolytica
PT infection), and disease associated with a leukotoxin, e.g., respiratory
PT disease.
XX
XX Claim 4; Fig 12; 70pp; English.
XX
XX The present sequence is Pasteurella (Mannheimia) haemolytica
CC modified leukotoxin-50 (lkt50) protein. The modification comprises
CC the removal of amino acids within the hydrophobic transmembrane
CC domain of a full length leukotoxin protein. Modified leukotoxin
CC sequences are used in vaccines to treat or prevent diseases associated
CC with leukotoxin, e.g., respiratory disease, and Mannheimia infection
CC (particularly M. haemolytica infection). In addition, the vaccine
CC is used to prepare a medicament. Furthermore, the plant transformed
CC with modified leukotoxin sequences is fed to an animal such as a
CC ruminant, to prevent or treat respiratory diseases.
XX
XX Sequence 450 AA;
SQ

Query Match 63.6%; Score 49; DB 22; Length 450;
Best Local Similarity 58.3%; Pred. No. 2.6;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDFHSGEGDDL 13
| | | | | : | | | |
Db 324 ndllhgykqdd 335

RESULT 8
AAE04636
ID AAE04636 standard; Protein; 608 AA.
XX
AC AAE04636;
XX
DT 10-SEP-2001 (first entry)
XX
DE Pasteurella haemolytica modified leukotoxin 66 (lkt66) protein.
XX
KW Leukotoxin 66; lkt66; respiratory disease; infection; therapy;
KW immunostimulant; antibacterial; vaccine; transgenic plant;
KW animal feed; mutant; muten.
XX
XX Pasteurella haemolytica.
OS Synthetic.
OS
PN WO200144289-A2.
XX
PD 21-JUN-2001.
XX
PF 15-DEC-2000; 2000WO-CA01498.
XX
PR 17-DEC-1999; 99US-0172148.
XX
XX (UYGU-) UNIV GUELPH OFFICE.
FA
FA Lo RYC, Shewen PE, Lee RWH, Hodgins D, Strommer JN;
PI WPI; 2001-408470/43.
DR N-PSDB; AAD08975.
XX
XX Modified leukotoxin polypeptide is useful in a vaccine to prevent or
PT treat Mannheimia (Pasteurella) infection (particularly M. haemolytica
PT infection), and disease associated with a leukotoxin, e.g., respiratory

PT disease -
 XX
 PS Claim 2: Fig 2: 70pp: English.
 XX
 CC The present sequence is Pasteurella (Mannheimia) haemolytica
 CC modified leukotoxin-66 (lkt66) protein. The modification comprises
 CC the removal of amino acids within the hydrophobic transmembrane
 CC domain of a full length leukotoxin protein. Modified leukotoxin
 CC sequences are used in vaccines to treat or prevent diseases associated
 CC with leukotoxin, e.g., respiratory disease, and Mannheimia infection
 CC (particularly M. haemolytica infection). In addition, the vaccine
 CC is used to prepare a medicament. Furthermore, the plant transformed
 CC with modified leukotoxin sequences is fed to an animal such as a
 CC ruminant, to prevent or treat respiratory diseases.
 XX
 SQ Sequence 608 AA:

Query Match 63.6%; Score 49; DB 22; Length 608;
 Best Local Similarity 58.3%; Pred. No. 3.6;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 NDIHSGEGDDL 13
 ||:| | | | | |
 Db 429 ndllhggkgddl 440

RESULT 9
 AAR10889
 ID AAR10889 standard; Protein: 924 AA.
 XX
 AC AAR10889;
 XX
 DT 11-APR-1991 (first entry)
 XX
 DE Leukotoxin 352 encoded by plasmid PAA352.
 XX
 KM LKT; vaccine; antigen; respiratory disease; shipping fever pneumonia.
 XX
 OS Pasteurella haemolytica A1 strain B122.
 XX
 PN CA2014033-A.
 XX
 PD 07-OCT-1990.
 XX
 PF 06-APR-1990; 90CA-2014033.
 XX
 PR 07-APR-1989; 89US-0335018.
 XX
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Acres SD, Babiuk LA, Potter AA, Lawman MUP;
 XX
 DR WPI: 1991-000097/01.
 DR N-PSDB: AAO10272.
 XX
 PT Pasteurella haemolytica proteins and genes - used for producing
 PT vaccines to protect animals esp. cattle from respiratory diseases
 PT e.g. pneumonia.
 XX
 PS Claim 13; Fig 5; 87pp: English.
 XX
 CC Plasmid PAA352 is derived from PAA114, a clone isolated from a
 CC genomic library of P. haemolytica. The protein, designated "new
 CC leukotoxin" or "LKT 352" is 98% homologous to authentic leukotoxin.
 CC LKT 352 and pref. antigenic fragments of it, can be used in
 CC vaccines to protect cattle from respiratory diseases. They can also
 CC be used to produce antibodies for immunoadfinity purificn. of
 CC further proteins. [fig. contg. sequence v. poor]
 CC See also AAR10890, AAR10909, AAR10910 and AAO10783.
 XX
 SQ Sequence 924 AA:

Query Match 63.6%; Score 49; DB 12; Length 924;
 Best Local Similarity 58.3%; Pred. No. 5.7;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 NDIHSGEGDDL 13
 ||:| | | | | |
 Db 745 ndllhggkgddl 756

RESULT 10
 AAR42385
 ID AAR42385 standard; Protein: 924 AA.
 XX
 AC AAR42385;
 XX
 DT 19-APR-1994 (first entry)
 XX
 DE Recombinant leukotoxin peptide from plasmid pCRR28.
 XX
 KW Haemophilus somnus; immunogenic; haemolysin; LppB; LppC;
 KW thromboembolic meningencephalitis; septicemia; arthritis;
 KW pneumonia; lktA gene; haemlin-binding protein; fusion protein.
 XX
 OS Pasteurella haemolytica.
 XX
 PN WO9321323-A.
 XX
 PD 28-OCT-1993.
 XX
 PF 05-APR-1993; 93WO-CA00135.
 XX
 PR 09-APR-1992; 92US-0865050.
 PR 04-JUN-1992; 92US-0893424.
 PR 04-JUN-1992; 92US-0893426.
 PR 29-MAR-1993; 93US-0038287.
 PR 29-MAR-1993; 93US-0038288.
 PR 29-MAR-1993; 93US-0038719.
 XX
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
 PI Rioux C, Theisen M;
 XX
 DR WPI: 1993-351733/44.
 DR N-PSDB: AAO51086.
 XX
 PT Haemophilus somnus immunogenic proteins used in vaccines -
 PT selected from haemlin-binding protein, haemolysin, LppB and LppC,
 PT and corresp. DNA
 XX
 PS Disclosure; Fig 11; 119pp: English.
 XX
 CC The lppB gene protein was expressed in E. coli as a fusion to the
 CC Pasteurella haemolytica leukotoxin gene lktA coded for by plasmid
 CC PAA352. The lppB gene fragment was taken from pMS11. lppB can be
 CC used in vaccines for preventing or treating H. somnus infections,
 CC which cause thromboembolic meningencephalitis, septicemia, arthritis
 CC and pneumonia in vertebrates.
 CC See also AAR42370-86.
 XX
 SQ Sequence 924 AA:

Query Match 63.6%; Score 49; DB 14; Length 924;
 Best Local Similarity 58.3%; Pred. No. 5.7;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 NDIHSGEGDDL 13
 ||:| | | | | |
 Db 747 ndllhggkgddl 758

xx	RESULT 11	
xx	AA042380	
ID	AA042380 standard; Protein; 924 AA.	
xx		
AC	AA042380;	
DT	19-APR-1994 (first entry)	
xx		
DE	Recombinant leukotoxin peptide (spllt) from plasmid pCCH4.	
xx		
KW	Haemophilus somnus; immunogenic; haemolysin; lppB; lppC;	
KW	thromboembolic meningococcal sepsis; septicemia; arthritis;	
KW	pneumonia; lktA gene; haemin-binding protein; fusion protein.	
xx		
OS	Pasteurella haemolytica.	
xx		
PN	MO9321323-A.	
xx		
PD	28-OCT-1993.	
xx		
PF	05-APR-1993; 93WO-CA00135.	
xx		
PR	09-APR-1992; 92US-0865050.	
PR	04-JUN-1992; 92US-0893424.	
PR	04-JUN-1992; 92US-0893426.	
PR	29-MAR-1993; 93US-0038287.	
PR	29-MAR-1993; 93US-0038288.	
PR	29-MAR-1993; 93US-0038719.	
xx		
PA	(UYSA-) UNIV SASKATCHEWAN.	
xx		
PI	Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;	
PI	Roux C, Theisen M;	
xx		
DR	WPI: 1993-351733/44.	
xx		
DR	N-PSDB; AA051082.	
xx		
PT	Haemophilus somnus immunogenic proteins used in vaccines -	
PT	selected from haemin-binding protein, haemolysin, lppB and lppC,	
PT	and corresp. DNA	
xx		
PS	Disclosure; Fig 6; 11pp; English.	
xx		
CC	The hmb gene encoding the haemin-binding protein was expressed in	
CC	E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene	
CC	lktA coded for by plasmid pA352. The hmb gene fragment was taken	
CC	from pRBP04 and starts at the codon for the 33 rd amino acid residue	
CC	of ORF1. The haemin binding protein can be used in vaccines for	
CC	preventing or treating H. somnus infections, which cause thromboembolic	
CC	meningo-encephalitis, septicemia, arthritis and pneumonia in	
CC	vertebrates	
CC	See also AA042370-86.	
xx		
SQ	Sequence 924 AA;	
xx		
QY	Query Match 63.6%; Score 49; DB 14; Length 924;	
	Best Local Similarity 58.3%; Pred. NO. 5.7;	
Matches	7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;	
Db	2 NDIHSGEGDDL 13	
	: : : :	
	747 ndllhggkgddl 758	
xx		
xx	RESULT 12	
xx	AA042378	
ID	AA042378 standard; Protein; 924 AA.	
xx		
AC	AA042378;	
xx		
DT	19-APR-1994 (first entry)	
xx		

DE	Recombinant leukotoxin peptide (split) from plasmid pCCH5.
XX	
KW	Haemophilus somnus; immunogenic; haemolysin; lppB, lppC;
KW	thromboembolic meningococcal septicemia; arthritis;
KW	pneumonia; lktA gene; haemin-binding protein; fusion protein.
XX	
OS	Pasteurella haemolytica.
XX	
PN	WO9321323-A.
XX	
PD	28-OCT-1993.
XX	
PF	05-APR-1993; 93WO-CA00135.
XX	
PR	09-APR-1992; 92US-0865050.
PR	04-JUN-1992; 92US-0893424.
PR	04-JUN-1992; 92US-0893426.
PR	29-MAR-1993; 93US-0038287.
PR	29-MAR-1993; 93US-0038288.
PR	29-MAR-1993; 93US-0038719.
XX	
PA	(UYSA-) UNIV SASKATCHEWAN.
PI	Hartland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
PI	Roux C, Theisen M,
XX	
DR	WPJ; 1993-351733/44.
DR	N-PSDB; AAO51081.
XX	
PT	Haemophilus somnus immunogenic proteins used in vaccines -
PT	selected from haemin-binding protein, haemolysin, lppB and lppC;
PT	and corresp. DNA
XX	
PS	Disclosure; Fig 5; 11pp; English.
XX	
CC	The hmb gene encoding the haemin-binding protein was expressed in
CC	E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene
CC	lktA coded for by plasmid PA352. The hmb gene fragment was taken
CC	from PAP501 and starts at the codon for the third amino acid residue
CC	of OREI. The haemin binding protein can be used in vaccines for
CC	preventing or treating H. somnus infections, which cause thromboembolic
CC	meningo-encephalitis, septicemia, arthritis and pneumonia in
CC	vertebrates.
CC	See also AAK42370-86.
XX	
SQ	Sequence 924 AA;
Query Match	63.6%; Score 49; DB 14; Length 924;
Best Local Similarity	58.3%; Pred. No. 5.7;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0.	
OY	2 NDIHSGEGDDL 13 : : :
Db	747 ndlhgykgddi 758
RESULT 13	
AAR14482	
ID	AAR14482 standard; Protein; 926 AA.
AC	AAR14482;
XX	
DT	15-JAN-1992 (first entry)
XX	
DE	LKT352.
XX	
KW	Antigen; leukotoxin; vaccine; lktA.
XX	
CS	Pasteurella haemolytica.
XX	
PN	WO9115237-A.

PD 17-OCT-1991.
 XX
 PF 17-OCT-1991; 91WO-CA00170.
 XX
 PR 05-APR-1990; 90US-0504850.
 XX
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Acres SD, Barluk LA, Potter AA, Lawman MJP;
 DR WPI; 1991-324967/44.
 XX
 PT Vaccines for Pasteurella haemolytica infection in cattle -
 PT comprise sub-unit antigens from P haemolytica fibrin protein,
 PT plasmin receptor, 50 K outer membrane protein and leukotoxin.
 XX
 PS Disclosure; Fig 5; 92pp; English.
 XX
 CC LKT352 is 98% homologous with authentic leukotoxin and migrates
 CC to the same position on gels.
 CC The LKT352 gene was prep'd as follows: Ikta, an MaeI fragment
 CC contg. the gene was ligated into the SmaI site of pUC13 to form
 CC pAI179. From this, two constructs were made in the pTac-based
 CC vector, pGH432:laci digested with SmaI. One, pAA342, consisted of
 CC the 5' AhaIII fragment from Ikta while the other, pAA345, contained
 CC the entire MaeI fragment. Clone pAA342 expressed a truncated
 CC leukotoxin peptide at high levels while pAA345 expressed full
 CC length leukotoxin at very low levels. The 3' end of the Ikta gene
 CC of pAA342 was therefore ligated to StyI/BamHI digested pAA342 to
 CC yield pAA352 contg. the LKT352 sequence. The protein expressed
 CC from the vector can be used to prepare a subunit vaccine with
 CC other P. haemolytica antigens, e.g. fibrin protein, plasmin
 CC receptor or 50K outer membrane protein. The vaccines can be used
 CC to protect cattle from respiratory diseases such as pneumonia, esp.
 CC Shipping fever pneumonia.
 CC See also AAR14481, 83, 84 and 85.
 XX
 SO Sequence 926 AA;

Query Match 63.6%; Score 49; DB 12; Length 926;
 Best Local Similarity 58.3%; Pred. No. 5.7;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIRHSGEGDDL 13
 ||:|:|:|:
 Db 747 ndlhgkgddl 758

RESULT 14
 AAR34545
 ID AAR34545 standard; Protein: 926 AA.
 XX
 AC AAR34545;
 XX
 DT 23-AUG-1993 (first entry)
 XX
 DE Leukotoxin 352 produced from pAA352.
 XX
 KW Vector; LKT 352; flanking; recombinant; antigen; somatostatin;
 KW gonadotropin releasing hormone; rotavirus viral protein 4;
 KW carrier protein; lactation; reproduction.
 XX
 OS Pasteurella haemolytica.
 XX
 PN WO9308290-A.
 XX
 PD 29-APR-1993.
 XX
 PF 15-OCT-1992; 92WO-CA00449.
 XX
 PR 16-OCT-1991; 91US-0779171.
 PR 14-OCT-1992; 92US-0960932.

XX
 XX (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Hughes HPA, Potter AA, Redmond MJ;
 XX
 DR WPI; 1993-152482/18.
 XX
 DR N-PSDB; AAQ41317.
 XX
 PT Immunological carrier system with enhanced immunogenicity -
 PT comprises chimeric protein comprising leuco:toxin peptide or
 PT homologous protein fused to antigen esp. somatostatin or
 PT gonadotropin releasing hormone
 XX
 PS Disclosure; Fig 3; 95pp; English.
 XX
 CC Gene libraries of P. haemolytica A1 (strain B122) were constructed
 CC in Lambda gtlI and pUC13. Resulting clones were used to transform E.
 CC coli and individual colonies were pooled and screened for reaction
 CC with serum from a calf which had survived a P. haemolytica infection
 CC and that had been boosted with a conc. culture supernatant of P.
 CC haemolytica to increase anti-leukotoxin antibody levels. Positive
 CC colonies were screened for their ability to produce leukotoxin by
 CC incubating cell lysates with bovine neutrophils and measuring the
 CC release of lactate dehydrogenase from the neutrophils. A 4kb
 CC fragment was obtd. Progressively larger clones were isolated by
 CC chromosome walking to isolate full length recombinants of ca. 8kb,
 CC in pAI14. The clone was subjected to restriction enzyme digestion
 CC to yield two clones, one expressing truncated leukotoxin peptide at
 CC high levels and the other expressing the full length leukotoxin at
 CC low levels. The 3' end of the Ikta gene from the full length clone
 CC was ligated to the truncated gene clone to yield plasmid pAA352. The
 CC clone was used to produce chimeric proteins by gene fusion with an
 CC antigen coding sequence, e.g. the coding sequence of somatostatin,
 CC gonadotropin releasing hormone or rotavirus viral protein 4, i.e.
 CC leukotoxin works as a carrier protein to bring about a larger
 CC immune response than the antigen alone. Immunisation with these
 CC antigens can regulate growth rate, lactation and reproductive
 CC efficiency. See also AAR34546-8.
 XX
 SO Sequence 926 AA;

Query Match 63.6%; Score 49; DB 14; Length 926;
 Best Local Similarity 58.3%; Pred. No. 5.7;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIRHSGEGDDL 13
 ||:|:|:|:
 Db 747 ndlhgkgddl 758

RESULT 15
 AAR50291
 ID AAR50291 standard; Protein: 926 AA.
 XX
 AC AAR50291;
 XX
 DT 06-OCT-1994 (first entry)
 XX
 DE Recombinant leukotoxin from plasmid pAA352.
 XX
 KW Vaccine; outer membrane protein; OMP; Haemophilus somnus;
 KW iron regulated protein; leukotoxin; Pasteurella haemolytica;
 KW LKT352.
 XX
 OS Pasteurella haemolytica A1 (strain B122).
 XX
 PN CA2099707-A.
 XX
 PD 03-JAN-1994.
 XX
 PF 29-JUN-1993; 93CA-2099707.

QY 1741 ggtcataagtaaaagcgtgcgaatgacatatacttgctggtcaaggtaaaatcg 1800
 DB 1972 ggtcataagtaaaagcgtgcgaatgacatatacttgctggtcaaggtaaaatcg 2031
 QY 1801 aatatgtagtgtagaagtgacacgactcgtgtcttctatagtaagaacggagatttgt 1860
 DB 2032 aatatgtagtgtagaagtgacacgactcgtgtcttctatagtaagaacggagatttgt 2091
 QY 1861 aatatgtagtgtagaagtgacacgactcgtgtcttctatagtaagaacggagatttgt 1920
 DB 2092 aatatgtagtgtagaagtgacacgactcgtgtcttctatagtaagaacggagatttgt 2151
 QY 1921 gttgctcgagtgatatacttaacagtgatgtgtaagcgtaagaacccaagtggtgtaaa 1980
 DB 2152 gttgctcgagtgatatacttaacagtgatgtgtaagcgtaagaacccaagtggtgtaaa 2211
 QY 1981 cgtactgaaactacccagatcgtgattatgaataagaagaattggtgatactgatacga 2040
 DB 2212 cgtactgaaactacccagatcgtgattatgaataagaagaattggtgatactgatacga 2271
 QY 2041 tctaccgataatttgataatcagtagaagaagaatgattggttctcaatttaatagtatctc 2100
 DB 2272 tctaccgataatttgataatcagtagaagaagaatgattggttctcaatttaatagtatctc 2331
 QY 2101 aaaggttcaaatctcaacgacatattccatagtggtgaagtgatgattactcgtggt 2160
 DB 2332 aaaggttcaaatctcaacgacatattccatagtggtgaagtgatgattactcgtggt 2391
 QY 2161 ggtgctggtgaacgacgctgtgttggtggtgaaagcaacgactcgtactctgagata 2220
 DB 2392 ggtgctggtgaacgacgctgtgttggtggtgaaagcaacgactcgtactctgagata 2451
 QY 2221 ggggaagatttactcgtggtggtgtgtgtgatagtatgataatggtggtggtggtat 2280
 DB 2452 ggggaagatttactcgtggtggtgtgtgtgtgatagtatgataatggtggtggtggtat 2511
 QY 2281 gatgtatatacttctcgaaaggtgtagtgaatgatacttctgacatggtgcgcggcaat 2340
 DB 2512 gatgtatatacttctcgaaaggtgtagtgaatgatacttctgacatggtgcgcggcaat 2571
 QY 2341 gataaattgcatctgacagatgcaataatactgataatgattgtaacgtaccaaagag 2400
 DB 2572 gataaattgcatctgacagatgcaataatactgataatgattgtaacgtaccaaagag 2631
 QY 2401 ggtatatagtttaaagaagaatgatacttcaagtagtataacatacacaagaatggtacata 2460
 DB 2632 ggtatatagtttaaagaagaatgatacttcaagtagtataacatacacaagaatggtacata 2691
 QY 2461 acatacaatttacaataattacaagaatgataacacgatacataaattgagcaactaatt 2520
 DB 2692 acatacaatttacaataattacaagaatgataacacgatacataaattgagcaactaatt 2751
 QY 2521 ggtaaagatgtagtatactcacttcgcgaatcaaatgataaaaatttgcgaagaataagaa 2580
 DB 2752 ggtaaagatgtagtatactcacttcgcgaatcaaatgataaaaatttgcgaagaataagaa 2811
 QY 2581 gatgtagacagtaatacattcaagaatgtaaaagcttgctgtagaataagagccaa 2640
 DB 2812 gatgtagacagtaatacattcaagaatgtaaaagcttgctgtagaataagagccaa 2871
 QY 2641 aaattctcgttcgacacttgcaagtagcttaataaactggttggtgcacatgagacta 2700
 DB 2872 aaattctcgttcgacacttgcaagtagcttaataaactggttggtgcacatgagacta 2931
 QY 2701 ttgtgtagcagaataatgtagttagttagtaacgcttaacgcaaatltacacaacaaactca 2760
 DB 2932 ttgtgtagcagaataatgtagttagttagtaacgcttaacgcaaatltacacaacaaactca 2991
 QY 2761 ggaatttggctccaagtggttag 2784
 DB 2992 ggaatttggctccaagtggttag 3015

RESULT 2
 AAQ10727
 ID AAQ10727 standard; DNA; 2788 BP.
 XX
 AC AAQ10727;
 XX
 DT 11-APR-1991 (first entry)
 XX
 DE Leukotoxin 352 gene in plasmid pAA352.
 XX
 KW LKT; vaccine; antigen; respiratory disease; shipping fever pneumonia;
 KW ds.
 OS Pasteurella haemolytica A1 strain B122.
 XX
 PN CA2014033-A.
 XX
 PD 07-OCT-1990.
 XX
 PF 06-APR-1990; 90CA-2014033.
 XX
 PR 07-APR-1989; 890US-0335018.
 XX
 PA (UYSA-) UNIV SASRATCHEMAN.
 XX
 PI Acres SD, Babiuk LA, Potter AA, Lawman MJP;
 DR WPI, 1991-000097/01.
 DR P-PSDB; AAR10889.
 XX
 PT Pasteurella haemolytica proteins and genes - used for producing
 PT vaccines to protect animals esp. cattle from respiratory diseases
 PT e.g. pneumonia.
 XX
 PS Claim 13; Fig 5; 87pp; English.
 XX
 CC Plasmid pAA352 is derived from pAA114, a clone isolated from a
 CC genomic library of P. haemolytica. The protein encoded by the
 CC plasmid, "new leukotoxin" or "LKT 352" is 98% homologous to
 CC authentic leukotoxin. LKT 352 and pref. antigenic fragments of it,
 CC can be used in vaccines to protect cattle from respiratory diseases.
 CC They can also be used to produce antibodies for immunofluorescence
 CC purification of further proteins. [Fig. contg. sequence v. poor]
 CC See also AAR10890, AAR20909, AAR10910 and AAQ10783.
 CC
 XX
 SQ Sequence 2788 BP; 928 A; 487 C; 597 G; 776 T; 0 other;
 Query Match 29.4%; Score 817.6; DB 12; Length 2788;
 Best Local Similarity 60.0%; Pred. No. 3.5e-171;
 Matches 1530; Conservative 0; Mismatches 964; Indels 54; Gaps 8;
 QY 53 caaagcttgatlaaanaacttacttgctcattcccaagaatatagtccgcaaaaag 112
 DB 29 caaagcttggtggcaaaaaaataatcatctctatattccccaataatcaaatatgactag 88
 QY 113 gtcggacttlaaagatttataaagctgctgataatgattgctgctttagcag 172
 DB 89 aacaagatttacaagatttagtcaaacggtccgaagagttgggattggtgataaagag 148
 QY 173 aagagcttaatacacttgtaaacagcaaaaaaattcgttgacacagtaatacagtttctc 232
 DB 149 aagaacgcaataatattgtaaacagctcaaaccaagtttaggcacgattcaaacgcgtattg 208
 QY 233 cctcacaacaactgtagtattcttctgcaacaacaattgaagaagttcttacaacaac 292
 DB 209 gcttaactgtagtggtgattggtatctcgcctccacaataattgataatgtcacaagaaa- 267
 QY 293 atttacaataatgtagccaaggttagacagtgtagaataataattgactgtaaatag 352
 DB 268 -----actaaagcagcgaagcattaggttctgcgcgaagcattgtaacaatatgcaa 319
 QY 353 gtaaaagcaagtaatgatatatacaacattagctcttttttggcactgcatagcgggta 412

Db 320 ataaagcaaaactgatatcttcgcatlcaatctatttagtccgatttggcttggaa 379
Qy 413 taagaacttgattcttaatacaaaaagtgatgctgacccgtgacttggcaagcta 472
Db 380 tgaattagatgagccttacagaa-----taacagcaaccaactgctcttgtaaaagt 436
Qy 473 gtaattgacttgatlaagataaattggttaactatctcagagtaactcaaaagatgaag 532
Db 437 gcttgaggttaacaactattctaattgaataattgtaattcagttaaaacacttgacg 496
Qy 533 catttctcaagcttgcaaaagttagtctcctatctatcgcgcgcaaaagccttcccta 592
Db 497 aatttgctgagcaaatagtcnaacttggttccaacatacaaaatatacaaaagctlaaggaa 556
Qy 593 alataaggaaacagtlgcnaaacttaaat---tttcttaaaacaactctggttggtaaa 649
Db 557 ctttagagagcaaacactcaaaaatatcggtgacttgataaagcgtgccttggttaagtg 616
Qy 650 taattactggttggctcaggaactcttcagagcttgctttagcggaataaaatgcata 709
Db 617 ttactcagggtctatlaicggcgcaaacgtgcacttgacttgcaagataaaatgctt 676
Qy 710 cgactggcaaaaagtgctgcagagtttgaattgaagaacatcaagttatggtaalgtaa 769
Db 677 caacagctaaaaaagtggtgcgggttctgaattgcaaacacaggtctggttaataata 736
Qy 770 caaaagcaattctctcaatagtttlaagacaacggtgtgctgctgctgctlaactaactg 829
Db 737 ccaaaagcgttctcttcaactttagccaacggtgtgcaagagtttacttctcaactg 796
Qy 830 gtgctgtgctgcttataacttcaactcagattagtgtgcaattagcccttggcattta 889
Db 797 ggccttggtgctgcttcaattgcttactgcttctcctgctgataagcccatlaagcattg 856
Qy 890 tgaatgacagagataaattcaatcatgctaagtctctgaagttggaacaaacttcc 949
Db 857 ccggtattgcgcgataaatttaactatgcgaaaagtttagagagttatgcgcgaacgcttta 916
Qy 950 gaaaattggtcatalgatgagggatcatcttatttgcgtgaatacagcgtggttgggtacta 1009
Db 917 aaaaattaggtatgacggagataattattatagcagataatcagcggggaacagagacta 976
Qy 1010 ttgaagcttcaataactacaacttagtaagcagataggtgcagttctcgtggttccg 1069
Db 977 ttgattgatacgtgatacgcacataactaatacgcgtatgcccgtatgctgggttgcctg 1036
Qy 1070 ctgctgtgtgaagatcgtcgtgtgtgtgcacgcgattgacattagttgcaggttgcag 1129
Db 1037 ctgctgcagcgcgctcgtgtattgtctcacgcgattgccttaattagttctcgggaattacg 1096
Qy 1130 gatgatcctctgnaattttgaagcgtctaaacagcgaatgtttgaaagtgtgctaacc 1189
Db 1097 gtgtaattcttaagattctgcaattatcttaacaagcaatggttggacgcttgcataa 1156
Qy 1190 gtttaacaggttaaattttagagtggtggaanaagcaaaatgvcggtcaaacattttgata 1249
Db 1157 aaattctaaacaataatgtgtgaalgggaaaaaaataatcgcgtgaagaaactacttgaaa 1216
Qy 1250 aagcctatgatttcgttatgctgcttatttagtaactaaactaaatttgcgtgagc 1309
Db 1217 atggttgcgtatgccggttactcttgcgaaatttaacagataataatgaatttcttaactga 1276
Qy 1310 taaataaagagttggaagcgtgaacgtgttatttgcaatcaccccaacacgttggatata 1369
Db 1277 taacaaagaggttacagcgacgaacgtgtcatcgtattactacagcagcaatgggataaca 1336
Qy 1370 atattgttggttagcgcggtattaccaaattgggtgaacgcataaagcggaagcct 1429
Db 1337 acatttggtatttgcgttgaatttagccgtttaggtgaaaagtccttagtggtaagcct 1396
Qy 1430 atcgaagtgcttttgaagatgagcaagaagtgtgaagctgttccaattacttggatg 1489
Db 1397 atgtgatacgtgttgaagaagcaaacacataaagccgaataaattagtaacgttgatt 1456
Qy 1490 ctaaaactggatcatagacattagtaattcaaatgggaanaaagcaacgcgttgatt 1549
Db 1457 cgggaacgcgttatatttgatggtgataattccgggtgaagaagcaaacctacacatactat 1516
Qy 1550 tcaactcgccttgtttaacagcaggaactgaatcgcgtgaacgctttaactaatgttaaat 1609
Db 1517 tcgaagaagccattattgaacgcgggaacagagacatcgtgaacgcgttaacaacaggttaaat 1576
Qy 1610 accttatattaaagaattaaatctcgaggtgttaaaaactcgggaagttacaggttagag 1669
Db 1577 atgaatatattcaacacccaatataatcaaccgtgtagatgctggaataattacagatggvt 1636
Qy 1670 aggcagttctaaattagatttctcctaagttatcagcgtgtgagccggaacaggaagca 1729
Db 1637 cagaagaattctactcttgatttaactaaagttgttcagcgttatgtgattgattagaca 1696
Qy 1730 cagaacgagattggtcttaatagttaaatgcaaaa-----gctgcgca 1768
Db 1697 atgcttggaatgttaactaaacccaagaacaaaataattatgccaacttgggtgaagtg 1756
Qy 1769 atgacgatcctctgtgtgcgaaggttaaatatgtaattggttggagatggagacagatc 1828
Db 1757 atgacaacgcatattgtgtgtctggttcggtacgcggaattggtgcggtgaaggttaagc 1816
Qy 1829 ggtctctctatagtaaaagcaggaagatttggtaatatattcagtagatgtaacgagtgcaa 1888
Db 1817 gatttctactatag---ccgttggaacatcatgtgtttaaactattgtatgcaacaagaaga 1873
Qy 1889 cagaagaagcagttataacagttaatcgttaagttgctgcaggtgatacttaccagaag 1948
Db 1874 ccgaagcaaggtatgtaaacgtaaatcgttctgtagaaaccggtlaaagcactaacagaa 1933
Qy 1949 ttgtgaagcgtlcaagaaaccaaagttggtgaacagttacgttaacatcagatcgttatt 2008
Db 1934 tgacttcaaacccataaccgcgaattagtggaacacgttgagaanaaataatagatatcgtcata 1993
Qy 2009 atgaattagaanaagttgggtatgtgtatcagttacgcgaataattgnaactagtagaag 2068
Db 1994 gcaataacccgcacccatg---ccggttattaccccaagaagataccttgaagcgttgaag 2050
Qy 2069 aagtaattggttctcaatttaagatgataatcaaaagttcaaatccaacagacatatcc 2128
Db 2051 aaattatcgttatacacaatacagatatcttcaaaagtaagtaagttcaatgaatgccttta 2110
Qy 2129 atagttgtaaggtgaatgaattactcogatgtgtgtgtgtgacgcgcgttcttgggt 2188
Db 2111 acggttggtatgtgttcgataactatgacggttaacgcgcaatgacgcgttatttgggt 2170
Qy 2189 gtaaaagcaacagatcgaacttctcgtgagaagaagcgatgaattactcagatgcggtctg 2248
Db 2171 gtaaaagcgatlgatattctcgaattcgtgtgaatgtgtatgttattcagtcggtcgaag 2230
Qy 2249 gtgatgtatgattaaatggtggtgtgtgtgtatgtatgtatctatcttccggaagggatg 2308
Db 2231 gcaacgacctattacaacggtggaagcgatgatatcttcgttcaacgctlaaagcgatg 2290
Qy 2309 gtaatgatacttgtacatgycgacgycgaatataaataatagcattgycagatgcaata 2368
Db 2291 gtaatgatatattacgcgattcgcagcgaatgataaataatatactctcgtatgtaact 2350
Qy 2369 tatcgtatatatgatgtaacgatacgaagaggtatataagttaaacgaatgatact 2428
Db 2351 taaaagaatttaacaattgaaaagtttaaaaa-----taactcttcatacagaattagaanaa 2407
Qy 2429 caggttagtattacaatacgaatlggttaataacatcaaatatttacaana-----tt 2479
Db 2408 aagagaagaagtgacacattcaaaacatggttccgaagaggttatttgcgttaagaagtgctta 2467
Qy 2480 atcaagaataaanaagcagatcaanaaatgtgaacacaaattgtgaagatggttattata 2539
Db 2468 attataaagcaactaaagaatgagaanaatcgagaanaatcatcgcgttcaaaaatgvcgagcgga 2527

Qy	2540	tcacttcgatcaaatgtataaattt	2567
Db	2528	tcactcaagcaagttgatgatcttat	2555

RESULT 3

AAT60032
ID AAT60032 standard; DNA; 3311 BP.

AC AAT60032;

DT 12-MAY-1997 (first entry)

DE Chimeric protein #1 coding sequence.

KM RFX cytotoxin; cytokine; immunogen; chimeric protein; cytokine; vaccine;
KM Interleukin-2; IL-2; gamma interferon; gamma IFN; leukotoxin; pneumonia;
KM Pasteurella haemolytica; LKT352; respiratory disease; shipping fever;
KM fibrinous pneumonia; cattle; therapy; ds.

05 Synthetic.

FH	key	Location/Qualifiers
FT	CDS	1..3297

PN US5594107-A.

PD 14-JAN-1997.

PF 22-AUG-1990; 90US-0571301.

PR 20-DEC-1993; 93US-0170126.

PR 16-OCT-1991; 91US-0777715.

PA (CIBA) CIBA GEIGY CANADA LTD

XX

XX

DR P-PSDB; AAW13866.

PT Immunogenic chimeric

XX

PS Claim 10; Column 25-32; 56pp; English.

CC AAT60032 and AAT60033 represent the co

AA1600032 and AA1600033 represent the coding sequences for immunogenic chimeric proteins of the invention. This sequence represents a chimeric protein containing the bovine interleukin-2 (IL-2) sequence and a leukotoxin sequence. The chimeric proteins of the invention comprise a cytokine, selected from interleukin-2 (IL-2) and gamma interferon (gamma IFN), linked to at least one RTX toxin epitope (preferably the sequence shown in AA163865). The RTX toxin used to provide the epitope sequence is preferably a leukotoxin, especially the full-length Pasteurella haemolytica leukotoxin. Alternatively, the leukotoxin is a truncated leukotoxin lacking leukotoxic activity, especially LK952. The chimeric proteins can be used for the production of vaccines against respiratory diseases such as pneumonia, particularly fibrinous pneumonia caused by *P. haemolytica*, including shipping fever, in cattle.

Sequence 3311 BP; 1113 A; 592 C; 699 G; 907 T; 0 other;

Query Match	29.3%	Score 815.6;	DB 18;	Length 3311;
Best Local Similarity	60.1%	Pred. No. 1e-170;		
Matches 1544; Conservative	0;	Mismatches 964;	Indels 60;	Gaps 9;

QY 39 aggcttgaaatccaacaagctcgatlaaaaatccttacttgcgtatcccaagat-- 96

Db	531	agccggcaggttccttaaaacctcgggcaaaaaaattacccttatatctcccaaatla	590
Qy	97	---tatgatccgcaaaaagttggagctttaaigtatttataagctcgtatgaaat	152
Db	591	ccaatgatatactgaacaagaagtaatggtttacagagattttagccaagcggccgaaggtt	650
Qy	153	aggtattgctcgcttttagcagaagaagcttaacactctgnaaagcaaaaaaatcgtgtga	212
Db	651	gggggtcttgaggtaacaagaagaaagacgaataatctgcaacggcccaacccagtttgg	710
Qy	213	cacagtaaatcagttcttcctctccacacaaactggtatgtcatcttcgcacaaaaatt	272
Db	711	caagatccaacccgctatttggttaactcggcgttggtcatttggtatccgtccacaat	770
Qy	273	agaaaagttccttcaaaaaacattcccaataagttagccaaagggttagacagtgtga	332
Db	771	tgataaattctgtacaagaa-----actaaagcaggccaaagcatttggtctgcgga	821
Qy	333	aaattatgacgttaatttagtaagaagaaagtaagtattatcaacataagctctttt	392
Db	822	aagcattgtacaaaaatgcaaaataaagccaaacactgtacatatctgcatccaatcattt	881
Qy	393	gggcactgcatlagcgggtatagaaactgtattccttaacaaaaaagggtgagtgtcaccc	452
Db	882	aggtcagatattgctggaatgtatttagtggccttacagaa---taacagaaacca	938
Qy	453	tgtatgctttgcttaaaagctatgtatgtatgtataatgtgttaactatctcca	512
Db	939	acatgtcctctgtcaaaactcggcttggagccacaacaaatcatatattgaaaatgtgc	998
Qy	513	gagtactcaaacgattgaagcattctctccacggttagcaaaagtttaggtctacatactc	572
Db	999	ttcagtaaaaacacttgcagaaattggttggagcaaattagtcaattgtgtccaactaca	1058
Qy	573	gcaggctaaaggtctctcctatataaggaacaaagttgcacaaactaaat---tttctca	629
Db	1059	aaataccaagcgtttagggactttaggagcaaaacccaataatctcgttggactgtataa	1118
Qy	630	aacaacatctgtcttggaataatlaetgatttgcatacgaacatcttcgcagcttgc	689
Db	1119	agctggccttgggtttagatgttatctcagggcattatctcgggcagcaacgctgcctgt	1178
Qy	690	tttagcggataaaaaatgcatacgcagtcgcaaaaagtctgcaggttttgaataagcaa	749
Db	1179	acttgcagataaaaatgcttccaacgctaaaagaagtggtgcgggttttgaattgcca	1238
Qy	750	tcaagttatttgtaattgaacaaagaattcttccaatggttttgagccaaacgtgttcg	809
Db	1239	ccaagttctgttaataatcaccaaaacgcttctcttccaatttttagcccaagtggtgc	1298
Qy	810	tgtctgtcatacacaactcagttgcgtctgtctgtcttaattacttcaactgatatgttcg	869
Db	1299	agcaggttatcttccaactttaggcgtcgtgcgtctttaatgtctactactgttctcttcg	1358
Qy	870	aattagctccttggcatttatgaatcgcagcagaataatccaatcagctcaatagccttga	929
Db	1359	gatttggccatttagcatttgcgggtatttgcgataaatttaacatgcagcaaaaagtttga	1418
Qy	930	tgaagttgcacaaacatccgcaaaatttgcgtatgatacgtatggtgagcatcttctgcgaata	989
Db	1419	gagttatgcgcgaagctttaaaaaattagcgtatgacgagataatttatatgacgaata	1478
Qy	990	tcaagctgtgtgtggtactatgaagctcattcaactacaataatgaagcattagtgctc	1049
Db	1479	tcaagcgggaaacaggagcatttgatgatcgttactgtcaataatgaacccgcatltagccg	1538
Qy	1050	agtttcctcctgtgttcccgctcgtcgtgtgagatactcgttgttggtagcccgatgcaat	1109
Db	1539	tattgcgtgtgtgtgtcctcgtcgtcgaacggcgtccgtttatctgtccacgattgcctt	1598
Qy	1110	attagtttcaggtgttctacagattgatctcttgaaatttttagaagcgttcaaacaggcaat	1169

Db 1599 attagatctcggtgattccggtgttaattcttaagcttctgcaatattcttaaacgaat 1658
 Qy 1170 gtttgaagtgctgtaacccgtttacaaggtaaaatttagatgggaaagcaaatg 1229
 Db 1659 gtttgagcagcttgcaataaaattcatacaaaaatttgtaaaggaaaaaatatca 1718
 Qy 1230 cggttcaaatattttgataaagctatgattctcgtatagctgctatttagctaat 1289
 Db 1719 cggtaagaactcttgtaaaagcttgtaagctgcgttacccttgcgaatttacaagata 1778
 Qy 1290 cttaaaattttctgctagcttaaaagagcttggaagctgcaacgtgttatgtcaatcac 1349
 Db 1779 tatgaattcttactgataacttaaacaaaggttaccagcgagaacgtgtcaatcttac 1838
 Qy 1350 ccaacaacgttgggataataatattgtgtgagtgacagtgatcaaccatgtggtagacg 1409
 Db 1839 tcagcagcaatgggataacaacattggtattagctggtatttgcgtttgagtgtaaaa 1898
 Qy 1410 catlaagagcggaagaacttatgacagctgtttgaaagatggcgagaagaattgaagctgg 1469
 Db 1899 agtcccttagtggttaagcctaagcttagtgatgcgttggaagaagcgcaaacattaaagcga 1958
 Qy 1470 ttccaatatcttggatgtctaaactggatcatatcatagacattagtaattcaattgggaa 1529
 Db 1959 taatttagtacaagtgtgatttcgcgaacggtattattgattggtgtaattcggtaagc 2018
 Qy 1530 aaaaacgcaagcgttgcaattcactgcgcttgttaacagcaggaactgaatcacgtga 1589
 Db 2019 gaaaactcagcatctctatcagaacgcctatttgacgcgcggagcaacagcgacgtga 2078
 Qy 1590 acgttaactaatgttaaatctcttatattatgaattaaacttcgacgctgtaaaaa 1649
 Db 2079 aacgctacaacaggttaaatatgatatataataccaaagctcaatttaccgtgtgagtag 2138
 Qy 1650 ctgcaagttacaatgtagagagcgtagttctaaattagattctctcaagtatttcagcg 1709
 Db 2139 ctgcaaaattacagatggtgcagcaagcttcaacttatttaactcaactgctgttcagcg 2198
 Qy 1710 tgtgacgagacagaagcacagcagatggtgttaattagtagtaattgtaaaaa----- 1761
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 Qy 1762 -----gctgcaatggacgatatcttgtgtgcaagtgtaaatgtaalatga 1808
 Db 2259 tgcgaacttggtggaaggtgtagacaacgtatttgtgtctgtaacgaggaattga 2318
 Qy 1809 tgtgtgagatgtagacagcgtgcttctctatagtaaaagcaggaattgtgtaattac 1868
 Db 2319 tggcgttgaaaggtttagcagcaggttccactatag--ccgtggaactatggtgtcttaac 2375
 Qy 1869 tgtagatgtgtagagtgcaacagagcagcgatatacaagttaacgttaaggtgtcgcg 1928
 Db 2376 tatgtatgaacccaagagaccggaagcaggtatgatatccgttaactgttcgcgtagaac 2435
 Qy 1929 aggtgatataccaatgaagtgtggaagcgtlcaagaaaccaaagtggttaaacgtactga 1988
 Db 2436 cggtaagacactacaagaagtactcaaccataccgcatlagtgggcaacccgtgaaga 2495
 Qy 1989 aactatccggtatcgtgattatgaattagaanaagtttggttgcgttaccgtaccca 2048
 Db 2496 aaaaatagaatcgtlcalagcaataaaccaagcaccatg---ccggtatatacaacaaga 2552
 Qy 2049 taattgaatacagtagaagaagtaattgtctcaatttaatgtatatacaaggttc 2108
 Db 2553 taccttgaaagctgttgagaagaattatcgtatcacatacgaattatctttaaggttag 2612
 Qy 2109 taattcaacagcatatccatagtggtggaaggtgatgatttaactcogatggtggtgcgg 2168
 Db 2613 taagttaaatgcttcaacggtgtgtagtgcgtatctatctgacgtgaacgagcg 2672
 Qy 2169 tgaagacgcgtgtgtgtggtgaagaagcagatcgcacttctgagagtagaagcgcatga 2228
 Db 2673 caatgacgccttattctgtgtgtaaaagcgatgatatctcgaatgtgtgaaatcgtgtgata 2732

Qy 2229 ttactcgaatggcgggttctcgtgtagatgataataatggtgtgtgtaatgtatca 2288
 Db 2733 ttattcgaatggcggtaaaaggaacgacctatttacaacggttgcaaggcgatgatttt 2792
 Qy 2289 tatcttcggaaggtgtagtgaatgatacttgttagatgacgacggcaatgataatc 2348
 Db 2793 cgttcacgtaaaagcgatgtagtgaattatattccgattcttgcgaatgataaatc 2852
 Qy 2349 agcatlttgagatgcaaatatatactgatatattgattgaacgttaccagaagggattat 2408
 Db 2853 atcaatcttcgtatcgaacttaaaagatttaacattgaaaaagttaaca---taactc 2909
 Qy 2409 agttaaacgaatgatalcattcaggtagattatatacacaacaaagtgtatatacaaa 2468
 Db 2910 tgtcatcaagaatagaaataaaagagaagaatgacattcaaacctgttcggagagctga 2969
 Qy 2469 tttaaaaa-----ttatcaaaagtataaacaagatcaataatgtgcaattat 2519
 Db 2970 ttgtgtaagaaggtgcttaattatataaagcaactaaagtgaagaatcgaagaatcat 3029
 Qy 2520 tggtaagaatgtagtattatatactcgcgatcaaatgtgtaaat 2567
 Db 3030 cggtaaaaatggcagcgagatccacccaagcaagttgattcttat 3077
 RESULT 4
 AAAT2483
 ID AAAT2483 standard; DNA; 3311 BP.
 AC AAAT2483;
 XX
 DT 19-DEC-2000 (first entry)
 XX
 DE Bovine IL-2/Pasteurella haemolytica leukotoxin fusion gene.
 XX
 KW Bovine IL-2; interleukin-2; leukotoxin; LKT; respiratory disease;
 KW pneumonia; shipping fever; cattle; livestock; anti-Pasteurella vaccine;
 KW immunogen; ds.
 XX
 OS Chimeric - Bos taurus.
 OS Chimeric - Pasteurella haemolytica.
 XX
 FH Key Location/Qualifiers
 FT 1..3297
 FT /*tag= a
 FT /product= "Bovine IL-2/Pasteurella haemolytica
 FT leukotoxin fusion protein"
 XX
 PN US6096320-A.
 XX
 PD 01-AUG-2000.
 PD
 XX
 PE 20-OCT-1997; 97US-0954418.
 XX
 PR 20-DEC-1993; 93US-0170126.
 PR 22-JUL-1996; 96US-0681479.
 PR 22-AUG-1990; 90US-0571301.
 PR 16-OCT-1991; 91US-0777715.
 XX
 PA (UUSA-) UNIV SASKATCHEWAN.
 PA (CIBA) CIBA GEIGY CANADA LTD.
 XX
 PI Campos M, Hughes HPA, Potter A;
 XX
 DR WPI; 2000-531543/48.
 DR P-PSDB; AAB21073.
 XX
 PT Vaccine for stimulating immunity against pneumonia comprises chimeric
 PT protein comprising gamma-interferon and leukotoxin derived from
 PT Pasteurella haemolytica -
 XX
 PS Example 1; Column 25-32; 56pp; English.

XX The invention relates to a novel vaccine composition comprising an
CC immunogenic chimeric protein that comprises gamma-interferon (gamma-IFN)
CC or an active fragment thereof, linked to an epitope of a Pasteurella
CC haemolytica leukotoxin (LKT). Pasteurella species, especially Pasteurella
CC haemolytica, are responsible for respiratory diseases in a range of
CC agricultural animals, most particularly cattle, but also sheep, pigs,
CC horses and fowl. Shipping fever is the most economically important
CC respiratory disease associated with Pasteurella species, affecting
CC 15-30% of exposed cattle and resulting in a 2-5% mortality rate in the
CC exposed population. The vaccine composition of the invention is
CC is useful for preventing or ameliorating respiratory diseases such as
CC pneumonia, particularly shipping fever pneumonia, in livestock. The
CC present sequence represents DNA encoding a fusion protein comprising
CC bovine Interleukin-2 (IL-2) and Pasteurella haemolytica leukotoxin.
CC which may also be used as an anti-Pasteurella vaccine.
XX
SQ Sequence 3311 BP: 1113 A; 592 C; 699 G; 907 T; 0 other;

Query Match 29.3% Score 815.6; DB 21; Length 3311;
Best Local Similarity 60.1% Pred. NO. 1e-170;
Matches 1544; Conservative 0; Mismatches 964; Indels 60; Gaps 9;

QY 39 aggcctgattccaacaagctcgtgattaaaaattcttacttgcttcccaagaat-- 96
DB 531 agccggcagcttcttaaaaaactggggcaaaaaaatctctctatctcccaaatla 590
QY 97 ----tatgacgcgaanaaaggcttggaactttaatgtattttaaagctgtgataat 152
DB 591 ccaatatgactgacacaaggtaatggtttacagatttagccaagcgcggaagatt 650
QY 153 aggtatgctcgttttagagaagaagcctaactcacactgaacagcaaaaaaatcgttga 212
DB 651 ggggattgaggtaacaagaagaacgcataatattgcaacagctcaacacagttagg 710
QY 213 caccgtaaatcagttctctctctccacaacactgtaattctatcttcgcaacaatt 272
DB 711 cagatccaacacgcgtatgtgcttaactgagcgtgagcttgtgtatcgcgtcccaat 770
QY 273 agaaagttcttcaaaaaacattctacaataagttagccaagggttagacagttgata 332
DB 771 tgataaatgtctacagaaa-----actaaagcagcgcaagcattaggtttcgcgca 821
QY 333 aaatcgtgatcgttaaataggtaagaagcaagtaatgatatcaacaatgaagcttttt 392
DB 822 aagcattgtcaaaaaatgcaaaaataaagccaaactgtatctatctggtcattcaatctt 881
QY 393 gggcactcattagcgggtatagaactgtattctttaacaaaaagttgtagctgcacc 452
DB 882 aggtctgaatttgctcguaatggatttagaagagccttacagaa---taacagcaacca 938
QY 453 tgaagcttctgctaagaagtagtattgactgtatagatagataatgtaactctca 512
DB 939 acatgctcttgctaagaagcttgctgagcttaacaatcatatgaatattgtaactaa 998
QY 513 gagtacccaacagattgaacatttctctcacagttagcaaaagttagttctactatc 572
DB 999 ttccgttaaaaacacttgcgaatttgcgtgacaaaattagtcgaatttgcgtcaaaactca 1058
QY 573 gcaagcctaaagcctctctataataggaagaagttgcaaaacttaaat---tttctcaa 629
DB 1059 aaatatacaaaagccttaggacttaggaagacaacatacaaaatatacgtgtaattgaa 1118
QY 630 aacaatcttggttgaataaatatctggttgcatacagcaattcttcgaagcttcg 689
DB 1119 agcttgaccttggttagatgtatctcagggtctatcaggcggaacagcgtcactggt 1178
QY 690 tttagcgataaaaatgcatacgtgcacaaaagttgctgcaggttttgaattgaacaa 749
DB 1179 acttgcaataaaaatgcttaacacagctcaaaaagttggtgcggttttgaattgcaaa 1238
QY 750 tcaagttattgtaatgtaacaagaacaaattctctcatatgttttagacaacgtgttcg 809

DB 1239 ccaagtttggttaattaccacaagccggttctcttcaaatcttagcccaacgctgtgc 1298
QY 810 tgcgtctataactactggtgctgtgtgcttcaattactcatcgatatagttgc 869
DB 1299 agcagttattctcaacatgagccgtgtgctgttcaattgcttaactggttctcttcgc 1358
QY 870 aattgctcttggtgattatgaatgacgagataaatcaatctcgtcaatgctgtca 929
DB 1359 gattgcccataagcattgcgcgcatgtgcgataaatcttaacatcagcaaaagtttga 1418
QY 930 tgaattgcaaaaacattccgaanaatttggtcatgtatgggagctcaatttgcgtaaa 989
DB 1419 gagtatgcccgaacgcttataaaaattggccataagcggaggaattattcttcggaata 1478
QY 990 tcaagcgtgtgtggttactatgtaagcttcaatcaatcaatagtaacgcatgtgtgc 1049
DB 1479 tcaagcgggaagaagcattgtatgcattcgttactgaataataacgcattgcccgcg 1538
QY 1050 agttctgctggtgttccgcgtgcgtgtagatcgtgtgtgtgtgcacgattgcact 1109
DB 1539 tatgtctgtgtgtgtctgtcgtgcgcgcgctcgtgtattgcttcaacgcatgtcct 1598
QY 1110 attagtcaaggtgttacaagatgatactctcgtgaattttagaagcgttcaacagcaaat 1169
DB 1599 attagatcgtggtatcaccggtgtatattctcagttccgatatcttcaacaagaat 1658
QY 1170 gttgaaagtggtgtcaacggttcaaggtaaattttagagtggtggaagaacaaatvg 1229
DB 1659 gtttgaagcagcttgcgaataaatcaatcaacaataattgtagatvggaaaaaataatca 1718
QY 1230 cgttcagacattttgtataaagcgtatgattctcgttatgctgtatttagtcaatba 1289
DB 1719 cgttgaagactactcttgaataatggttaccggttactcttgcgaatttcaagataa 1778
QY 1290 cttaaaatttctgtcgtgctaataaagaagttggaagcgtgagctgtatttgcatacgc 1349
DB 1779 tatgaattcttaccgaacttaacaagaaggttaccaggaagcgtgtcatctatctac 1838
QY 1350 ccaacaacgttvggataataatattgtgtgtagttagcaggtattaccaaattvggtgacg 1409
DB 1839 tcaagcagatvggataaacaacattggtttagctgtttagtcggttttagtgaanaa 1898
QY 1410 catgaagcggaaaagccttagcagatgtctttgaagtggtgcaagaagttgaagctvg 1469
DB 1899 agtcttagtggtaagccttagtgaagctgttgaagaaggtcaacaacattaaagccga 1958
QY 1470 ttccaattacttggatggtcaaacgtgtatcatagacattgaattccaattgysaa 1529
DB 1959 taatttagtacaagttggtatcggtcaaacggttatattgtagtgaattcgtgtaagc 2018
QY 1530 aaaaaacgaagcgtgtgcatlctactcgtcttgtttaaagcaggaactgaatcagtyga 1589
DB 2019 gaaaactcagcatatcttattcagaagccattatttgacgcgggaacagagatctgga 2078
QY 1590 acgtttaactaatgttaataactcttatataataagttaaaatcgcgaagcgttaaaaa 1649
DB 2079 acgcttacaanaaaggtataatagatataattccaagcctcaatlaaacggttagatag 2138
QY 1650 ctgcaagtttacaagttgagagcgtgtctaaatttagattctctcaagtattcagcg 1709
DB 2139 ctggaataattacaagatgtgtgcagcaagttctacacttgaattcaactaaagttgttcagcg 2198
QY 1710 tgaagcagagacagaagcacagacagatgtgtcttaatagtaaatgtaacaa----- 1761
DB 2199 tatgttatgtattagacaatgctggaatgttaacttaaaaacagaagaacaaatattat 2258
QY 1762 -----gctgcgaatgacgatatcttctgttgcgaaggttaaaatgaatga 1808
DB 2259 tgcacaacttggltgaaggtgtagacaacgtattctgttctgtgtacagcggaaattga 2318
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FT		/note= "GrNH DNA"
XX		
FN	W09308290-A.	
XX		
PD	29-APR-1993.	
XX		
PF	15-OCT-1992;	92WO-CA00449.
XX		
PR	16-OCT-1991;	91US-0779171.
XX		
PA	14-OCT-1992;	92US-0960932.
XX	(UYSA-) UNIV SASKATCHEWAN.	
P1	Hughes HPA,	Potter AA, Redmond MJ;
DR	WPt: 1993-152482/18.	
XX	P-FSDB; AAR34547.	
XX		
PT	Immunological carrier system with enhanced immunogenicity -	
PT	comprises chimeric protein comprising leuco-toxin peptide or	
PT	homologous protein fused to antigen esp. somatostatin or	
PT	gonadotropin releasing hormone	
PS	Example 2; Fig 8; 95pp; English.	
XX		
CC	Oligonucleotides contg. sequences from bovine gonadotrophin	
CC	releasing hormone (GNRH) gene were constructed on a Pharmacia Gene	
CC	Assembler using standard phosphoramidite chemistry. The oligo-	
CC	nucleotides were annealed and ligated into vector pAA352 (contg.	
CC	the Pateurella haemolytica leuko-toxin gene) which had been digested	
CC	with BamHI. The ligated DNA was used to transform E. coli strain	
CC	MH3000. Transformants contg. the oligonucleotide inserts were	
CC	identified by restriction endonuclease mapping and the recombinant	
CC	plasmid designated PA502. The chimeric protein produced from the	
CC	plasmid works to bring about a larger immune response than the antigen	
CC	alone. i.e. the leukotoxin works as a carrier protein.	
CC	See also AAQ41317-23.	
XX		
S0	Sequence 2817 BP; 933 A; 495 C; 606 G; 782 T; 1 other;	
	Query Match	29.3%; Score 815; DB 14; Length 2817;
	Best Local Similarity	60.2%; Pred. No. 1.3e-170;
	Matches 1538; Conservative	0; Mismatches 956; Indels 60; Gaps
QY	53 caaaagctcgtgaataaaaaaatcttaacttggtgcattcccaagaat-----tatgatccgc	106
Dd	29 caaaaacctggggccaanaaaaatatcttcctatattcccatcccaaatattcaccaatagtaccy	88
QY	107 aaaaggtggcgaccttaaatgattatttaaagctgcgtgagatgaattagttatgtctcgtt	166
Dd	89 aacaagtaatggttllltagaaggattllagtcocaaagcgycgaagaagttgggattggagtac	148
QY	167 tagcgaagagcgcctaatacaactggaacaacgcaaaaaaatctgtgacacagtaaatcagt	226
Dd	149 aaaggaagaagcgcataatatttgcacaacgcccacaacagtttagcgatgtcaaacgc	208
QY	227 ttctctctccacacaacatggtatttgtctattttgtgcacaacaaatlagaanaagttctac	286
Dd	209 ctatggcttaactagcgtgctgattgtttacgccctccacaanaattgtataattgtac	268
QY	287 aaaaacatttcaaccaataagttagcgcaaaaggtttagaacgftgtaaaaaatattgatacga	346
Dd	269 agaaa-----actaaagcaggcccaagcattgagttctgcgaaagacattgtacaaa	319
QY	347 aattgggttaagcgaagttaatgtattatatacaactaagctcttcttttggcgactgcatag	406
Dd	320 atgcaaataaagccaaaactgtattatcttcggtattcaatcatcttttagctcgaattgg	379
QY	407 cgggtatagaactgattctttaatcaaaaagaagtgatgctgcacattgactgttggcta	466
Dd	380 ctggaattgatttagatgagccttacagaa---taacagcaacaacatgcttcttgcta	436

QY	467	aagctagctatgctctgtatgaatagataatggtgtaacctatccagagctacaaagca	526
DB	437	aagctgtgttggaactcaacaactatcatatgtaaatatgtctaattccgtataaacaac	496
QY	527	ttgaagcaattctctccagctttagcaagtttaggtttctctatalcgcagcgctaaagct	586
DB	497	ctgcagcatctnctgtagcgaacttagtccaatttggcttcaaaaactacaagt	556
QY	587	tcctcaatataggaacaagtctcaaaccttaaat---ttctctaaacaacttggct	643
DB	557	taggagctttagagagacaacaactcaaaaatacgtgtagctgtataaagctggtcttgct	616
QY	644	tgsaataatbactbgtgttgcatacagcaattctgcaggtcttgccttagcggataaa	703
DB	617	tagatgttatctccaggcgtatcttcgvcgcacagctgcattctacttgcagataaa	676
QY	704	atgcatacgactgugaaaaaagttgcgcaggttttgaattgaatacgaactaagttagta	763
DB	677	atgcttcaacgcgcaaaaaagtcgvcggttttgaattgcaaaccaagtgtgtgtga	736
QY	764	atgtaacaaagcgaacttctctcaatgattttagcaacaacgttttgcctgtcgtacaa	823
DB	737	atattacaaagccggttctctctctacattttagcccaagtcgtgcagcaggttatctt	796
QY	824	ctactbgtbctgtctgcgtcttaatactatctcaalcgataigtgttgcaattagtccttbg	883
DB	797	caactbgtccctgtgcgtcttaattbgtcttactgttctctcttggttagcccatlag	856
QY	884	catttatgaatgcgcgcgataaattccaatcactatgctctatgcttgaagtgttgcacaac	943
DB	857	catltgcgcgtatgtccgataaatttaatacgtcaaaaagttttagagagttatgcgcgac	916
QY	944	aattccgaaaaatttgctctgtagtggagatcaatttatgttgtaatacgcgttgctg	1003
DB	917	gcttataaaaactagtcatacgtacgcggaataatttatacttagcagaatacgcgcgggaacag	976
QY	1004	gtaactatgaagctctcaattcaatacaatttagtcgcgcatlaagtgcagttctctgcctgtg	1063
DB	977	ggactatgtatgcatacgttctacgtcaataataccgcatlgtgcgtatgtcgttggtg	1036
QY	1064	tttcgcgtcgtctgtatgagatcgtcgtgttggtgcacgcgattgcataatagtgtgcagtg	1123
DB	1037	tgctgcgtcgtcgcgcgcgcgtctcgttatgtcttcaacgcgattgccttatagtatctggga	1096
QY	1124	ttacagcgattgatactcctcgtgaattttagaagcgtctcaaaagcgaattgtttgaagtgctg	1183
DB	1097	ttacgcgtgttaattcttcagcatctcgcataatctcaataacgaacgaatgtttgcagcgtg	1156
QY	1184	ctaacgcgtttcaacagtgtaaaattcttagagtggtggaagaacgaattgcgctgcgaacttt	1243
DB	1157	caaatataaatcatacaacaataattgtgaaatggtgaaaaataatacgcgttaagaactact	1216
QY	1244	ttgataaagcgtatgattctcgttatacgtcgtctatgtatttagctataactaaattttgtc	1303
DB	1217	ttgaaaaatgtgtttagcagatccgcgttatctctgcgaaatttcaagaataatagttaattcttacc	1276
QY	1304	ctgcgactaaataaagagtttggaaagcgtgaacgcgttttatactgaatcccaacaacggttg	1363
DB	1277	tgaacttaaaaaaagagcttacaagcgcgaagcgtgtccatacttaccatccagcgcgaatggg	1336
QY	1364	ataataatattgtgtagtttagcagagttatccaacaatttgggtgtaacgcgtttaaagcggaa	1423
DB	1337	ataacaacattgtggtatttagcgtctatgaccggttttaggtgtaaaagtctcttggtgtata	1396
QY	1424	aagcttatgcagatgcttcttgaaatgcgcagaagaagttgaaagtcggttcccaatatctt	1483
DB	1397	aagcctatgtgtgtagtcggttttgaaagagcgcaacaacataaagcgcgataaatatgtagcgt	1456
QY	1484	tgggtcttaaaaacgcgtgatacagataagcaatttagtaattccaatgtggtgaaaaaagcgaagcgt	1543
DB	1457	tggatctcgcgcgaagcgtgataatcgtatgtagtgaatttccgtgtaaagcgaacacccgcata	1516
QY	1544	tgcattccaactgcgcctttttagaacgcaggaactgaatcaacggttgaacgctttaactaatg	1603

[illegible]

ID	AAQ41323	standard; DNA; 2861 BP.
XX	AAQ41323;	
AC	23-AUG-1993	(first entry)
XX	Rotavirus VP4-leukotoxin gene fusion.	
DE	Vector: LKT 352; flanking; recombinant; antigen; somatostatin;	
KW	gonadotropin releasing hormone; rotavirus viral protein 4; ds;	
KW	carrier protein; lactation; reproduction; SRIF.	
XX	Synthetic.	
OS		
XX		
PH	Key	location/Qualifiers
FT	misc_feature	1..2778
FT		/tag= a
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FT	misc_feature	2779..2861
FT		/tag= b
FT		/note= "Rotavirus VP4 DNA"
PN	W03508290-A.	
XX	29-APR-1993.	
PD	15-OCT-1992;	92WO-CA00449.
XX	16-OCT-1991;	91US-0779171.
XX	14-OCT-1992;	92US-0960932.
PR	(UWSA-) UNIV SASKATCHEWAN.	
XX	Hughes HPA, Potter AA, Redmond MJ;	
PI	WPI: 1993-152482/18.	
XX	P-PSDB; AAR34548.	
DR	Immunological carrier system with enhanced immunogenicity -	
XX	comprises chimeric protein comprising leuco:toxin peptide or	
PT	homologous protein fused to antigen esp. somatostatin or	
PT	gonadotropin releasing hormone	
PT		
XX	Example 2; Fig 10; 95pp; English.	
PS	Oligonucleotides contg. sequences from bovine Rotavirus viral	
XX	protein 4 (VP4) gene were constructed on a Pharmacia Gene	
CC	Assemblr using standard phosphoramidite chemistry. The oligo-	
CC	nucleotides were annealed and ligated into vector pAA352 (contg.	
CC	the pateurella hemolytica leuko-toxin gene) which had been digested	
CC	with BamHI. The ligated DNA was used to transform E. coli strain	
CC	MH3000. Transformants contg. the oligonucleotide inserts were	
CC	identified by restriction endonuclease mapping and the recombinant	
CC	plasmid designated pAA501. The chimeric protein produced from the	
CC	plasmid works to bring about a larger immune response than the antigen	
CC	alone, i.e. the leukotoxin works as a carrier protein.	
CC	See also AAQ41317-22.	
XX		
CC	Sequence 2861 BP; 947 A; 504 C; 615 G; 794 T; 1 other;	
XX		
QY	Query Match	29.3%; Score 815; DB 14; Length 2861;
DB	Best Local Similarity	60.2%; Pred. No. 1.3e-170;
	Matches 1538; Conservative	0; Mismatches 956; Indels 60; Gaps
QY	53 caaagctcgtatcaaaaactcttacttgcgtatcccaagaat-----tatgacgcg	106
DB	29 caaaaactggggcaaaaaaattatccctcatattcccaaaattaccaatgatgac	88
QY	107 aaaaagctgggaccttaaatgatttatataagctcgtatgataagtgattgctcgt	166
DB	89 aacaaggtatattgcttaccagatttatcaaacgacggaaggttgggattgaggtac	148

QY	157	ttagcagaagcgctaatacacaatgaaacgcaaaaaaatactgtgtgacacgtaaatcaat	226
Db	149	aaagagaagcaagcaataatgtcacacgctccaacaaagtttagcagcattcaaacg	208
QY	227	ttctctctccacaacaacgtgattgttcattcttcgcacaacaatttagaaagttctac	286
Db	209	ctattgcttaacacgacgtgtgcattgtttatccgcctccacaataatgtataattgtac	268
QY	287	aaaaactctacccaataaagttagccaagaaggttagacagttgttagaaataatgtactga	346
Db	269	agaaa-----actaaagcagcgcaagcattagttctgcgcaaaagcattgtacaaa	319
QY	347	aattagcgaagcagaatgaatgtatccaacttaagcctcttttttggcgcctcattag	406
Db	320	atgcacaataaagccaaaacggtatctatccggcatccaatctatatttaggcacgattgg	379
QY	407	cgggtatgaaactcgattcttctaatacnaaaagtgatgtgcacatgtattgttgcta	466
Db	380	ctggaaatgtatttagatgagcgcttaacaga--taacagcaaccaaatctcttgcta	436
QY	467	aagctagatctgactgtatgaatgaagataatgtgtatctatctcaagtgatccaacga	526
Db	437	aagcgtgcttgtagaactaacaattcatatgaataatgtcattcgaatgaanaaac	496
QY	527	ttgaagcctttctctccacagttagcaagttagttctctatcatalcgcagcgtaaaagct	586
Db	497	ttgaagcaattntgtgagcaaatgaatgcactttgttccaactacaataatcaacaagct	556
QY	587	tctctaataaggaacaagttgcacaacttaaat---tttctaanaacaactctgtct	643
Db	557	tagggaactttaggaacacaactcaaaaataatcggttgacttgaataagctgtgcctgtgt	616
QY	644	tggaaataattacgtgtttgtctacacagcattctcgcagcttgcctttagtcggaataaa	703
Db	617	ttagatgtattctcagggcgtatattatccggcgcaacgctgcagcttgaacttgcagtaaa	676
QY	704	atgcatacgactgccaanaaagtgtcgcaggttttgaattaagcaatacgaattatgtga	763
Db	677	atgcttcaacagctaaaagaatgtgtgtgcggttttgaattgcaaaccaagttctgtgtga	736
QY	764	atgtaacaagaacattctcttcacatgtttttagacaacgtgtgtgtgtctgtcatcaaa	823
Db	737	ataatcaacaagcgttctctcttaacatttagoccaacggtgtgtgaagaggttatctt	796
QY	824	ctactgtgtgtgtgtgctttaatactcaatcogaltatgtgtgcattagtcctttgg	883
Db	797	caactgtgcctgtgtgctttaatgtcttaactgttttctcttgatgaatgaocattag	856
QY	884	cattatgaatgacgaataatcaatcaatcogltgaatgtctgtgtgtgtgttcgaacac	943
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QY	944	aattcogaanaattgtcatgatagtggagatcaattatgtgtgaataatcagcgtgtgtgtg	1003
Db	917	gctttaaaaataatgacgtatgacgcaggaataattatttagagaataatcaocgcgggaacag	976
QY	1004	gtactatgaagctcaatcaataactacaatgaacgagcattaggtgtgcagtttctgtcgtgtg	1066
Db	977	ggactattgatcatcogtgttactgaatcaataacacgattgtgcgcattgtgtgtg	1036
QY	1064	tttcgcgtctgtgttagagatctgtgtgtgtgtgacagcattgcacattagttgcaggtg	1122
Db	1037	tgtctgtcgtcgaacgcgcgtcctggttattgtcttaacgagattgcttattgatactcggga	1096
QY	1124	ttaacagatgatcctcgtgaatttttagaagcgtctaaacagcgaatgtttgaagtgtgtg	1188
Db	1097	ttacgcgttgaaattctacgattctgcgaattcttaacaacagcaatgttttagcacgtgtg	1156
QY	1184	ctaacgcgtttacaaggttaaatatttttaggtgtgtggnaaagcgaataatggcggtcaaacatt	1244
Db	1157	caaatataaattctaaacaattttgttagaattgtggaaaaaataatcaacaggttaagaaactact	1216

OY	1244	ttgataaagctatgatctctcgttatcgtcgtctattttagctataactataactaaatttttgt	1303
Db	1217	ttgaaaatgtgttaagatgcccgttatctctgtcgaatttcaagaataaltaatgtattcttacc	1276
OY	1304	ctggagctaaataaagatttggaaagcgtgaacggtgtatcttgcaatcccaacaacgttggg	1353
Db	1277	tgaaacttaacaacaagagttacagagcgaacggtgtccatctctatctcagacgaatlygg	1336
OY	1364	ataataatattggtgaacltgcagcagttatcaccaaatctgggttaaacgcataaagacgga	1423
Db	1337	atacaagaatttgttgatttgcttgcgtcatctacgctttagtgtaaaaagtccttggtgta	1336
OY	1424	aagcttatgcgaatgcttcttgaaatgctgcaagaagaattgaaagcgtgtcttccataattact	1483
Db	1397	aagccttatgtgatcgttcttgaaaggaacaaacacataaagccgataattatgtatagct	1456
OY	1484	tgtgtgtctaaaacctggtatcatatgacaattgaattccaatggtggaaaaaacgcgaagcgt	1543
Db	1457	tgtgattctgcgcaaaaaggtatatttgaatgtgaaatattcgggttaaaagcgaatactagcata	1516
OY	1544	tgcatacttaccctcttcttgtaacgcggaacgtgaaatcagatgaaagctttaactaag	1603
Db	1517	tctattctcgaagacgcattcttgaacgcggtgacgaagacatcgtgtaaacggtlcaaaaaag	1576
OY	1604	gtaaatactcttatattatnaaagttaaatactcgaaacgtgttaaaaagcctgcggaattcacg	1653
Db	1577	gtaaataatgatattatattaccagaagctcaatattaaacggtgtatgatacggtgaataatcaag	1636
OY	1664	atggagaagcgtatgtcttaaaatagattatctcttaaaagttaacagctgtatgcggaagacg	1733
Db	1637	atgggtcagaagaagttcttacccttgattttaaactaagcgtgttcaagctatgtatgtaat	1696
OY	1724	aaggcagagacggagatttggctcttaagtgaatgtcaaaa-----g	1762
Db	1657	ttagcaatgtcgtgaaatgtaactaaacccaagaacaaataatcttgcacaacttggtg	1756
OY	1763	ctggcaatctgacgaatatctcttctgtgtgtcgaaggttaaaatgtatattgattgtagatgtgac	1832
Db	1757	aagtgatgtaaaagaagctatttctgtgtctcgtgtaacgacgaaatgtatgtgcggtgaaggtt	1816
OY	1823	acgaatcgtgtctctatagttaaaagcgggaagatctgttaatacttaccgtatgactgtacga	1882
Db	1817	acgacgcgagtttcaactaag---ccgtgtgaaactatgtgtctttaaactatgtatgaaacca	1873
OY	1883	gtgcacaagaagcgggagatattacagtttaactgttaactgttctcgaaggtgatatactacc	1942
Db	1874	aaggacccggacaaggatagttatataccgttaaatctgtctgtagaaaaacggttaagaactac	1933
OY	1943	atgaagttgtgtgaagcgtctcaagaacacaaaggtgtgttaaaagtcttaaatccagatactc	2002
Db	1934	acgaagtgacttcaaccataccgcatcttaggtgtggacacgcgtgaagaaaaatagaatactc	1993
OY	2003	gtgatattgaaatlaagaagaagttgggtatgtatcagttcactcgcgataatttgaatactag	2052
Db	1994	gtctatgaacaataaccagaccacatg---ccggtattatcacccaagaatcctctgaaagctg	2050
OY	2063	tagaagaagtgatgtgtcttccaattatagaatgtatcaaaagttcgaattcaatcaacgaca	2122
Db	2051	cttgaagaataatcatcgtgtacataccataacgaatacttcaaaaggtatgatttcaatgtctg	2110
OY	2123	tattccatagtgtgtgaagagtgatattcaactcgaatgtgtgtctgtgtgaacgcgcgtgt	2182
Db	2111	cccttaacggtgtgtatgtgtctgatactatgtgaacgtatgaacgaacgacaagcgaatccgttat	2170
OY	2183	cttgggtgttaaaagcgaacgatacgaacttctcgtgagaatgaagacgaaatgaactcgaatgcg	2242
Db	2171	cttgggtgttaaaagcgtgatatactctcgaatgtgtgaagaatgtatgtatttcaatcgaatgcg	2230
OY	2243	gtctcgtgtgaatgatactttaaagtgtgtgtgtcgtgtgaatgattgtctatattcttcgaaag	2302
Db	2231	gttaaaagcaaacgaccttacttacaacggtgtgcgaaggtcgaaatgtatcttctgtccacgttaag	2290
OY	2303	gtgaatgtgttaatgatacttctgaatcgtgcgaacggtgacatgataataatgaacttgcagaagt	2362

Db	2291	gcatgataagatatattaccgalttcgaagcgaatataatcatcattcttcgatt	2350
Qy	2353	caaatatctgatattatgatgtgaacggtaccaaagaggtatattgaacgaaatg	2422
Db	2351	cgaaacttaagaagatttacaattcgaaagaattbaaca---taattctgtcatcagaata	2407
Qy	2423	atcattcaggtagatttaacataccaagaaggtacatacacaattacaaaa----	2477
Db	2408	gcaaaaagagaagaagtgcaccatccaactggtccgagaggtgattttgctaagaag	2467
Qy	2478	----ttatcaagaataaaaaagcatcataaattgagacaactaatgtgtaagaatgta	2533
Db	2468	tgcctaattataaagaacaaatgaagaaatggaagaataatcatcgtgtcaaaatgcg	2527
Qy	2534	gtatatactctccgatccaattgataaaattt	2567
Db	2528	agcgatcacctccaagaagaatttgatgattctt	2561

RESULT 7

AAQ14238
ID AAQ14238 standard; DNA; 2794 BP.

AC AAQ14238;

DT 15-JAN-1992 (first entry)

DE LKT352 gene.

KW Antigen; leukotoxin; vaccine; Ikta; ds.

05 *Pasteurella haemolytica*.

PN W09115237-A.

PD 17-OCT-1991.

PF 17-OCT-1991; 91WO-CA00170.

PR 05-APR-1990; 90US-0504850.

PA (UYSA-) UNIV SASKATCHEWAN.

PI Acres SD, Bariuk LA, Potter AA, Lawman MJP;

DR WPI; 1991-324967/44.

PT Vaccines for *Pasteurella haemolytica* infection in cattle -

PT plasmin receptor, 50 k outer membrane protein and leukotoxin.

PS Disclosure; Fig 5; 92pp; English.

The LKT352 gene was prep'd. as follows: 1kta, an *Mae*I fragment contg. the gene was ligated into the *Sma*I site of pUC13 to form pAA179. From this, two constructs were made in the *pac*-based vector. pGH432::laci digested with *Sma*I. One, pAA342, consisted of the 5' *Aha*II fragment from 1kta while the other, pAA345, contained the entire *Mae*I fragment. Clone pAA342 expressed a truncated leishotoxin peptide at high levels while pAA345 expressed full length leishotoxin at very low levels. The 3' end of the 1kta gene of pAA345 was therefore ligated to *Sty*I/*Bam*HI digested pAA342 to yield pAA352 contg. the LKT352 sequence. The protein expressed from the vector can be used to prepare a subunit vaccine with other *P. haemolytica* antigens, e.g. fimbrial protein, plasmid receptor or 50K outer membrane protein. The vaccines can be used to protect cattle from respiratory diseases such as pneumonia, esp. shipping fever pneumonia.

Sequence 2794 BP; 930 A; 487 C; 599 G; 778 T; 0 other;

Query Match 29.3%; Score 814.4; DB 12; Length 2794;
Best Local Similarity 60.2%; Pred. No. 1,8e-170;
Matches 1538; Conservative 0; Mismatches 956; Indels 60; Gaps 9;

QY 53 caaagcttgatataaaatcttacttgctctcccaagat-----tatgaccgc 106
DB 29 caaaaactgggcaaaaaaatatctatctctatctcccaaatatccaatgatgac 88
QY 107 aaaaagctggactttaaatgatcttattaaagctgcgtatgaattagatgctgcgt 166
DB 89 aaaaagtgatggtttacacggatttgatccaagcgcgaaggttggggtatgaggtac 148
QY 167 tagcagaagagcctaatacactgtgaacagcaaaaaaatctgtttgacacagtaatcagt 226
DB 149 aagaagagaagcgaataatattgtcaacagctcaaacaggttttagagcagatccaacg 208
QY 227 ttctctctcaacaacactggtatgtctattcttcgcaaaaaattagaaaattcttac 286
DB 209 ctatgtgcttaactgtgcgtgcatctgttaccgcctccacaatattgataaattgctac 268
QY 287 aaaaactctaccaataagttagccaaggttagacaggtgagaaaatattgctgta 346
DB 269 agaaa-----actaaagcagcgcaagcattaggttctgcgcaaaagattgtacaa 319
QY 347 aattagtgaaagcaagtaattgatatcaacatlaagctctttttgggcactgcatlag 406
DB 320 atgcaataaagcgaacaaactgtatattctgcattcaactatttttagtcagatlag 379
QY 407 cgggtatagacttgattcttcttaatacaaaaagtgtgtcgcacccgagcttggtcta 466
DB 380 ctggaaatggatttagatgagccttacagaa---taacagcaaccaacagcctctgtcta 436
QY 467 aagctatgattgacttgattatagataatgtgtaactatctacagatgactacaaga 526
DB 437 aagctgcttgaggcgtacaacaattcaattatgtaaatattgcttaattctgataaaacac 496
QY 527 ttgaagcattctcttcacagttgcaaggttaggttcttactatactgcgaggtcaaggtc 586
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QY 587 tctctaataataggaacagttgcaaaacttaaat---tttctcaaaaacalcttggtc 643
DB 557 taaggactttagaggaacaaactccaataatcgtgtgacttgataaagctgcgcttggtc 616
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QY 704 atgcatcactgycgaacaaagttgctgcaggttttgaaatgaagcaatcagttatgta 763
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QY 1064 ttccgctgtcgtctgtagatctgtgtgtgacacgattgacactattagttgcaggtg 1123

DB 1037 tgtctgtcgtcagcgcgctcggttatgtcttcacggattcctattagatctcggga 1096
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QY 1364 atataatattggttgagttagcaggtattacaacaattgggtgaaacgcatlaagcggaa 1423
DB 1337 atacaacattggttgaatttagctgttatlagccggtttagtgaaaaagttcattgtgta 1396
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QY 1883 gtgcacaagaagcaggtatatacagtttaactogtlaaggttgcgtgaggtgatatctacc 1942
DB 1874 aagagaccggacgaagtagtattacgltlaaactgcttctgtagaanaacgggtlaaagcattac 1933
QY 1943 atgaagtttggaaagcgtccaagaacaaaggttgggtlaagcttactgaaacatccagratc 2002
DB 1934 acgaagtgaacttcaaccataccgcatltagtggcaacgcgttgaagaaataatgaaatatac 1993
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RESULT 8

AA041317
 ID AA041317 standard: DNA: 2794 BP.

XX AC AA041317;
 XX AC 23-AUG-1993 (first entry)
 DT XX
 DE Leukotoxin 352 gene in plasmid pAA352.
 XX KM Vector; LMT 352; flanking; recombinant; antigen; somatostatin;
 KM gonadotropin releasing hormone; rotavirus viral protein 4; ds;
 XX carrier protein; lactation; reproduction.
 OS Pasteurella haemolytica.
 XX
 FH Key Location/Qualifiers
 FT misc-feature 1..30
 FT /*tag= a
 FT /note= "flanking vector region"
 FT misc-feature 30..2772
 FT /*tag= b
 FT /note= "recombinant leukotoxin 352 DNA"
 FT misc-feature 273..2794
 FT /*tag= c
 FT /note= "flanking vector region"
 XX
 PN WO9308290-A.
 XX PD 29-APR-1993.
 XX PF 15-OCT-1992; 92MO-CA00449.
 XX PR 16-OCT-1991; 91US-0779171.
 XX PR 14-OCT-1992; 92US-0960932.
 XX
 PA (UWSA-) UNIV SASKATCHEWAN.
 PI Hughes HPA, Potter AA, Redmond MJ;
 XX WPI: 1993-152482/18.
 DR P-PSDB: AAR34545.

XX Immunological carrier system with enhanced immunogenicity -
 PT comprises chimeric protein comprising leucotoxin peptide or
 PT homologous protein fused to antigen esp. somatostatin or
 PT gonadotropin releasing hormone
 XX
 PS Disclosure: Fig 3; 95pp; English.
 CC Gene libraries of P. haemolytica A1 (strain B122) were constructed
 CC in lambda gtl1 and pUC13. Resulting clones were used to transform E.
 CC coli and individual colonies were pooled and screened for reaction
 CC with serum from a calf which had survived a P. haemolytica infection
 CC and that had been boosted with a conc. culture supernatant of P.
 CC haemolytica to increase anti-leukotoxin antibody levels. Positive
 CC colonies were screened for their ability to produce leukotoxin by
 CC incubating cell lysates with bovine neutrophils and measuring the
 CC release of lactate dehydrogenase from the neutrophils. A 4kb
 CC fragment was obtd. progressively larger clones were isolated by
 CC chromosome walking to isolate full length recombinants of ca. 8kb,
 CC in pAA114. The clone was subjected to restriction enzyme digestion
 CC to yield two clones, one expressing truncated leukotoxin peptide at
 CC high levels and the other expressing the full length leukotoxin at
 CC low levels. The 3' end of the lktA gene from the full length clone
 CC was ligated to the truncated gene clone to yield plasmid pAA352. The
 CC clone was used to produce chimeric proteins by gene fusion with an
 CC antigen coding sequence, e.g. the coding sequence of somatostatin,
 CC gonadotropin releasing hormone or rotavirus viral protein 4, i.e.
 CC leukotoxin works as a carrier protein to bring about a larger
 CC immune response than the antigen alone. Immunisation with these
 CC antigens can regulate growth rate, lactation and reproductive
 CC efficiency. See also AA041318-23.
 XX
 SQ Sequence 2794 BP; 930 A; 487 C; 599 G; 778 T; 0 other:

Query Match 29.3%; Score 814.4; DB 14; Length 2794;
 Best Local Similarity 60.2%; Pred. No. 1,8e-170;
 Matches 1538; Conservative 0; Mismatches 956; Indels 60; Gaps 9;

QY 53 caaagctggtatataaaatcttacttggtcttcccaagat-----tatgatcgc 106
 Db 29 caaaaacttggtggaataaaatattatctctctatctcccaaaattccaatgatgactg 88
 QY 107 aaaaaggtggaactttaaatgattttataaagctgtgagatgagttggtccggt 166
 Db 89 aaaaaggtatggtttacaggtatttgtaaaagcgcgaaggttggggatggaagttac 148
 QY 167 tagcagaagagccatacacaactgaaacagcaaaaatctgttgacagataatcagt 226
 Db 149 aagaagaagaagcgaataatattgcaacagctcaaacagtttaggcagatccaacg 208
 QY 227 ttcctctctcaacaactgtgtatgtctattctcgcacaacaattagaagaattcttac 286
 Db 209 ctatgtgcttaactgagcgtgtgcatgtgttalcgcgcacacaattgtataaattgttac 268
 QY 287 aaaaactcttacaataagtttagccaaggggtgacaggtgtaagaatattgacgtga 346
 Db 269 agaaa-----actaaagcagccaaagcattagttctgcgaagaagcattgtcaaa 319
 QY 347 aattagtaagaagtaagtattatcaacattaaagctcttcttgggacgtgacttag 406
 Db 320 atgcaataaagcgaacactgattatctgcatcaactcaattcttaggtcagttggtg 379
 QY 407 cgggtatagaactgtattcttatacaaaaaggtgatgctgacactgtgacttgctga 466
 Db 380 ctggaatggaattagatgagcccttacagaa---taacagcaaaccaactgctcttgta 436
 QY 467 aagctagattgactgtatgaatgagataattgtaattctcactcagagttaccacaaga 526
 Db 437 aagctggtcttgaggttaacaatcattatgtaaatatgtcaattcagtaaaaacac 496
 QY 527 ttgaagcattcttcacagtttagcaagtttagttctcactaatcagcaggtcaaaaggt 586

Db 497 ttgacgaatttggtgacaaattagtcgaatttggttcaacaactacacaatalcaaaagcgt 556
QY 587 tctctaataaggaaacaagtgtgcaaaacttaaa- - -tttctaacaacaaatcttggt 643
Db 557 taaggacttaaggacaaactcaaaaatcgtgtgactgtgaaagcgtggtgtgt 616
QY 644 tggaaataattactgtgtgttgcacgtgttcgcagcgtgttcgtttagcggttaaa 703
Db 617 tagatgtatctcgaagcttatacgtggtcgcaacagctgcaactgttaactgtcgataaaa 676
QY 704 atgcatactgacggcaaaaaggtgtgcaaggttttgtaataagcaatcaagttatgtgta 763
Db 677 atgcttcaacaagcttaaaaaggtgtggtcggtgtttgaattgtgcaaaccaagctgtgtgta 736
QY 764 atgtaacaaaagcaattcttcatagttttagacaaggtgtgtgtgtgtgtgtgtgt 823
Db 737 atattacaagaagcgtgttcttcttacaatttagcccaagcgtgtgtgcaaggttactt 786
QY 824 ctactgt 883
Db 797 caactgt 856
QY 884 caattatgaatgtcagacgaataaattcaatcaatgctaaagtgtgtgtgtgtgtgtgtgt 943
Db 857 cattgtcggtatgtgcgataaatttaacatgcaaaaagtttagagagttatgtccgaac 916
QY 944 aattcgaaaaattgt 1003
Db 917 gctttaaanaatttagctatgacgagataattatctagcgaataatcagcggggaacg 976
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Db 1037 tgtctgt 1096
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QY 1244 ttgataaaggt 1303
Db 1217 ttgaaaatgt 1276
QY 1304 ctgagcttaataaagagttgtgagctgtgacgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1363
Db 1277 tgaacttaacaaaaggt 1336
QY 1364 ataataatattgt 1423
Db 1337 ataacaactgt 1396
QY 1424 aagcttatgacaggt 1483
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Db 1697 tagacatgtctgtgaatgtgaataaaccagaagaacaaaattatgtccaaactgtgtgt 1756
QY 1763 cggcaatgtacatattctgt 1822
Db 1757 aaggt 1816
QY 1823 acgactgt 1882
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QY 1883 gt 1942
Db 1874 aaggaacagacagaggt 1933
QY 1943 atggaatgt 2002
Db 1934 acgaaggt 1993
QY 2003 gt 2062
Db 1994 gt 2050
QY 2063 tagaagaagtaattgt 2122
Db 2051 tgaagaanaattcgt 2110
QY 2123 tattcctatgt 2182
Db 2111 cctttaaaggt 2170
QY 2183 ttgt 2242
Db 2171 ttgt 2230
QY 2243 gt 2302
Db 2231 gtaagaacagacacataatcaacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2290
QY 2303 gt 2362
Db 2291 gcatgt 2350
QY 2363 caatatatctgtatattatgt 2422
Db 2351 cgaacttaaaaagatttaacattgtgaaaagttaaaa- - -taactgtgtcatcagaata 2407
QY 2423 atcatcaggt 2477
Db 2408 gcaaaaagaaggaagt 2467
QY 2478 - - -ttatcaagtaataaacaagatcaataaattgtgtgtgtgtgtgtgtgtgtgtgt 2533
Db 2468 tgcctaatattaaagcaactaaagatgtgaaataatcgtgaagaatcgtgtgtgtgtgt 2527
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RESULT 9

AAQ44760

ID AAQ44760 standard; DNA; 2794 BP.

AAQ44760;

XX 06-Oct-1994 (first entry)

QY 1304 ctgagctaaataaagagltggaagctgaaagctgtatgtcaatcaccacaacgttggg 1363
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 Db 1337 ataacaacattgtgtatttagctgtttagcgttttagtgaaanaagtccttagtgla 1396
 QY 1424 aagcttatgcagatcgtcttgaagaatggaagaagttggaagcgtgttccaatattactt 1483
 Db 1397 aagcctatgtgtatgctgttttgaagaagcaacacatlaaagccgataatattagtcagt 1456
 QY 1484 ttgagctgtaaaactgtgtatcagaacattagtaattcaaatlyggaaaaaacygaagcgt 1543
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 QY 1544 tgcatttcacttcgcttctgttgaacaggaagtaacatcgtggaagagtttaactatgt 1603
 Db 1517 tcttatcagaacgcctattatcgcgcgggaacagagcatcgtgaaacgttacaacag 1576
 QY 1604 gtaatacctctatataataaagtaaaatcgcgaagcgtlaaaaaactgcgaagttacag 1663
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 QY 1823 acgctgtgtcttctatagtaagaacggaagattgtgtaaatattactgtatgtgtaaga 1882
 Db 1817 acgacgcaggtcactatag---ccgtggaactatgtggtccttaacttattgtacaaca 1873
 QY 1883 gtgcaacagaagcagcaggtatatacagttacgtlaaagttgtccgcgaggtatattacc 1942
 Db 1874 aagagacgcgaagcaagtgatgataccgttaacgttctcgtgtaaaacggtataagcactac 1933
 QY 1943 atgaagttgtgaagcgttcaagaacaaagcgtggttaaacgtactgaactatccagttac 2002
 Db 1934 acgaagtgacttcaacccatccatcagattagtggtgcaacgcgtgaagaaaaataatattc 1993
 QY 2003 gtgattatgaattaagaagaattgtgtatgtgtatcagttcagcagataattgtaattag 2062
 Db 1994 gtcatlaacaataacacagacacatg---ccgttattacaacaaagaattaccttgaagcgtg 2050
 QY 2063 taagaagaagtaattgtgtctcaaatatgaatgattcaacaaagttcaaatcaacagca 2122
 Db 2051 ttgagaagaattatcgttaacacatacagaatccttaagaagtgatgaagttaaatgtatg 2110
 QY 2123 tattccatagtgtggaaggtgatagtattactcagatgtgtgtgtgtggaagcgcgtgtgt 2182
 Db 2111 cctttaaagcgtgtgagtggtgtcgtactatgtacggtlaaagcgcgaatgacgcgttat 2170
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 QY 2423 atcattcaggtatgatttaacttaacaaagtgtgtatcaactcaatttacaana----- 2477
 Db 2408 gcaaaaaagagaagtgacacttcaaaaactgttccgagagcgtgatttgcataaagaag 2467
 QY 2478 ----ttacaaagtaataaagacagatcaataattgagcacttaattgttaagatgta 2533
 Db 2468 tgcctaatataaagcaactaaagaatgagaanaacogagaataatcgtgtcaaatggtcg 2527
 QY 2534 gtatatacttcgcagatcaaatgtataaatttt 2567
 Db 2528 agcgatcacctcaagaagtgatgattctat 2561
 RESULT 10
 ID AAV61530 standard; DNA; 2794 BP.
 AC AAV61530;
 XX
 DT 24-DEC-1998 (first entry)
 DE
 XX Nucleic acid encoding Leukotoxin 352.
 DE
 KW Gonadotropin releasing hormone; GnRH; chimera; leukotoxin polypeptide;
 KW multimer; vaccine; tumour; Leukotoxin 352; LKT 352; Lkta; plasmid PAA352;
 KW cytotoxic; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..2781
 FT /*tag= a
 FT MISC_feature 31..2772
 FT /note= "Encodes recombinant leukotoxin peptide"
 XX
 PN W09806848-A1.
 PD 19-FEB-1998.
 XX
 PF 08-AUG-1997; 97WO-CA00559.
 PE
 PR 09-AUG-1996; 96US-0694865.
 XX
 PA (UWSA-) UNIV SASKATCHEWAN.
 XX
 PI Manns JG, Potter AA;
 DR WPI; 1998-159540/14.
 DR P-PSDB; AAW79568.
 XX
 PT Chimeric protein of leukotoxin and gonadotropin releasing hormone -
 PT useful for, e.g. preparation of vaccines for reduction of incidence
 XX of mammary tumours in mammals
 PS
 XX
 PS Disclosure; Figure 3.1-9; 118pp; English.
 CC The present sequence represents a recombinantly produced or chemically
 CC synthesized nucleic acid encoding leukotoxin 352 (LKT 352), derived from
 CC the Lkta gene that is present in the plasmid PAA352. This gene produces
 CC a truncated protein that has an estimated molecular weight of about
 CC 99 kDa and lacks the cytotoxic portion of the molecule. Thus this gene
 CC has a higher expression level than that of the full-length molecule.
 CC This can be used in the construction of a chimeric protein that comprises
 CC a leukotoxin polypeptide, several multimers, and a GnRH sequence. The
 CC chimeric protein can be used as a vaccine to help reduce the incidence of
 CC mammary tumours in a mammalian individual.
 XX
 SQ Sequence 2794 BP; 930 A; 487 C; 599 G; 778 T; 0 other;

Query Match 29.3% Score 814.4 DB 19 Length 2794;
Best Local Similarity 60.2% Pred. No. 1.8e-170;
Matches 1538; Conservative 0; Mismatches 956; Indels 60; Gaps 9;

QY 53 caaagcttgatgataaaatcttacttgctacttcccaaaagat-----tatgatcgcg 106
DB 29 caaaacttgaggcaaaaaaattatctctatattccccaatttccaatatgatgactcg 88
QY 107 aaaaagtgaggacttaaatgatattatcaaaagctgctatgaattagatgtgcgtc 166
DB 89 aacaaagtgatggtttactcaggaatttagtcaaaagcgccgaagaggttgggagttgaggtac 148
QY 167 tagcaaaagagcctaatacctacgctgaagcaaaaaaatctgttgcacagatcaatcag 226
DB 149 aagagaaagacgcaataatattgcacagctcaaaacaggtttagtcagatccaacgcg 208
QY 227 ttctctctccacacaactggtatgtctattcttcgaacaanaattagaaaagttcttac 286
DB 209 ctattgcttaacttgagcgctggtcattgtgttaccgcgtccacaatattgataattgctac 268
QY 287 aaaaacattcacaataagtttagccaaggttagacaggtgtagaanaatattgactcgtta 346
DB 269 agaaa-----actaaagcagcgcaagcattaggtcttcgcggaagacattgtacaac 319
QY 347 aattaggttaagcaagtaagtattatcaacatlaagctctctttttgggcactgcatlag 406
DB 320 atgcaataaagcaaaaacgttattatcttgcattcaatcttatttaggtctcagatttgg 379
QY 407 cgggtatagacttgattcttcttaatacaaaaaggtatgctgcacgtgactgcttgcta 466
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DB 677 atgcttccaacagctaaagaagtggtgcgggttttgatggaacaaaccaaagctgttggtta 766
QY 764 atgtaacaagaacaaattcttctcaatgatttttagcacaagctgtgctgcgtgccttaca 823
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QY 884 catttatgaatgacagagataaaatccaatcatgctaaatgctctctgatagtttgcaaac 943
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QY 1004 gtactattgaaagctcaatcaatacgaattagtaacgcatataggctacggttgcgttggt 1063
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DB 1037 tgcctcgtcgtcagcgcggtcgtgttatctgtctcaacggactgctcttatgtatctcggga 1096
QY 1124 ttacaggaattgactccttggaatttttagaagcgtctcaaacggaacatgtttgaaagtgtg 1183
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QY 1604 gtaatacctcttatataatcaagtttaaatctcgagcgtgtgtaaaaactggaagctacag 1663
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QY 2003 gtgattatgaattaaagaanaagtttggtatgttatacagctcaccagaataatttgaaatcag 2062
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QY	2003	gtgattatgaatgaagaaaagttgggtatggttatacagttaccgataatctggaatcag	2062
Db	1994	gtcatatgcaataaacccgacaccatg---ccggttatataccacaaagataacttggaaagt	2050
QY	2063	tgaagaagaatattgcttctcaatttaatgatacgtatccaagggttctaattcaacgaca	2122
Db	2051	tgaagaagaattatcgttacatcacatacagatattctttaaaggtagtaagttcaatgat	2110
QY	2123	tattccatagtggtgtaaggtgagatattactcgaatggttgctgctggagagaccgctgt	2182
Db	2111	cccttaacggtctgtctgtgtgctgcatacctatgcacggttaacgacgcaatgacgcgttat	2170
QY	2183	tctgttgtaaaagcacaacgatacgcacttctctggaagatgaagcgatgatctacgtgctg	2242
Db	2171	tctgtgtgtaaaagcgatgatattctcogatctgtgtggaatctgtgataatttatacgtatg	2230
QY	2243	gtctctgtcatgatacgtataaatggtgtgtgtgtgtaatgatacgtatataccttcggaa	2302
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Db	2291	gcgattgtatgtatattatataccagatcttcgaagcgcaatgataaattacatctctcgat	2350
QY	2363	caataatactctgaataattatgtgaacgtccaaaggggtattatagttaaaacgaatg	2422
Db	2351	cggaacttaaaaggttttaacattgtgaaaaagttaaaca---taactctgtcatcgaata	2407
QY	2423	atcattcaggttagtattataacataccaagatggtacataacatcaaatcttacaana	2477
Db	2408	gcataaaagagaagatgacatccaacgtgtccgagaggtctgattttgtctaagaag	2467
QY	2478	---tatccaagtataataaacgatacatataaatttggcacaactatgtgtaagaatgta	2533
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RESULT 12			
AAV61531			
ID	AAV61531 standard; DNA; 2934 BP.		
XX	AAV61531:		
AC			
XX			
DT	24-DEC-1998 (first entry)		
XX			
DE	Nucleic acid encoding LKR-GnRH.		
XX			
KM	Chimeras: pCB113; LKT 352; GnRH; Gonadotropin releasing hormone; multimer		
KW	cytotoxic activity; antigen presentation; immune response; vaccine;		
KW	tumour; ss.		
XX			
OS	Synthetic.		
XX			
Key	Location/Qualifiers		
FT	1..2934		
FT	CDS		
	/*tag= a		
XX			

PN WO9806848-A1.
 XX 19-FEB-1998.
 PD 08-AUG-1997; 97WO-CA00559.
 PF 09-AUG-1996; 96US-0694865.
 XX (UYSA-) UNITV SASRATCHEMAN.
 XX
 PA Manns JG, Potter AA;
 PI WPI, 1998-159540/14.
 DR P-PSDB; AAM79569.
 XX Chimeric protein of leukotoxin and gonadotropin releasing hormone
 PT useful for, e.g. preparation of vaccines for reduction of incidence
 PT of mammary tumours in mammals
 PS Disclosure; Figure 5.1-8; 118pp; English.
 XX
 XX The present sequence represents the nucleic acid encoding the LKT-GNRH
 CC chimeric protein from PCB113. This plasmid contains the LKT 352
 CC polypeptide (AAM79568) fused to four copies of the GNRH peptide. This
 CC chimera lacks cytotoxic activity which enables there to be an increase
 CC in antigen presentation and thus an optimal immune response. The removal
 CC of this region also enables the truncated LKT to be expressed at much
 CC higher levels and allows the amount of antigen administered to be
 CC reduced. This chimeric protein comprises a leukotoxin polypeptide,
 CC several multimers, and a GNRH sequence. The chimeric protein can be used
 CC as a vaccine to help reduce the incidence of mammary tumours in a
 CC mammalian individual.
 XX
 SQ Sequence 2934 BP; 950 A; 529 C; 650 G; 805 T; 0 other;
 Query Match 29.3%; Score 814.4; DB 19; Length 2934;
 Best Local Similarity 60.2%; Pred. No. 1.8e-170;
 Matches 153; Conservative 0; Mismatches 956; Indels 60; Gaps 9;
 QY 53 caaagcttgatataaaatcttactgtgctatcccaagat-----tatgacgcg 106
 DB 29 caaaactcgggcaaaaataatccctatattccccaatataccaatagatctcg 88
 QY 107 aaaaagtgaggacttaattatttaagctcgtatgaatagttatgctcgtt 166
 DB 89 aaaaagtgaaatggtttacagattatgcaagcgccgaagagttggagttgagttac 148
 QY 167 tagcagaagagcttaatacactcgaacgaacaaaataatcgttgacacagtaatacgt 226
 DB 149 aaagaagaagacgcaataatattgcaacagcacaacagtttaggcagattcaaacg 208
 QY 227 ttctctctcaacaactgtgattgtattcttcgcaaaaataatgaagaagtctac 286
 DB 209 ctaatggtctactcgtgagcgttggtatggtatccgcacaaatgataaattgctac 268
 QY 287 aaaaactctcaacaatagttagcgaaggttagacagtgtagaataatgtagctga 346
 DB 269 agaaa-----actaaagcagcgcaagcattaggttcgccaagcattgtaaaa 319
 QY 347 aattggttaagcaagatgatatatacaacatagctctttttggcactgattag 406
 DB 320 atgcaataaagcaaaactgtatattctgcatcattcaatcttttagcctagattcgg 379
 QY 407 cgggtatagaacttattcttcaatcaaaaaggtgacgtgcactgagcttggtgta 466
 DB 380 cgggaatggtatttagatgagccttacagaa---taacagcaaccaaatgctcttgta 436
 QY 467 aagctagtttgaactgattatgagataatgtgtaatactatcgaagttactacaaga 526
 DB 437 aagctggtcttgagcgaacaaatcattgaataatgtaataatgtaataaagaacac 496
 QY 527 ttgaagcattctctcaacagttagcaagttaggttctactatalcgacgagtaagct 586

DB 497 ttgaagcattctctcaacagtttagcaagtttaggttctactatalcgacgagtaagct 556
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 QY 644 tggaaataattactgttctgcatcagcattcttcgagccttgctttagcagataaa 703
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 QY 704 atgcactgactgcaaaaagttgctcgaagtttgaattgaataagcaatcaagttgta 763
 DB 677 atgctcaacagcgtcaaaaaggtggtggttggattggaatggcaacaaactgttgta 736
 QY 764 atgtaacaacaaactcttcataatgttttagcaacaacggttgctggtcgtatcaa 823
 DB 737 atataccaacgcttctctcttcttcttcaattttagcccaacggttgacagattatctt 796
 QY 824 ctactggtgctgtgctgcttcaattactcagatattgattggaattagctcttggt 883
 DB 797 caactggtcctgtgctgcttcaattgcttctactcgttctctctcttgagttccattag 856
 QY 884 catltagatgacagagataaattcaatcagtcgaatgctcttgatagttgcaaac 943
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 QY 944 aattccgaataattggtcgtatgagtggtggtatattatggtcgtatatacagcgtgtg 1003
 DB 917 gctttaaataattagcgtatgacgagataattatagcagaataacagcgggaaacag 976
 QY 1004 gtactattgaagcttcaataactcaacatagtagcagattaggtcagtttctggtg 1063
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 QY 1064 ttccgctcgtctgtgagatcgtcgtgtgtgacacgaattgcactatagttgaggtg 1123
 DB 1037 tgcctcgtcgtcagcgcgctcgttattgcttcaacggttgccttattagttatctgga 1096
 QY 1124 ttacagatgtatcctgtgaattttagaagcgtcacaacagcaatggttgaagtgtg 1183
 DB 1097 ttaccggtgtaattctcagatctcgaatattcctaacaacgaatggtttagcagcgtg 1156
 QY 1184 ctacacgtttacaagtttaaatgttaggtggtggaagaacgaatggtcgtcgaactat 1243
 DB 1157 caataaaatctcaacaacaaatgttagaattggaataaaataacacggttaagaactact 1216
 QY 1244 ttgataaaggctatgattctcgtatgctgattatttagctaaataaattttgt 1303
 DB 1217 ttgaataatgtttagcgttgcgttctcttgcgaatttacaagataataatgaaattctt 1276
 QY 1304 ctgagcttaataaagattggaagcgtgaagcgtgtttagtgaatccacaacagcgttgg 1363
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 QY 1364 ataataattgtgtgattgacggtatcaacaaattggttgaacgcataacgaacgttgg 1423
 DB 1337 ataacaacattgtgtattgacggtatgacggtttaggttagtgaagaagctttaggtga 1396
 QY 1424 aagctttagcagatgctttagaagatggaagaagttgaagcgtgttccaataactt 1483
 DB 1397 aagctttagttagcgtttagaagaagcacaacatcaatgaacgcgtatgaattagtcagt 1456
 QY 1484 tgaatgtcaaacgtgatatcatagactttagtgaattgaataatggaataaagcaacgct 1543
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 QY 1544 tgcatttcaactcgtttagtcaacagcaggaatcagttacgtgtaacgtttagt 1603
 DB 1517 tcttattcagaagcgaattatgacgcgggaagaacagcgtggaacggttacaacag 1576
 QY 1604 gtaatactcttatataatgaatgaatcgaagcgtgtaaaaactgcaagttacag 1663

Db	1577	gtaataatgatatattatccaagctcaataataaccggtgtagatgctcggaanaattcaag	1636
Qy	1664	atggagagcctaattcttaaatagattctctaaagttaatcaocgctgttagccgagaacg	1723
Db	1637	atggtgagaagaattctactactttgatttctaactacagcttgctoaagtgattgattgaat	1696
Qy	1724	aaggccagacgagatttgctctaatatgtaatgcaaaa-----g	1762
Db	1697	tagacaatagtcttgaaattgtaactaaaccaaagaacaaaataattatgcgaacttggtg	1756
Qy	1763	ctcgcaaatgcgctaacttctgtgtgtgcgaagcgaaataatgaattatgattggtgaatgac	1822
Db	1757	aagggtgatgcgaacgcatattgtgtgtcttcgcgtgacagcggaaattgatgtcgtgtaaaggtc	1816
Qy	1823	acgacgtgctctctatagtaaaagcagcgaggatttggttaataattacgttagatgtaacga	1882
Db	1817	acgacggattctactatag---ccgtggaataactatggtgctttaaactatgtaacaa	1873
Qy	1863	gtgcacaagagagagcgagttatacagtttaacgtgaactcgtgaagtgtgtcagaggtgatatcacc	1942
Db	1874	aagagacaggcgcaaggtatgataaccgttaaacctgttcctgtagaaacgggtataagcactaac	1933
Qy	1943	atgaagctgtgaagcgtctacagaagaaccaaaggttggtgttaaaacgttaactgaactatccagtaatc	2002
Db	1934	acgagagtgacttcaaccataccgcatcttagtggtgcacacggtagaagaaanaataagatatatc	1993
Qy	2003	gtgatattgataatgaanaaaagttggtgatgtgtatccagttacgcgtatacgaataattgaaatcacg	2062
Db	1994	gtctaatcaataaaccgacacacatg---ccggttatatacccaagaagatacctcttgaagactgt	2050
Qy	2063	tagaagaagaataattggtcttccaaatgaataagatattcaaaagttcttaattcaaacgaca	2122
Db	2051	ttgaaagaataattacggtatcacatcacataaagaatactttaaaggttgatgaattcaatgattgt	2110
Qy	2123	tattccatagttggtgaaggttgatgataatttcaactgcgaatggtgtgtgtgtgcagacccgctgt	2182
Db	2111	cccttaacggttggtgattgtgtgcgtacattgacgtatgcggtgaagcagcgcaatgacccgttat	2170
Qy	2183	ttggtgtgtaagcgcaacgatacgactcttcctgcgagatggaagcggaatgataattactgatatgcg	2242
Db	2171	ttcgtgtgttaaaagcgatgataatctcgaatgcgtggaaggttgatgataatttccatgatgcg	2230
Qy	2243	gtctcgtgtgattgattatgaataggtgcgtgcgtgaatgatgtatcttcaatacttccggaag	2302
Db	2221	gtaaagcgcaacgacctataacacggtgcggaaggtgcgattatcttgcgttaaccggttaag	2250
Qy	2303	gtgatgtgtaattgatacttgtaacgtatgcgtgcagcggaatgataaattagcaatttgcgaatg	2362
Db	2291	ggcgtgtgtaatgattatratatraccgattctgcagcgcaatgataaattatcatcttcctgatt	2350
Qy	2363	caaatatattcgtatatatgatattggaacggtacccaagaaggttatatatgtaataacgaatg	2422
Db	2351	cgaaacttaaaagattttaaactttgttaaaaaggttaaaca---taactgttcatcgcgaata	2407
Qy	2423	atcatacaggtagattatgaacataccaagaatgtgtacataacataccaatttacaacaa-----	2477
Db	2408	gcataaaaaggaaggtgacatcatcaaaactggttcccggaaggtcgtattttgctaaagag	2467
Qy	2478	-----tatacaagtaataaacaacagatcataaaattgagcaactaattgtgtaagaatgta	2533
Db	2468	tgcttaattataaagcaactaaagatgtagaanaatacgaaanaatacgttcaaaatgcg	2527
Qy	2534	gttatatacacttccgatccaattatgataaaatttt	2567
Db	2528	agcggatcacctccaagaaggttattgatacttat	2561

RESULT	13
AA054213	
ID	AA054213 standard; cDNA to tRNA; 3229 BP.
XX	
AC	AA054213;
XX	

DE	01-JUL-1994 (first entry)
XX	
DE	Bovine IFNgamma/LKT chimeric gene from plasmid pAA497.
XX	
KW	Bovine: Interleukin-2; IL2; P. haemolytica; leukotoxin; LTK; IFN;
KM	ltkA; chromosome walking;; fusion protein; vaccine; interferon; gamma;
KW	monoclonal; polyclonal; antibody; ds.
XX	
OS	Pasteurella haemolytica - chimera.
OS	Bos taurus - chimera.
XX	
FH	Location/Qualifiers
FT	CDS
FT	1..3210
FT	/*tag= a
FT	/product= IFNgamma-LKT chimeric protein.
XX	
FN	US5273889-A.
XX	
PD	28-DEC-1993.
XX	
PF	22-AUG-1990; 90US-0571301.
XX	
PR	22-AUG-1990; 90US-0571301.
ER	16-OCT-1991; 91US-0777715.
XX	
XX	(CIBA) CIBA GEIGY CANADA LTD.
PA	(UYSA-) UNIV SASKATCHEWAN.
XX	
PI	Campus M, Hughes HPA, Potter A;
XX	
DR	WPI, 1994-006687/01.
DR	P-PSDB; AAR52748.
XX	
PT	Immunogenic fusion proteins of gamma-interferon and immunogenic
PT	leukotoxin - used in vaccines and to raise monoclonal and polyclonal
PT	antibodies
XX	
PS	Claim 3; Fig 7; 56pp; English.
XX	
CC	This sequence encodes a fusion between bovine gamma interferon
CC	(IFNgamma) and Pasteurella haemolytica leukotoxin (LTK). The
CC	leukotoxin gene, ltkA, was isolated from a gene library of P.
CC	haemolytica by chromosome walking. Immunogenic fusion proteins
CC	such as this can be used in vaccine compositions. It can also be
CC	used to raise mono- and polyclonal antibodies.
XX	
XO	Sequence 3229 BP; 1085 A; 571 C; 690 G; 883 T; 0 other;

Query Match	29.3%	Score 814.4	DB 15	Length 3229
Best Local Similarity	60.2%	Pred. No. 1.9e-170		
Matches 1538	Conservative 0	Mismatches 956	Indels 60	Gaps 9
QY	53	caaaagctcgtgataaanaaatcttactctgctatcccaagaat-----tatgacgcg	106	
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QY	107	aaaaagctgagacttaaaatgattatataaagctgcatgtaathagtgatgctcgt	166	
DB	89	aacaagatgatactggtttaccaggaatttagtcaaaagcgccgaagaagttggatctggatc	148	
QY	167	tagcgaagagcgctaatcactatgcacagcaacgaaaaaatctgtctgcacagtaaatcagt	226	
DB	149	aaaggaagaacgcataataattatgcacagctcaacagctttagcagcatccaacg	208	
QY	227	ttctctctccacacaacatggtbattgctattcttcgcaacaaattagaaaaagttcttc	286	
DB	209	ctattgcttaactgagcgtgagcatgtgttatccgctccacacaatgtgtaaatgtctac	268	
QY	287	aaaacattctccacataagttagcccaaaaggttagacagctgtagaanaattatgacgta	346	
DB	269	agaa-----actaaagcagggccaaagcatggtcttcgtccgaaaacattgtacaa	319	

QY 347 aattggttaagcaagtaatgtatatatacaactaagctctttttggcgacttag 406
Db 330 atgcaataaagccaaactatattatctgcatcaactatcttaagctcagatattg 379
QY 407 cgggtataagacttgattctttaacaaaaggtgagtgcgactgctgttggtgcta 466
Db 380 ctgggaatggtatttaagtgcgaccttaacgaa---taacagcaaccaacgtccttgcta 436
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Db 437 aagctgcttgagcttaacaaattcatttaattgaaaataattgcttaattcagtaaaaaacac 496
QY 527 ttgaagcatttcttcacaggtagcaaggttaggttctactataatcgagcgtlaaggtc 586
Db 497 ttgaagcaatttggtgaagaataatgacatlttggttcaaaaataacatacaaggtc 556
QY 587 tctcaataatagaacaaagttgtcaaaacttaaat---tttcttaaaaactctgtgt 643
Db 557 tagggaactttaggaacaaactcaaaaataatcgtgtgacttgataaagcttgcttggt 616
QY 644 tggaaataattactggtttgtctatcaggaattcttcgaggtcttgcttaagcgataaa 703
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QY 704 atgcacgcagctggcaaaaagttgctgcaggttttgaattgaagcaatcaagttatgta 763
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Db 1337 atacaacattgtgtatttagctgtattagcgttttagtgaaanaagttcccttagtgta 1396
QY 1424 aagcttatgcagatgcttllagaagtgcgaagaaggtgaagcgtgttccacataattactt 1483

Db 1397 aagctatgtgtagtgcgttttgaagaaggaacacacattaaagccgataaattagtagcgt 1456
QY 1484 tggatgcttaaaaactggttctatagacatttagtaattcaaatggtggaanaaaagcgaagct 1543
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Db 1517 tcttatacgaacgcgcattattatgacgcgggagacagacatcgttgaacgctgaacaacag 1576
QY 1604 gtaaatctctatataatlaaagttaaatctcgagcgtgtgaaaaaactgycgaattacag 1663
Db 1577 gtaaatatgaataatattccaaagcctcaatlaaacggtgtagatagcttgaanaattacag 1636
QY 1664 atggagaggtggttcttaattagatttctcaaatgttatcgaatttagcgttgagcggagac 1723
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Db 1934 acgaagttgactcaaccataccgcatlagttggtgcaacggttgaagaaanaatlaagatalc 1993
QY 2003 gtgattatgaatttaagaanaagtttgggtatggttatcagttctacgaataatttgaataag 2062
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QY 2063 tagaagaatattgttctcaattlaaagtatlaaaggttcaaatcaacagca 2122
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QY 2423 atcatcaggttagatttaacatbacaagatgttatacatcaatcaaatlacaaaa----- 2477
Db 2408 gcaaaaaagagaagtgacacttcaaaaactgttcccgaggtgctgatttgcataagaag 2467
QY 2478 ----ttatcaagaatataaacagatctcaaaaatttgagcaactaattgttgaagatgtta 2533

DB 2468 tgcctaatataaagaactaagatgagaaaaatcgaagaataatcgcgtgcaaaatgagcg 2527
QY 2534 gtatataccttcgcgcgaatgatgataaattt 2567
DB 2528 agcgcgatccactcaagaagtgatgattctat 2561

RESULT 14
AAT60033
ID AAT60033 standard; DNA: 3229 BP.
XX
XX AAT60033;
AC
XX
DT 12-MAY-1997 (first entry)
XX
DE Chimeric protein #2 coding sequence.
XX
XX RTX cytotoxin; cytokine; immunogen; chimeric protein; cytokine; vaccine;
KW Interleukin-2; IL-2; gamma interferon; gamma IFN; leukotoxin; pneumonia;
KW Pasteurella haemolytica; LKT352; respiratory disease; shipping fever;
KW fibrinous pneumonia; cattle; therapy; ds.
XX
OS Synthetic.
XX
XX
XX Key Location/Qualifiers
FH CDS 1..3210
FT /*tag= a
FT /product= chimeric protein #2
FT
FT
FT
FT
PN US5594107-A.
PN 14-JAN-1997.
XX
XX 22-AUG-1990: 90US-0571301.
XX
XX 20-DEC-1993: 93US-0170126.
PR 22-AUG-1990: 90US-0571301.
PR 16-OCT-1991: 91US-0777715.
XX
XX (CIBA) CIBA GEIGY CANADA LTD.
PA (UYSA-) UNIV SASKATCHEWAN.
XX
XX Campos M, Hughes HPA, Potter A;
PI
XX MPI: 1997-099529/09.
DR P-PSDB; AAM13867.
XX
XX Immunogenic chimeric proteins comprising cytokine linked to RTX
PT toxin - useful in vaccines, esp. against shipping fever in cattle
PS
XX Claim 13: Column 37-46; 56pp: English.
XX
XX AAT60032 and AAT60033 represent the coding sequences for immunogenic
CC chimeric proteins of the invention. This sequence represents a chimeric
CC protein containing the bovine gamma interferon (gamma IFN) sequence and a
CC leukotoxin sequence. The chimeric proteins of the invention comprise a
CC cytokine, selected from Interleukin-2 (IL-2) and gamma IFN, linked to at
CC least one RTX toxin epitope (preferably the sequence shown in AAM13865).
CC The RTX toxin used to provide the epitope sequence is preferably a
CC leukotoxin, especially the full-length Pasteurella haemolytica
CC leukotoxin. Alternatively, the leukotoxin is a truncated leukotoxin
CC lacking leukotoxic activity, especially LKT352. The chimeric proteins
CC can be used for the production of vaccines against respiratory diseases
CC such as pneumonia, particularly fibrinous pneumonia caused by
CC P. haemolytica, including shipping fever in cattle.
XX
XX
XX Sequence 3229 BP; 1085 A; 571 C; 690 G; 883 T; 0 other;

Query Match 29.3%; Score 814.4; DB 18; Length 3229;
Best Local Similarity 60.2%; Pred. No. 1.9e-170;
Matches 1538; Conservative 0; Mismatches 956; Indels 60; Gaps 9;

QY 53 caaagctggtattaaanaatcttacttggctatctcccaaat-----tatgattccg 106
DB 29 caaaactggtgggcaaaaaaattatccctcattatccccaattaccatattgattcgt 88
QY 107 aaaaagtggtgacttaaatgatttattaaagctgctgattgattgattgattcgcgtt 166
DB 89 aacaagtgattgtttaccagatttagtcaaaagcgccggaagatttgggtattgaggtac 148
QY 167 tagcagaagagccttaacacagcgaacgaacaaanaatctgttgcacagtgattatcagt 226
DB 149 aagaagaagaagcgaataaataattgcaacagctcaaacagatttaggcagattccaacgc 208
QY 227 ttctctctccacacaactggtattgctatttctgcacaanaattagaagaagttctac 286
DB 209 ctattgcttaacttgcgtgctgatttggcttattccgtctccacaattgataattgttac 268
QY 287 aaaaacttaccataaagtagccaagaaggttagacagtgtagaanaattgattgctga 346
DB 269 agaaa-----actaaagccagccagcattaggttctgcggaagaagctgtacaaa 319
QY 347 aattaggtaaagcaagtaagatttatcaacattgaagctctttttgggagctgattag 406
DB 320 atgcaataaagccaaaacggtattatctgcatlcaattcattttaggtcagattgtg 379
QY 407 cgggtatagactgtattctttaaatacaaaaaggtgtagtgcacctgattggtgcta 466
DB 380 ctggaatggttttagatgaagccttacaaga-----taacagcaacaaacagctcttgcta 436
QY 467 aagctagattgacttgattgaatgaatattggttaattcattcagatgattccaacga 526
DB 437 aagctgcttgtagcttaacaaattcattgaataattgtcatttgcgttaaaaaaacac 496
QY 527 ttgaagatttttcttcagtttagcaagtttagtttactattatgcagcgttaaaagct 586
DB 497 ttgacgaatttggtagcaaatattgtaatttgggttcaacaatacaaaatatacaagct 556
QY 587 tctctaataagaaagaattgcaaacattaaat---tttctaaacaacttgggt 643
DB 557 taggaatttaggaagaataaactcaaaaatatcgttgacttgtaaaagctggttgggt 616
QY 644 tggaaataattggttgcctatcaggaattctgcagagcttgcgttgcggaataaa 703
DB 617 tagatgtattcctcaggtctattatcggtgcgaacagctgcatgttcttgcagataaaa 676
QY 704 atgcattgactggaacaaaaggtgctgcaggttttgaattgaacgaatcaagttatgta 763
DB 677 atgcttaacagcgttaaaaaggtggtggtgtttagatggcaaacaaagttgtgta 736
QY 764 atgtaacaaagcaatttcttcataatgttttagcacacagtggtgcgtgctatcaaa 823
DB 737 atattaccaagcgtttcttcttaccattttagcccaagtggtgcagcaggttattcctt 796
QY 824 ctactgtgctgttgcgttcttaattacttcattcattatgatttggcaattagtccttgg 883
DB 797 caactggtcgtggtgcgttcttaattgcttcttactgttcttctgtcattagccattag 856
QY 884 cattatgaatgcagcagataaattcaatcatgtaattgcttgcagattgttgcacaaac 943
DB 857 catttgcgttattgcccgaataattatcatcatgaanaaagtttagagattagtcgcaag 916
QY 944 aattccgaanaatttggcgtatgagtgatcatattatggtcgtgaatacagcgttgggtg 1003
DB 917 gctttaaanaattaggtctatgacggagataattattatagcagaataatcagcggggaacag 976
QY 1004 gtaatttgaagcttcaatlaactaaattagtagcagcattaggttgcgttgcgttgcgtg 1063
DB 977 ggaattattgattgcattcgttaccgttaataataaccgattggtgcgttgcgttgcgtg 1036
QY 1064 ttccgctgctgctgtagatctgctgtgtgtggtgcacagcattgcaattatgattgcaggtg 1123
DB 1037 tgcctgctgctgagccgctggtatttcttaccagcattgcttattagttatcgttggaa 1096
QY 1124 ttacagattgattcctcgtgaattttagaagcgtctaaacggcaattgttggaaagtgtg 1183

Db 1097 ttacccggtgtaattcttcacgattcttcgcaatattcctaacaacgaacgaattgttagcacgttg 1156
 Qy 1184 ctaacccgttctaagagtaaaattttaagatggaagcaaaagcggtgcgaacattt 1243
 Db 1157 caaataaattcctaacaacaaattttagaattggaagaaanaaaataatcgcgttaagaactt 1216
 Qy 1244 ttgataaagcgtatgattctcgttatgctgtcttatttagactaactaaattttgt 1303
 Db 1217 ttgaaataggtttagcgtcccggttattcttgcaatttacaagataatgaaattttac 1276
 Qy 1304 ctgagcttaataaagagttgaagctgaacgtgttattgcaatcccaacaacgttgg 1363
 Db 1277 tgaacttaacaagagttacaagcgacgltgcattcgtcttacttaagaacgaattgg 1336
 Qy 1364 ataataatattggtgagttagaaggtatcacaatttggtggaacgcaatagaacggaa 1423
 Db 1337 ataacaacattggtgattttagctgtattagcgttttagcggaanaagctccttagtgta 1396
 Qy 1424 aagcttatgcagatgcttttgaagatggaagaaagttgaagctgtgtccaaattactt 1483
 Db 1397 aagcctatggtatgcgttttgaagaagcaacacattaaagccgataatttagtaagct 1456
 Qy 1484 tggatgtcaaaacgtgatacctagaacattagtaattcacaatggggaanaaaacgaagct 1543
 Db 1457 tggattcgcgaacacgtattatttgaatgtagtaattcgggtlaaagcgaaacacgaata 1516
 Qy 1544 tgcatttactcgccttctgttlaacagcaagcaatgaaacgttgaacgttcaactaatg 1603
 Db 1517 tctatttcgaacgcacattatttgaacgcgggaacagacacgtgaaacgttacaacaaag 1576
 Qy 1604 gtaataactcttataatataagtaaaatcgcgaacgttgaanaaaactgcgaattacag 1663
 Db 1577 gtaaatatgaaataattacacagctcaaatlaaacggttagatagctggaanaattacag 1636
 Qy 1664 atggaagagcgagttcctaatttagattctctaagattacagctgctgaacggagacag 1723
 Db 1637 atgtgtgcagcagattctacacttatttgaactaacggttgcacggttattgttgaat 1696
 Qy 1724 aagcacaagcagatgtgtctaaatagtaaaatgcaaaa-----g 1762
 Db 1697 tagacaatgtcgtgaatgttaactaaacaaagaacaaataattatgccaactgtgtg 1756
 Qy 1763 ctggcaatgacgatacttctgttgcgaagtaaaatgaaatagatgtgtgagatggac 1822
 Db 1757 aaggtgtgatacaacgtatttctgttctgttgcacggaacgaatgatggcgttgaagtt 1816
 Qy 1823 acgctcgtcttcttataagtaagaacgaggaattgtggaatattacgttagatgtgacga 1882
 Db 1817 acgacccagttcacataag-----ccgtggaacactgtgtgcttactatgtatgacaaca 1873
 Qy 1883 gtgcaacaagaagcagagtagtatalacagttlaactglaaggtgtcgaagtgatattctacc 1942
 Db 1874 aagagaccgagcagagtagtattacacgtlaaatcgttctgtagaaacggtlaaagcacctac 1933
 Qy 1943 atggaagtgtggaagcgtcaaaaaccaaagtggtgaaacgtacgtgaacactaccagatc 2002
 Db 1934 acgaagtgtacttcaaccataccgcatagtggtggaacccgtgaagaaataaataaataatc 1993
 Qy 2003 gtgatttgaatgaagaaagtgtgtagtattcagttcagttacggaatattgaatcag 2062
 Db 1994 gtctatgaataaaccagcacatg-----ccggtattacacaaagaataccttgaagaagctg 2050
 Qy 2063 tagaagaagtaattggttctcaatttaattgattatcaaaagttctaataccaagaca 2122
 Db 2051 ttgagaagaattatcgttaccatcacatacagaatattccttaagaagtgaatgaatgattg 2110
 Qy 2123 tatcccatagtggtggaaggtgattatctcagtggtgtgctggtggaacgcgcctgtg 2182
 Db 2111 cctttaaagtggtgtagtggtgcatactattgacggtlaaagcgaatgacgtctat 2170
 Qy 2183 ttggtgtaagcgaacgattgacttctgagatggaagcgaattactgcatgagcg 2242

Db 2171 ttggtgtaaagcgatgatatactcgaatgtgtggaatgtgatattttagcatgagcg 2230
 Qy 2243 gtctcgtgatgatgatataatgtgtgtgtgctggtgaatgatgtcatatactttcggaag 2302
 Db 2231 gtaaaagcaacgacctattacaacggtgcaagggagatgatatttctgtcacgtaag 2290
 Qy 2303 gtgagtgaatgatattctgttcagatggaacggtgcaatgaataatgacatttgcagatg 2362
 Db 2291 gggatggaatgatattatctacgattctgacggtgcaatgaataattatcattctctgtt 2350
 Qy 2363 caataatactgataattttagattgaacgtaccaaaagaggtattatagttaaacgaatg 2422
 Db 2351 cgaacttaaaagatttaacatttgaanaaagttaaca-----taattctgtcatcagaata 2407
 Qy 2423 atcatcaggtgagtatttaacacagatgtgtatatacatcaaatcacaana----- 2477
 Db 2408 gcaaaaaagaaagatgtaccccttcaaaactggttccggagagcgattttctaagaag 2467
 Qy 2478 -----tlatcaaaagtaataaacaagatcataaaatgagcaactaattgtlaaagatgta 2533
 Db 2468 tgcctaattataaagcaactaaagatgagaataatcgaagaatactcgtgtaaaatgagc 2527
 Qy 2534 gttatatacttccgattcaaatgtataaattt 2567
 Db 2528 agcgtatcaccctcaagcaagttgatgtcttat 2561

RESULT 15
 AAAT2484
 ID AAAT2484 standard; DNA; 3229 BP.
 AC AAAT2484;
 XX 19-DEC-2000 (first entry)
 DT
 XX
 DE Bovine gamma-IFN/Pasteurella haemolytica leukotoxin fusion gene.
 XX
 KW Bovine gamma-IFN; gamma-Interferon; leukotoxin; LKT; respiratory disease;
 KW pneumonia; shipping fever; cattle; livestock; anti-Pasteurella vaccine;
 KW immunogen; ds.
 XX
 OS Chimeric - Bos taurus.
 OS Chimeric - Pasteurella haemolytica.
 OS
 XX
 FH Location/Qualifiers
 FT CDS 1..3297
 FT /tag= a
 FT /product= "Bovine gamma-IFN/Pasteurella haemolytica
 FT leukotoxin fusion protein"
 FT
 PN US6096320-A.
 PD 01-AUG-2000.
 XX
 PE 20-OCT-1997; 97US-0954418.
 XX
 PR 20-DEC-1993; 93US-0170126.
 PR 22-JUL-1996; 96US-0681479.
 PR 22-AUG-1990; 90US-0571301.
 PR 16-OCT-1991; 91US-0777715.
 XX
 PA (UWSA-) UNIV SASKATCHEWAN.
 PA (CIBA) CIBA GEIGY CANADA LTD.
 PI Campos M, Hughes HPA, Potter A;
 XX
 DR WPI: 2000-531543/48.
 DR P-PSDB; AAB21074.
 XX
 PT Vaccine for stimulating immunity against pneumonia comprises chimeric
 PT protein comprising gamma-Interferon and leukotoxin derived from
 PT Pasteurella haemolytica
 XX

PS Example 5: Column 37-46; 56pp; English.

XX This sequence represents DNA encoding a fusion protein comprising
CC bovine gamma-interferon (gamma-IFN) and Pasteurella haemolytica
CC leukotoxin (Lkt). The fusion protein is immunogenic, and may be
CC used in an anti-Pasteurella vaccine composition. Pasteurella
CC species, especially Pasteurella haemolytica, are responsible for
CC respiratory diseases in a range of agricultural animals, most
CC particularly cattle, but also sheep, pigs, horses and fowl. Shipping
CC fever is the most economically important respiratory disease associated
CC with Pasteurella species, affecting 15-30% of exposed cattle and
CC resulting in a 2-5% mortality rate in the exposed population. The vaccine
CC composition of the invention is useful for preventing or ameliorating
CC respiratory diseases such as pneumonia, particularly shipping fever
CC pneumonia, in livestock.

XX Sequence 3229 BP; 1085 A; 571 C; 690 G; 883 T; 0 other;

Query Match 29.3%; Score 814.4; DB 21; Length 3229;
Best Local Similarity 60.2%; Pred. No. 1.9e-170;
Matches 1558; Conservative 0; Mismatches 956; Indels 60; Gaps 9;

QY 53 caaagctggtatataaaatcttacttggctatcccaagat-----tatgctcgc 106
DB caaaaactgggcaaaaaataatctctatattcccaaaattaccataatgatactg 88
QY 107 aaaaagctggacttttaagatttttaagctgctgataagattgatactgctc 166
DB 89 aaaaagctggacttttaagatttttaagctgctgataagattgatactgctc 148
QY 167 tagcagaagagccttaacacatggaacgaacaaataatctgttgcacgtaatac 226
DB 149 aagaagagagccttaacacatggaacgaacgaacgaacgaacgaacgaacga 208
QY 227 tctctctccacaacaactggtatcttctgcacaacaaatgaaagttctac 286
DB 209 ctatgcttaacagcagcgtgctgttctatccgcctccacaacgaatgataatgctac 268
QY 287 aaaaacattacacaatagttgacaaaggttagacagttgataaataatgatac 346
DB 269 agaaa-----actaaagcagcgaacgaatagttctgcgaagaactgtacaa 319
QY 347 aattaggttaagcagaatgaatgatatcaacatgaactgttcttggagcagctag 406
DB 320 atcgaacaaagcgaacaaatgataatcgcgcacatcaatcatttgaagcagctag 379
QY 407 cgggtatagactgtatcttcttaacaaaaggtgtagctgcacgtgactgtgcta 466
DB 380 ctggaatgagtttagatgagccttacagaa---taacagcaacacacatgctctgcta 436
QY 467 aagctgatactgactgtatgaatgaatgaatgatactatcctcagagtaacaga 526
DB 437 aagctgactgtgagtaacaaatcattatgaataatgataatgataatgataacac 496
QY 527 ttgaagatttctcactgagttgacaaagttagttactatatacgcagctaaagct 586
DB 497 ctgaagatttctcactgagttgacaaagttagttactatatacgcagctaaagct 556
QY 587 tctctaataaggaacaaatgcaaaacttaaat---tttcttaacaaatcttgg 643
DB 557 taggacttttagagagaacaaatcacaataatcgttgaactgtgaaagcgcgctgtg 616
QY 644 tggaaataatctactgtgtctatcaggaatctcgcagcgttgcgttgcgataaa 703
DB 617 tagatgtatctcactgaggtctatcgcgcgaacagctgactgttacttgcagataaa 676
QY 704 atgcatgactgcaaaaaggtgctgcaggtttgaaatgaacgaacgaatgataatg 763
DB 677 atgcttcaaacagctaaaggtggtggtggttgcaggttgcagcaacgaatggtgta 736
QY 764 atgtaacaaagcaatctctcatatgttttagacaaagctgtgtgcgtgctatcaaa 823

DB 737 atattacaagccgttctcttactatattagccaagctgttgcagcagttatcct 796
QY 824 ctctgt 883
DB 797 caactggcgt 856
QY 884 catltaagaatgcagcaacaaatcacaatcagtaatgctgtgaagttgcaaac 943
DB 857 catltaagaatgcagcaacaaatcacaatcagtaatgctgtgaagttgcaaac 916
QY 944 aatccgaaaattgtgtatgagtgaggaatcattatgtgtgaatcagcgtgtgtg 1003
DB 917 gctttaaataattgactatgacgagagataattattagcaaatcacaacgaggaac 976
QY 1004 gtactatgaagcttcaatcaatcaatgtaagcattagagcaggtttctgtgtg 1063
DB 977 ggaactatgacgtcgt 1036
QY 1064 ttccgctgt 1123
DB 1037 tgtctgt 1096
QY 1124 ttacaggaatgactcctgtgaattttagaagcgtctaaacgaggaatgttgaag 1183
DB 1097 ttacaggaatgactcctgtgaattttagaagcgtctaaacgaggaatgttgaag 1156
QY 1184 ctacagcgttacaaggaatattttagaagcgtctaaacgaggaatgttgaagcag 1243
DB 1157 caataaataatcacaacaaatgtgaaatgaggaataaataacgaagtaagaact 1216
QY 1244 ttgaataagcgtatgactcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1303
DB 1217 ttgaataagcgtatgactcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1276
QY 1304 ctgagcctaaataagagttgaaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1363
DB 1277 tgaacttaacaaagagttgaaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1336
QY 1364 atataatattgt 1423
DB 1337 atataatattgt 1396
QY 1424 aagcttgcagagctgt 1483
DB 1397 aagcttgcagagctgt 1456
QY 1484 tgaatgtcaaaactgtatcatatagacatagtaattcaaatgaggaataaagcag 1543
DB 1457 tgaatgtcaaaactgtatcatatagacatagtaattcaaatgaggaataaagcag 1516
QY 1544 tgaatgtcaaaactgtatcatatagacatagtaattcaaatgaggaataaagcag 1603
DB 1517 tgaatgtcaaaactgtatcatatagacatagtaattcaaatgaggaataaagcag 1576
QY 1604 gtaaatctcttaataatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 1663
DB 1577 gtaaatctcttaataatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 1636
QY 1664 atgagaagcgt 1723
DB 1637 atgagaagcgt 1696
QY 1724 aaggaacagcagagatgt 1782
DB 1697 tagaacaatgt 1756
QY 1763 ctggaatgt 1822
DB 1757 aaggaacagcagagatgt 1816
QY 1823 acgactgt 1882
DB 1817 acgactgt 1873

QY 2534 gtataatcacttcgcgatacaattgataaatltt 2567
||||| | | ||| ||||| | |||
Db 2528 agcggatcacctcaagaagcgtgatgatcttat 2561

Search completed: September 15, 2002, 11:57:05
Job time: 10587 sec

SCOT D

RESULT 4
AAR10889
ID AAR10889 standard; Protein: 924 AA.
XX
AC AAR10889;
XX
DT 11-APR-1991 (first entry)
XX
DE Leukotoxin 352 encoded by plasmid PAA352.
XX
KM LKT; vaccine: antigen; respiratory disease; shipping fever pneumonia.
XX
OS Pasteurella haemolytica A1 strain B122.
XX
PN CA2014033-A.
XX
PD 07-OCT-1990.
XX
PF 06-APR-1990; 90CA-2014033.
XX
PR 07-APR-1989; 89US-0335018.
XX
PA (UTSA-) UNIV SASKATCHEWAN.
XX
PI Acres SD, Babluk LA, Potter AA, Lawman MJF.
XX
PI WPI: 1991-000097/01.
DR N-PSDB: AAO10272.
XX
PT Pasteurella haemolytica proteins and genes - used for producing
XX vaccines to protect animals esp. cattle from respiratory diseases
XX e.g. pneumonia.
PS Claim 13; Fig 5; 87pp; English.
XX
XX Plasmid PAA352 is derived from PA114, a clone isolated from a
CC genomic library of P. haemolytica. The protein, designated "new
CC leukotoxin" or "LKT 352" is 98% homologous to authentic leukotoxin.
CC LKT 352 and pref. antigenic fragments of it, can be used in
CC vaccines to protect cattle from respiratory diseases. They can also
CC be used to produce antibodies for immunofluorescent purification of
CC further proteins. (Fig. contg. sequence v. poor).
CC See also AAR10890, AAR10909, AAR10910 and AAO10783.
CC
XX
XX Sequence 924 AA;
SQ

Query Match 75.4%; Score 43; DB 12; Length 924;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
II IIIII:II
Db 422 flnlknkelaqae 433

RESULT 5
AAR42385
ID AAR42385 standard; Protein: 924 AA.
XX
AC AAR42385;
XX
DT 19-APR-1994 (first entry)
XX
DE Recombinant leukotoxin peptide from plasmid pCRR28.
XX
KM Haemophilus somnus; immunogenic; haemolysin: LppB; LppC;
XX thromboembolic meningoencephalitis; septicemia; arthritis;
XX pneumonia; lktA gene; haemin-binding protein; fusion protein.
XX Pasteurella haemolytica.
XX
XX WO9321323-A.
PN

XX
PD 28-OCT-1993.
XX
XX
PF 05-APR-1993; 93WO-CA00135.
XX
XX
PR 09-APR-1992; 92US-0865050.
XX
PR 04-JUN-1992; 92US-0893424.
XX
PR 04-JUN-1992; 92US-0893426.
XX
PR 29-MAR-1993; 93US-0038287.
XX
PR 29-MAR-1993; 93US-0038288.
XX
XX
XX (UTSA-) UNIV SASKATCHEWAN.
XX
XX
XX Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
PI Rioux C, Theisen M;
XX
XX
DR WPI: 1993-351733/44.
XX
DR N-PSDB: AAO31086.
XX
XX
XX Haemophilus somnus immunogenic proteins used in vaccines -
XX PT selected from haemin-binding protein, haemolysin, LppB and LppC,
XX PT and corresp. DNA
XX
XX
XX PS Disclosure; Fig 11; 119pp; English.
XX
XX
XX The lppB gene protein was expressed in E. coli as a fusion to the
CC Pasteurella haemolytica leukotoxin gene lktA coded for by plasmid
CC PAA352. The lppB gene fragment was taken from pMS11. LppB can be
CC used in vaccines for preventing or treating H. somnus infections;
CC which cause thromboembolic meningo-encephalitis, septicemia, arthritis
CC and pneumonia in vertebrates.
CC See also AAR42370-86.
CC
XX
XX Sequence 924 AA;
SQ

Query Match 75.4%; Score 43; DB 14; Length 924;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
II IIIII:II
Db 424 flnlknkelaqae 435

RESULT 6
AAR42380
ID AAR42380 standard; Protein: 924 AA.
XX
AC AAR42380;
XX
DT 19-APR-1994 (first entry)
XX
DE Recombinant leukotoxin peptide (split) from plasmid pCCH4.
XX
KM Haemophilus somnus; immunogenic; haemolysin: LppB; LppC;
XX thromboembolic meningoencephalitis; septicemia; arthritis;
XX pneumonia; lktA gene; haemin-binding protein; fusion protein.
XX Pasteurella haemolytica.
XX
XX WO9321323-A.
XX
XX
XX 28-OCT-1993.
XX
XX
XX 05-APR-1993; 93WO-CA00135.
XX
XX
XX 09-APR-1992; 92US-0865050.
XX
XX 04-JUN-1992; 92US-0893424.
XX
XX 04-JUN-1992; 92US-0893426.
XX
XX 29-MAR-1993; 93US-0038287.
XX
XX 29-MAR-1993; 93US-0038288.
XX
XX

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 14, 2002, 22:25:42 ; Search time 2862.36 Seconds
(without alignments)
13127.462 Million cell updates/sec

Title: US-09-884-696-1

Perfect score: 2784
Sequence: 1 atgccaataataatgtat.....tttggcccaagtgttag 2784

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estda:*
2: em_esthm:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_pln:*
15: em_gss_pln:*
16: em_gss_vtl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123.2	4.4	450	12	AF307787 AF307787
2	109.6	3.9	463	12	AF307788 AF307788
3	82.4	3.0	908	12	AZ548467 ENTKE30TR
4	79.8	2.9	843	12	AZ551618 ENTDV54TR
5	78.8	2.8	877	12	AZ531291 ENTBO34TR
6	78.2	2.8	912	12	AZ551092 ENTFC22TR
7	74.8	2.6	849	12	AZ546009 ENTFC64TR
8	73.6	2.6	726	12	AZ196050 SP_1031_A
9	73.2	2.6	905	12	AZ550256 ENTVE58TR
10	72.2	2.6	976	12	BH149983 ENTOD93TR
11	71	2.6	582	12	CNS0173R Tetradon
12	70.4	2.5	795	12	AZ528485 ENTFC64TR
13	70.4	2.5	833	12	AZ676218 ENTFC36TR
14	70.4	2.5	843	12	BH139532 ENTFC86TR
15	70.4	2.5	931	12	BH160272 ENTQV49TR
16	66.8	2.4	816	12	AZ535744 ENTQ25TR
17	66.6	2.4	900	12	AZ549980 ENTDD94TR

C	18	65.4	2.3	1101	12	CNS0039G	AL063921 Drosophila
C	19	65	2.3	891	12	AZ683582	ENTKK47TR
C	20	64.8	2.3	866	12	CNS02C24	AL180587 Tetradon
C	21	64	2.3	598	10	BMI70666	BMI70666 EST573189
C	22	64	2.3	605	10	BMI63520	BMI63520 EST566043
C	23	64	2.3	747	10	BMI62732	BMI62732 EST565255
C	24	64	2.3	943	12	AZ211711	AZ211711 SP_0157_B
C	25	63.6	2.3	479	12	BH211305	BH211305 SMI_50G22
C	26	63.6	2.3	794	10	BMI59906	BMI59906 EST562429
C	27	63.4	2.3	774	12	CNS02A2C	AL188841 Tetradon
C	28	63.4	2.3	890	12	AZ530768	AZ530768 ENTBM54TR
C	29	63.2	2.3	487	12	BH200321	BH200321 SMI_50O20
C	30	63	2.3	474	9	BE059711	BE059711 sn35h05_Y
C	31	63	2.3	717	10	BMI60500	BMI60500 EST563023
C	32	62.4	2.2	541	12	AQ242166	AQ242166 1E13-28C
C	33	62.4	2.2	838	10	BG535503	BG535503 602563188
C	34	62.4	2.2	880	12	AZ669474	AZ669474 ENTIV88TR
C	35	62.2	2.2	550	12	AQ403310	AQ403310 HS_5061_B
C	36	61.8	2.2	476	10	BFS66802	BFS66802 UT-R-BJ06
C	37	61.8	2.2	548	12	BH200391	BH200391 SMI_39D16
C	38	61.8	2.2	906	12	BH153606	BH153606 ENTTS83TR
C	39	61.8	2.2	1101	12	CNS0106X	AL098595 Drosophila
C	40	61.6	2.2	824	12	BH396872	BH396872 AG-ND-101
C	41	61.4	2.2	548	10	BMI59818	BMI59818 EST562341
C	42	61.4	2.2	810	12	CNS0272N	AL184136 Tetradon
C	43	61.2	2.2	645	10	BMI65350	BMI65350 EST567873
C	44	61	2.2	815	12	BH356455	BH356455 C1230-163
C	45	60.6	2.2	493	10	BMI70559	BMI70559 EST573082

ALIGNMENTS

RESULT 1
AF307787 450 bp DNA linear GSS 17-JAN-2001
LOCUS AF307787 Escherichia coli CF073 Escherichia coli genomic clone
DEFINITION 2b11-593, DNA sequence.
ACCESSION AF307787
VERSION AF307787.1 GI:12250177
KEYWORDS GSS.
SOURCE Escherichia coli.
ORGANISM Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

REFERENCE 1 (bases 1 to 450)
AUTHORS Bahrani-Mougeot,F.K., Pancholl,S., Daoust,M. and Donnenberg,M.S.
TITLE Identification of putative urovirulence genes by subtractive
cloning
JOURNAL J. Infect. Dis. (2001) In press

COMMENT Contact: Bahrani-Mougeot, FK
Department of Medicine-Division of Infectious Diseases
University of Maryland
MSTF Rm 9.00 -10 S. Pine St., Baltimore, MD 21201, USA
Tel: 410-706-7560
Fax: 410-706-8760
Email: fBahrani@umaryland.edu
Class: unknown.
Location/Qualifiers

FEATURES
source 1..450
/organism="Escherichia coli"
/strain="CF073"
/db_xref="taxon:562"
/clone="2b11-593"
/note="Escherichia coli CF073"
/note="uropathogenic; isolated based on subtractive
hybridization with Escherichia coli K12; putative
urovirulence genes"

BASE COUNT 142 a 61 c 122 g 121 t 4 others
ORIGIN

Query Match 4.4%; Score 123.2; DB 12; Length 450;

method for isolate identification. Exp. Parasitol.

light size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999)."

BASE COUNT 319 a 72 c 175 g 229 t

Query Match 2.5%; Score 70.4; DB 12; Length 795;
Best Local Similarity 44.8%; Pred. No. 0.00044;
Matches 269; Conservative 0; Mismatches 331; Indels 0; Gaps 0;

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DB 193 gtaattaatgctttttatatttttaacattcactaaacgtaagaacacgttgatttaaat 232
QY 1912 aacgtgaaggttcgcgaagtgatatacaccatgaagcttgcaagaacgaag 1971
DB 253 tatgatgaattcgaatttagaagaataatgtaacgaagaataatgtaacgtgcaatgca 312
QY 1972 gtgggtaaacgtactgaacataccagtcgtgattgataaataaagaagtggat 2031
DB 313 gatgatgatgaattgaattgaattgaattgaattgaattgaattgaattgaattgaatt 372
QY 2032 ggtatcagctcagcgaataattggaatcgtagaagaattggttcccaattaat 2091
DB 373 gat 432
QY 2092 gatgatcagaagttcacaacacacataatccatcagtcgtggaagtgatgattta 2151
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DB 493 gatgacgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgat 552
QY 2212 ggaagatgaaggaaggaaggaaggaaggaaggaaggaaggaaggaaggaaggaagga 2271
DB 553 gat 612
QY 2272 gctgtgaatgctatatacttcgcgaaggtgagtgatgatactatgtaacgagtc 2331
DB 613 gatgatgacgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgat 672
QY 2332 acgggcaatgataaatacattgcagatgcaaatatatactatgattgaagcgt 2391
DB 673 gacgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgat 732
QY 2392 accaagaagggtatagtttaagtaagaatgatactcagtcagtcagtcagtcagtcag 2451
DB 733 aaacaaatgtcAAAAAAATCCAAACTATTAAATAATTAATTAATTAATTAATTAATTA 792

RESULT 13
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DEFINITION ENTKE36TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
genomic, DNA sequence.
ACCESSION A2676218
VERSION A2676218.1 GI:11813364
KEYWORDS GSS.
SOURCE Entamoeba histolytica.
ORGANISM Entamoeba histolytica.
Eukaryota; Entamoebidae; Entamoeba.

REFERENCE 1 (bases 1 to 823)
AUTHORS Loftus, B., Van Aken, S., and Fraser, C.
TITLE Determination of clone end sequences from Entamoeba histolytica
JOURNAL HMI:IMSS sheared DNA library
COMMENT Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjlloftus@ligr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 17
High quality sequence stop: 810.
Location/Qualifiers
1. 823
/organism="Entamoeba histolytica"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica sheared DNA"
/note="Vector: PHOS1; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
light size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999)."

BASE COUNT 228 a 206 c 86 g 303 t

Query Match 2.5%; Score 70.4; DB 12; Length 823;
Best Local Similarity 44.8%; Pred. No. 0.00045;
Matches 269; Conservative 0; Mismatches 331; Indels 0; Gaps 0;

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DB 782 gtaattaatgctttttatatttttaacattcactaaacgtaagaacacgttgatttaaat 723
QY 1912 aacgtgaaggttcgcgaagtgatatacaccatgaagcttgcaagaacgaag 1971
DB 722 tatgatgaattcgaatttagaagaataatgtaacgaagaataatgtaacgtgcaatgca 663
QY 1972 gtgggtaaacgtactgaacataccagtcgtgattgataaataaagaagtggat 2031
DB 662 gatgatgatgaattgaattgaattgaattgaattgaattgaattgaattgaattgaatt 603
QY 2032 ggtatcagctcagcgaataattggaatcgtagaagaattggttcccaattaat 2091
DB 602 gat 543
QY 2092 gatgatcagaagttcacaacacacataatccatcagtcgtggaagtgatgattta 2151
DB 542 gatgatgacgatgacgatgacgatgacgatgacgatgacgatgacgatgacgatgacgat 483
QY 2152 ctgcagatggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 2211
DB 482 gatgacgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgat 423
QY 2212 ggaagatgaaggaaggaaggaaggaaggaaggaaggaaggaaggaaggaaggaagga 2271
DB 422 gat 363
QY 2272 gctgtgaatgctatatacttcgcgaaggtgagtgatgatactatgtaacgagtc 2331
DB 362 gatgatgacgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgat 303
QY 2332 acgggcaatgataaatacattgcagatgcaaatatatactatgattgaagcgt 2391
DB 302 gacgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgat 243

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2002, 07:01:13 : Search time 102 Seconds
(without alignments)
6704.350 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	815.6	29.3	3311	1	US-07-777-715-6 Sequence 6, Appl1
2	815.6	29.3	3311	1	US-08-170-126-1 Sequence 1, Appl1
3	815.6	29.3	3311	3	US-08-954-418-1 Sequence 1, Appl1
4	814.4	29.3	2794	1	US-07-960-932-1 Sequence 1, Appl1
5	814.4	29.3	2794	1	US-07-908-253-1 Sequence 1, Appl1
6	814.4	29.3	2794	1	US-08-455-970A-1 Sequence 1, Appl1
7	814.4	29.3	2794	1	US-08-387-156-5 Sequence 5, Appl1
8	814.4	29.3	2794	2	US-08-694-865-5 Sequence 5, Appl1
9	814.4	29.3	2794	2	US-08-878-748-5 Sequence 5, Appl1
10	814.4	29.3	2794	2	US-08-535-837-1 Sequence 5, Appl1
11	814.4	29.3	2794	3	US-09-124-491-5 Sequence 5, Appl1
12	814.4	29.3	2794	6	5476657-2 Patent No. 5476657
13	814.4	29.3	2817	1	US-07-960-932-9 Sequence 9, Appl1
14	814.4	29.3	2817	1	US-08-455-970A-11 Sequence 11, Appl1
15	814.4	29.3	2838	1	US-07-960-932-8 Sequence 9, Appl1
16	814.4	29.3	2838	1	US-08-455-970A-9 Sequence 9, Appl1
17	814.4	29.3	2861	1	US-07-960-932-10 Sequence 10, Appl1
18	814.4	29.3	2861	1	US-08-455-970A-13 Sequence 13, Appl1
19	814.4	29.3	2934	1	US-08-387-156-7 Sequence 7, Appl1
20	814.4	29.3	2934	2	US-08-694-865-7 Sequence 7, Appl1
21	814.4	29.3	2934	2	US-08-878-748-7 Sequence 7, Appl1
22	814.4	29.3	2934	3	US-09-124-491-7 Sequence 7, Appl1
23	814.4	29.3	3229	1	US-07-777-715-8 Sequence 8, Appl1
24	814.4	29.3	3229	1	US-08-170-126-3 Sequence 3, Appl1
25	814.4	29.3	3229	1	US-08-954-418-3 Sequence 3, Appl1
26	814.4	29.3	3646	3	US-08-619-812-7 Sequence 7, Appl1
27	800.4	28.8	2802	1	US-08-215-805A-79 Sequence 79, Appl1

28	800.4	28.8	3848	1	US-08-215-805A-1 Sequence 1, Appl1
29	775	27.8	4731	2	US-08-488-706-2 Sequence 2, Appl1
30	775	27.8	4731	3	US-08-772-270A-9 Sequence 9, Appl1
31	636.8	22.9	4190	2	US-08-488-706-3 Sequence 3, Appl1
32	629	22.6	3828	5	PCT-US93-10500-1 Sequence 1, Appl1
33	629	22.6	7721	3	US-08-772-270A-14 Sequence 14, Appl1
34	488.8	17.6	3762	3	US-08-772-270A-3 Sequence 3, Appl1
35	485.6	17.4	8370	2	US-08-488-706-1 Sequence 1, Appl1
36	403	14.5	2278	1	US-08-258-188-1 Sequence 1, Appl1
37	403	14.5	2278	1	US-08-526-813-1 Sequence 1, Appl1
38	403	14.5	2278	5	PCT-US95-08554-1 Sequence 1, Appl1
39	343.2	12.3	2102	2	US-08-694-865-15 Sequence 15, Appl1
40	343.2	12.3	2102	3	US-09-124-491-15 Sequence 15, Appl1
41	341.8	12.3	1635	1	US-08-387-156-9 Sequence 9, Appl1
42	341.8	12.3	1635	2	US-08-694-865-9 Sequence 9, Appl1
43	341.8	12.3	1635	2	US-08-878-748-9 Sequence 9, Appl1
44	341.8	12.3	1635	3	US-09-124-491-9 Sequence 9, Appl1
45	308.2	11.1	6850	4	US-09-298-367B-2 Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-07-777-715-6
; Sequence 6, Application US/0777715
; Patent No. 5273889
; GENERAL INFORMATION:
; APPLICANT: Potter, Andrew
; APPLICANT: Campos, Manuel
; APPLICANT: Hughes, How P.A.
; TITLE OF INVENTION: CYTOKINE-LEUKOTOXIN GENE FUSIONS AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; City: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07777, 715
; FILING DATE: 1991016
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Rodins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 29310-2001320
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3311 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3294
; ;
; US-07-777-715-6
Query Match 29.3%; Score 815.6; DB 1; Length 3311;
Best Local Similarity 60.1%; Pred. No. 1.6e-177;
Matches 1544; Conservative 0; Mismatches 964; Indels 60; Gaps 9;

39 aggcgttaattcaacaagaagctcgatattaaaaacttacttggtatcccaagaag-- 96
Db 531 AGCGGAGAGTCTTTAAAACTGGGCGAAAAAATATTCCTCTATATTTCCCAAAATTA 590
Qy 97 ----tatgacccgaagaagtgaggactttaatgatttatataaagctgctatgaat 152
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Qy 153 aggtatgctcgctttagcagaagaagcctataacacggaacacgcaaaaaactgltga 212
Db 651 GGGGATTGAGGTACAAAGAGAAAGAACCAATATATTGCAACACCTCAACCAATTAGG 710
Qy 213 cagagtaaatcagttctctctcccaacaacggtatgctatcttcctgcaaaaaat 272
Db 711 CACGATTCAAAACCGCTATTGGCTTACCTGAGCGCTGCGATTCGTATCCGCTCCACAAAT 770
Qy 273 agaaagttcttacaanaaacattctaccaataagltagcgaaggggttagacagltaga 332
Db 771 TGATTAATTTGCTACGAAA-----ACTAAAGCAGGCCAACATTTAGGTTCTGCGGA 821
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Db 822 AAGCATTTGTACAAAATGCAAAATTAAGCCAAATGTTATTTGTCATTCATTTATTT 881
Qy 393 gggcactgcatlagcgggtatagaactgtatctttaacaaaaaaggltgctgcaac 452
Db 882 AGGCTCATGATTGGCTGGAATGGATTTAGATGAGGCTTTACAGAA---TAACAGCAACCA 938
Qy 453 tgaatccttgctaaagctagttatgactgtatgaatgaatgaatgaatgaatgaatga 512
Db 939 ACATGCTCTGCTTAAAGCTGGCTTGAGCTTAAACAAATTCATTAAATTTGAATTTGCTAA 998
Qy 513 ggaatctcaagaagattgagaacattctctcaacagltagaagtttactatatac 572
Db 999 TTTCAGTAAAAACACTTGAAGATTTGGTGAAGCAATTTAGTCAATTTGGTTCAAAATCA 1058
Qy 573 gcaagctaaaggctctctcaatataagaaacagltgcaaaaactaaat---tttctaa 629
Db 1059 AATATTCAAAAGGCTTAGGAGACTTTAGGAGACAAACCTCAAAAATATCGGTGAGCATGATTA 1118
Qy 630 aacaaactctggttgggaataataactggttgcatacagcacttctgcaaggtctgc 689
Db 1119 ACCTGGCCTTTGGTTTAAAGATTATCTCAGGCTATTATTCAGGCGCAACAGCTGCACTTGT 1178
Qy 690 tttagagataaagaatgactgcagctgcgaagaagttgcgtgaggtttgtaataagca 749
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Db 1239 CCAAGTTGTTGGTAAATATTAACCAAGCCGTTCTTCAATTTTAGCCCAACGTTGTC 1298
Qy 810 tgcgtctatacaactacagtggtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 869
Db 1299 AGCAGGTTTATCTTCAACGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1358
Qy 870 aattagtccttggcattatgaatgcagcagataaatacaatcatgtaactgcttga 929
Db 1359 GATTACCCCATTTAGCATTTGGCGGTATTCGCCATAATTTAATCATGAAAAAGTTTGA 1418
Qy 930 tgaagttgcgaagaacatccgaagaatttggctatggtgggtgatttatttggctga 989
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Qy 990 tcaagctgt 1049
Db 1479 TCAGCGGGGACAGAGGACTATTAATGATCGATTACTGCAATTAATACCGCATTTGGCCG 1538
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Qy 1170 gtttgaagatgt 1229
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Db 1719 CGGTAAAGACTACTTGTAAATGTGTACGATGCCCTTATCTTGGCAATTTTCAAGATTA 1778
Qy 1290 cttaaatcttctcgt 1349
Db 1779 TATGAATTTCTTCTGACTTAAACAAAGATTACAGGCAAGCGTGTATGCTTATTC 1838
Qy 1350 ccaacaagcttggataataatattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1409
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Qy 1410 cattaaagcgcgaagaactatgcaagtgctttagaagltgcaagaaggttgaagctg 1469
Db 1899 AGTCTTAGTGTAAAGCCTATGTGATGCTTTGAAAGAGGCAACACATTTAAACCCA 1958
Qy 1470 ttccaataactcttgatgt 1529
Db 1959 TAAATTAATGTAAGTGTGATTTGGCAACGCTATTTATTTGATGATGATTTGCGGTAAAC 2018
Qy 1530 aaaaacgcagcgttgcattctacttcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1589
Db 2019 GAATTAATGATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 2078
Qy 1590 acgtttaaactaatgttaataactcttatataatgaatgaatgaatgaatgaatgaatga 1649
Db 2079 ACGGTACAAACAGGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2138
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Db 2199 TATTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2258
Qy 1762 -----gctgcaatgacgaatcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1808
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Qy 1809 tgtgtgagatgtagacagctgtgtctctatagtaagaagcggagatttggtaatatct 1868
Db 2319 TGGCGGTGAAGGTATACAGACGAGTTCACTATAG---CCGTGGAATTAATGTTGCTTTAAC 2375
Qy 1869 tgaagatgtagcagtgtagcaagaagaagcaggtatatacagttatcgttaagttgtgc 1928
Db 2376 TATTGATGCAACCAAGAGCAGGCAAGGTATTAATTAATTAATTAATTAATTAATTAATTAAT 2435
Qy 1929 aggtgatcttccatggaatgtgtgaagcgtcgaagaacaaaggltgggtlaaacgtatga 1988
Db 2436 CGGTAAACACTACACGAGTGTACTTCAACCCATTAACGCAATTAATTTGGCAACCGTGAAGA 2495
Qy 1989 aactacagatcgtgtatgaatgaagaagaagtttggatagttatcagttacccga 2048
Db 2496 AAAAAATGATATGCTGATTAACCAATTAACCAACACCATATG---CCGTTATTAATTAACCAAGA 2552
Qy 2049 taattgaatcagtagaagaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2108
Db 2553 TACCTTGAAGCTGTGTGAAGAAATTTATGCTATCAATTAACGATTAATCTTTAAAGGTAG 2612
Qy 2109 taattcaacagcatatccatagtggtgtgaaggtgtatatttactcgtgtgtgtgtgtgt 2168
Db 2613 TAACTTCAATGATGCTTTAAACGTTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2672
Qy 2169 tgaacacgcgt 2228

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/908, 253
FILING DATE: 19920702
CLASSIFICATION: 420
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000-0026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2794 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2778
US-07-908-253-1

Query Match 29.3%; Score 814.4; DB 1; Length 2794;
Best Local Similarity 60.2%; Pred. No. 2.9e-177;
Matches 1538; Conservative 0; Mismatches 956; Indels 60; Gaps 9;

53 caaagctcgatataaaatcttacttgcgtatcccaaat-----tatagtcgc 106
29 CAAAACCTGGGGCAAAAATTTATCTCTATTTCCCAAAATTAACCAATATGATCTG 88
107 aaaaagcgggactttaaatgattataaagcgtcgtatgaattagttatgctcgt 166
89 AACAGGTAATGCTTTTACAGATTTAGTCAAGCGCGCAAGAGTTGGGAGTTAGGTAC 148
167 tagcagaagacctaatacactgaaacagcaaaaatcgtgtgacacagtaaatcagt 226
149 AAGAGGAAGAACGCAATATATTTGCAACAGCTCAACAGTTAGGACGATTCAACCG 208
227 ttctctctcacacaactggtatgtctatcttcgcaacaataatlaaaaagctcttac 286
209 CTATTGGCTTAACGATGAGCGTGGCATTTGTGTATCCGCTCCCAAAATTGATAATTGCTAC 268
287 aaaaacattctacaaatagtagcgaagggtagacagtgtagaataatltgactgta 346
269 AGAA-----ACTAAGCAGCGCAAGCATTTAGGTTCTGCGCAAAACATTGTACAAA 319
347 aattagtaagcaagtaatgtatatacaacataagctcttcttttgggcaactgcatag 406
320 ATGCAAAATTAACCCAAACGTATATTTCTGGCATTCAATCTATTTTAAAGCTCAGTATGG 379
407 cgggtatgaacttattcttataacaaaagtgatgctgacactgacgtatgttgctta 466
380 CTGGATGTGATTTAGATGAGCGCTTACAGAA---TAAACGACACCAACATGCTCTTGCTTA 436
467 aagctagatitgactgtatataagataatgtgatactatctcagagtaactacaaga 526
437 AAGCTGGCTTGAAGCTTAACAAATTCATTATGAAATTTGCTATTCAGTAATAAAGC 496
527 ttgaagcatttctcacaagtagcaagtgtaggttctactatatacgcaggtcaagct 586
497 TTGAGCAATTTGCTAGCAAAATTAATGCAATTTGGTTCAAAACATCAAAATATCAAAAGCT 556
587 tctcacaataggaacaaagttgcaaaactaat---tttcttaaaacaactcttggt 643
557 TAGGACCTTTAGGAACAACATCAAAATATCGGTGACTGTATTAAGCTGAGCTTGCTG 616
644 tggaaataatitactgttctcacaagcattctcgaagcttcttgaagggataaa 703
617 TAGATGTTATCTCAGGCGCATTTATCGGCGCAACAGCTGCATTTGACTTGGACGATTA 676
704 atgcatcgacttggcaaaaagttgctgcaagtttgaattaaagcaatcaagttatgtta 763

677 ATGCTTCAACAGCTAAAAAGCTGGCGGCTTTGAAATGGCAACCAAGTTGTGTA 736
764 atgtaacaaagcaatttctcacaatgttagaacaacggtgtgtgtgtgtatcaaa 823
737 ATATTACAAAGCGCTTCTTCTTACATTTTAGCCCAAGGTGGACACAGATTATCTT 796
824 ctactgt 883
797 CAACGTGGCGCTGTGCTCTTAAATGCTTGTAGCTTGTCTGCTGCAATGAGCCATTA 856
884 cattatgaatgcaagcaataatcaatcagtaatgctcctgtatgagtgttgaacac 943
857 CATTGGCCGATTCGCCATTAATTAATCAATGCAAAAAGTTTGAAGATTGACCGGAC 916
944 aattccgaaaatttggcgtatgaggaatcaatcttctgccaatcagcgtgtgtgtg 1003
917 GCTTAAAAAATTTAGGCTATGACGAGATTAATTTATGCAAGATATACGGGGGAACG 976
1004 gtactatgaagctcattcaatcaatcagtaagtagcagttatgtgtgtgtgtgtgt 1063
977 GAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1036
1064 ttccgctgt 1123
1037 TGTCTGCTGCTGACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1096
1124 ttacagagtgatctctgtaattttagaagcgtcgaacagcaagctgttgaagtggt 1183
1097 TTACCGGTGATTTCTCAGATTCGCAATATTCATAACAGCAATGTTTACGACGCTTG 1156
1184 ctaacggttacaagtaaaatttagagtgaggaaagcaaatggtggtcagaactct 1243
1157 CAATTAATTAATTCATTAACAAATTTGTAATGGGAAAAAATTAACGCTTAAGACT 1216
1244 ttgataaagctatgatactctgtatgctgtctatctttagcctaataacttaattt 1303
1217 TTGAAAATGTTAGCATGCGCGCTTATCTTGCAATTTCAAGATTAATTAATTTCTTAC 1276
1304 ctgaagctaaatgaagagtggaagctgaagctgtatctgcaatcccaacaacgtgtg 1363
1277 TGAATTTAAACAAAGAGTTTACAGCGAAGCGTGCATTTCTCAGACGAAATGG 1336
1364 ataatacatgt 1423
1337 ATAAACAAATGCTGATTTAGCTGATTTAGCTGATTTAGCTGATTTAGCTGATTTAG 1396
1424 aagctatgacagatgcttctttagaagtagcaagaagttgaagctgttccaatctact 1483
1397 AAGCTATGTGTGATGCTGTTGAAGAGCAACACATTAACCCGATTAATTAATTAATTA 1456
1484 tgaatgctaaacgtgtatcatalagacatagtaattcaaatlgygaaaacagcaagct 1543
1457 TGGATTCGCAAAAGCGTATTTATGATGAGTAATTCGGGTAAACGAAACCTCGACTA 1516
1517 TCTTATTCAGAACGCAATTTATGAGCGCGGACAGACATTCGTAAACGCTCAAAACG 1576
1544 tgcatttcaacttcgcttltgttaacagagaactgaatcagctgaacgttctaacta 1603
1604 gtaatactcttataataaagtaaatctcgagcgtgtgtaaaaacagcagtaagtaag 1663
1577 GTAATATGAATATATTCACCAAGCTCAATATTAACCGGTGATATGCTGGAAATTTACG 1636
1664 atgagagagctagcttcaaatagattctcctaagattatcaagcgttgaacgagag 1723
1637 ATGTGACAGCAAGTTCTACTCTTGTATTAACTAACGTTGTTGAGCTATTTGATTAAT 1696
1724 aagcagcagcagagatltgtcctaataagtaaatlgycaaaa-----g 1762
1697 TAGACAAATGCTGGAATTAACCTAAACCAAGAAACAAATTAATTCGCAAACTTGGTG 1756
1763 ctggcagtagcagatcttctgtgtcaagtgtaaaatgaatattgaatgtgtgagatgac 1822

Db 1757 AAGGTGATGACAACTATTGTTCTGTGTACAGCAAAATTGATGCGGTGAAGTT 1816
 Qy 1823 acgatcgtctctctataaagaacgagatttgtaataatcagtgatgtaacga 1882
 Db 1817 ACGACCGAGTCTACTATAG--CCGTGGAACATGATGGTCTTAACTATGATGATCAACCA 1873
 Qy 1883 gtgcacaagaagcagcagttatcaatcgaatcgaatgctgcaggtgatataacc 1942
 Db 1874 AAGGACCGACGACAGTAGTATACGTAATCGTTTCGTGGAACCGTAACGACTAC 1933
 Qy 1943 atgaagltgtgaagcgtcaagaacaaagtgaggtaaacgtactgaactacaglatc 2002
 Db 1934 ACGAAGTGAAGTCAACCCATACCGCATTAGTGGCAACCGTGGAAGAAAATAGATATC 1993
 Qy 2003 gtgatctgtaataaagaagttgggtatggtatcagttaccgataattgaatcag 2062
 Db 1994 GTCTATGCAATTAACACACACCATG--CCGTATATTACCAAAAGATACCTTGAACCTG 2050
 Qy 2063 taagaagaagtaattggtctcaatttaattgattcctcaaggtctcaaatcaagaca 2122
 Db 2051 TTGGAAGAAATTATCGTACATCAGATACGATATCTTTAAAGTAGTAAGTTCAATGATG 2110
 Qy 2123 tatcacaagtgatgaaggtgatgattactcgaatggtggtgctggtgacgacgctgt 2182
 Db 2111 CCTTTACGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2170
 Qy 2183 ttgggtgaaggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2242
 Db 2171 TTGGTGTAAAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2230
 Qy 2243 gtctgtgtaattgatttaattgattgattgattgattgattgattgattgattgattg 2302
 Db 2231 GTAAAGCAACGACTTTTACAGCGTGGCAAGGCGATGATTTTGGTTTACCGTTAAAG 2290
 Qy 2303 gtgatgtaattgacttgatgacgacgacgacgacgacgacgacgacgacgacgacg 2362
 Db 2291 GCGATGTAATGATATTATACCGATCTGACGCAATGATGATGATGATGATGATGATGATG 2350
 Qy 2363 caaatatctgatatgattgattgattgattgattgattgattgattgattgattgattg 2422
 Db 2351 CGAAGTTAAAGATTTAACTTTGAAAAAGTTAAACA--TAACTTGTCTATCAGATA 2407
 Qy 2423 atcatcagtaattgattgattgattgattgattgattgattgattgattgattgattg 2477
 Db 2408 GCAAAAAAGGAAAGTACCATTTAAACATGCTTCCGACGAGCGTGAATTTTCTTAAAG 2467
 Qy 2478 ----tatacaagtaataaagcagatcataaattgacgaactaattgataaagtgta 2533
 Db 2468 TGCGTAATTATTAAGCAACTAAAGATGAGAAATCGAAGAAATCATCGTCAAAATGCGC 2537
 Qy 2534 gtataatcattccgacgaactgataaatttc 2567
 Db 2528 AGCGATCACCTCAAGCAAGTATGATCTTAT 2561

RESULT 6
 US-08-455-970A-1
 ; Sequence 1, Application US/08455970A
 ; Patent No. 5708155
 ; GENERAL INFORMATION:
 ; APPLICANT: PORTER, ANDREW A.
 ; APPLICANT: REDMOND, MARK J.
 ; APPLICANT: HUGHES, HWM P.A.
 ; TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: REED & ROBINS
 ; STREET: 285 HAMILTON AVENUE, SUITE 200
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: UNITED STATES OF AMERICA
 ; ZIP: 94301

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/455,970A
 ; FILING DATE: 31-MAY-1995
 ; CLASSIFICATION: 424
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/960,932
 ; FILING DATE: 14-OCT-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: ROBINS, ROBERTA L.
 ; REGISTRATION NUMBER: 33,208
 ; REFERENCE/DOCKET NUMBER: 9001-0016.10
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 327-3400
 ; TELEFAX: (415) 327-3231
 ; INFORMATION FOR SRO ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2794 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..2778
 ; US-08-455-970A-1

Query Match 29.38; Score 814.4; DB 1; Length 2794;
 Best Local Similarity 60.28; Pred. No. 2.9e-177;
 Matches 1538; Conservative 0; Mismatches 956; Indels 60; Gaps 9;

Qy 53 caaagtcgtgaattaaatcttactctgctgctcccaagat-----tatgacgcgc 106
 Db 29 CAAAACTGGGGGCAAAAAATTATCTCTATTTCCCAAAATTTACCAATATGATCTG 88
 Qy 107 aaaaagtgaggacttaaatgattttaaagctgctgataagttgattgattgattgattg 166
 Db 89 AACAGGAATGATGTTTACAGATTTAGTCAAAAGCGCGAAGAGTGGGATGAGGTAC 148
 Qy 167 tagcagaagagcccaatcacctgaacagcaaaaaaatcgttgacacagtaatacagt 226
 Db 149 AAAAGAAAGAAAGCAATTAATTTGCAACAGCTCAACAGTTTGAAGCAGATTAACCG 208
 Qy 227 ttctctctcacacaacactgtaattgctattcttgcaacaanaattgaagaagttctac 286
 Db 209 CTATTTGGCTTACGTAGCGTGGCATTTGTGTTATCCGCTCCCAAAATTTGATTAATTC 268
 Qy 287 aaaaacattctacataagtttagcacaaggggttagacagtgtagaanaattgattcgta 346
 Db 269 AGAAA-----ACTAAACAGAGCCAGACATTAAGTTTGGCCGAAGACATTTGACAAA 319
 Qy 347 aattaggtaaagcaagtaagtattatcaacaataaagctcttttttggaacgtcattag 406
 Db 320 ATGCAAAATTAAGCCAAACCTGATTAATCTGGCATTTCAATCTATTATAGGCTCACTATGG 379
 Qy 407 cgggtatagaactgattctttaaataaagaagttgctgcgaaccgtgactcttggtga 466
 Db 380 CTGGAATGATTTAGATGAGGCGCTTACAGAA--TAAACAGAACCAACATCTCTTGCTA 436
 Qy 467 aagctaglatgacttgattatagataattgtgtaactatcgaagtaactcaacga 526
 Db 437 AAGCTGCTTGAGAGCTAAACAATTCATTAATTAAGAAATATGCTAAATTAAGTAAACAC 496
 Qy 527 ttgaagcatttcttcacagttagcaagttaggttctactatactcgaagcgaagcgt 586
 Db 497 TTGACGAATTTGGTGGCAAAATTAATGATTAATTAATTAATTAATTAATTAATTAATTA 556
 Qy 587 tctctaataagaaacaagttgcaaaacttaatt-----tttctaaacaactcttggtt 643

Db 557 TAGGACCTTTAGAGACAACTCAAAAATATCGGAGCATTTGATTAACCTGGCCCTTGCTT 616
Qy 644 tggaaatattactggttgcatacagcattctgcagagcttgcctttagcggataaa 703
Db 617 TAGATGTTATCTCAGGGCTATTATCGGCGCAACAGCTGCACCTTACTTGACATTA 676
Qy 704 atgacatgcactgycacaaaagttgcgcaggtttggaaatgaacaaatgaattatgta 763
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Qy 764 atgtaacaaaagcaattcttcataatgttttagcaaacggttgctgcgtcgtatcaa 823
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Qy 824 ctactgagctgctgctccttaattactcaatgataatgttggaattagtccttgcg 883
Db 797 CAACGGGCGCTGTGCTGCTTAAATGCTTCTACTGTTTCTCTTCGATTAACCCATTAG 856
Qy 884 cattatgaatgcagcagataaataatcaatcatgctaaatgcttcttgatgagtttgcaaac 943
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Db 917 GCTTTAAAAAATTAGGCTATGACGAGATTAATTTATGACAAATATAGCGGGAGACAG 976
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Db 1217 TTGAATAATGGTATCGATCCCGCTTATCTTTCGCAATTTTACAAATTAATTAATGAAATTTCTTAC 1276
Qy 1304 ctgagctaaataaagaatgttggaagctggaagcggtatagcaatcccaacaagttgg 1363
Db 1277 TGAACCTTAACCAAGAGTTTACAGCGCAACGTTGATCGCTATTTACTGACGCAATGGG 1336
Qy 1364 ataaatatttgcgtgagttgaggtatattaccaaatltgggtgaacgcatlaagacgga 1423
Db 1337 ATTAACAACATTGCTGATTTAGCTGATATTAGCCGTTTAGTGTAAGAAAGCTTATAGTGA 1396
Qy 1424 aagcttatgcagatgcttltggaagatggaagaagaatgtgaagcgtgttccaatlactt 1483
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Qy 1544 tgcattcactcgcgcttgttaacagcagagcaatgaatcaatgaatgacgttgaatga 1603
Db 1517 TCTTATTGAGAACGCCATTATTGACGCGGGAACAGAGATGCTGTAAGCCGTAAACAACG 1576
Qy 1604 gtaaatcacttataatataaagttcaaatcgcagcggtgaataaaactgycagatgaag 1663
Db 1577 GTAATATGAAATATATTACCAAGCTCAATATTAACCGCTGATGATGCTGGAATAATTAAG 1636
Qy 1664 atgagagagctgattcttaaatgatttctcaagttatagaggtgagccgagcag 1723

Db 1637 ATGTGACGACAGTTCTTACCTTTGATTTAACTAACTGTTTCCAGGATTTGATTAAT 1696
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Qy 1763 ctggcaatgcagatattcttgttgcagagtaaaatgaataatgagtgagtgagtgac 1822
Db 1757 AAGGTGATGACAAACGATTTTGTGTTGCTGTACAGCAGCAAAATGATGCGGTGAAGGTT 1816
Qy 1823 aagatcgtct 1882
Db 1817 ACGACCGAGTTCTACTATAG---CCGTGGAACCTATGCTGCTTTAATCTATGATGACCA 1873
Qy 1883 gtcacacagacagcagcagcttataacagtaacgtgaatgtgtctcagagtgataltacc 1942
Db 1874 AAGAACCGGAGAGAGGTATATACCGTAATTCGTTTGTGTAAGAACCGGTAAAGCATAC 1933
Qy 1943 atgaagtgtgaagcggttaagaacaaaggttggtgaacgactgaactccagttac 2002
Db 1934 ACGAAGTGAATTCACACCCATCCGATTAAGTGGCGCAACCGTGAAAGAAAATAGAAATTC 1993
Qy 2003 gtgattatgaatlaagaaaagtttggtatgttattcagttcagcagataattgaatcag 2062
Db 1994 GTCATGCAATTAACCGACCAATG---CCGTTATTACCAACCAATACCTTTGAAGCTG 2050
Qy 2063 tagaagaagtaattgtctcctaattlaaagtatgtaattcaaaagttcctaattcaacgaca 2122
Db 2051 TTGAAGAATTAATCGGTACATACATACATATCTTTAAAGGTATGTAAGTCAATGATG 2110
Qy 2123 tatccatagtggtgaaggtatgattatcactcagatgtgtgtgtgtgtgtgtgtgtgtgt 2182
Db 2111 CCTTTAACGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2170
Qy 2183 ttggtgtgaaggaacagcagcagcttctggaagtgagagtgagagtgagagtgagagtg 2242
Db 2171 TTGGTGTGAAGCGCATATATCTCGATGTTGGAAGAAAGGTGATGATTTTATCGATGCGC 2230
Qy 2243 gtctcgtgatgatgattataatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2302
Db 2231 GTAAAGCGACAGCACTATTACACGCTGCAAGGCGAGGATGATTTTCTGTTACCGTAAG 2290
Qy 2303 gtgatgtgaatgatactcttgcagtgcaacgggaatgataatgaatcatttgcagtg 2362
Db 2291 GCGATGGAATGATATTTTATCCGATTTCTGACGGAAGATTAATTAATCAATTCCTGTGAT 2350
Qy 2363 caaatatcagatattatgataagcaglaccaagaggtatattagttaaagcaatg 2422
Db 2351 CGAATTTAAAGATTTTAACATTTGAAAAAGTTAAACA---TATCTTGTCAATCAGCAATA 2407
Qy 2423 atcattcaggtgattataacataccaagatggtatataacatacaatlttacaana----- 2477
Db 2408 GCAAAAAAGAGAAAGTGAACATTTCAAACTGTTCCGAGAGCTGATTTTCTGTAAGAAG 2467
Qy 2478 ----ttatcaaggtataaacaagatcataaattgagcaactaatttglytaagtgta 2533
Db 2468 TGCCTAATTAATTAACCACTAAAGATGAGAAATGGAAGAAATCAATCGTCAAAATGGCG 2527
Qy 2534 gtatatacactcgcagcaaatltgtaaaattt 2567
Db 2528 AGCGATCACCTCAAGCAAGTTGATGATCTTAT 2561

RESULT 7
US-08-387-156-5
; Sequence 5, Application us/08387156
; Patent No. 5723129
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: REDMOND, MARK J.
; APPLICANT: HUGHES, HOW P. A.
; TITLE OF INVENTION: GHRH-LEUKOTOXIN CHIMERAS
; NUMBER OF SEQUENCES: 28

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,156
FILING DATE: 10-FEB-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2794 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2778
US-08-387-156-5

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Query Match	29.3%	Score 814.4	DB 1	Length 2794
Best Local Similarity	60.2%	Pred. No. 2.9e-177		
Matches 1538	Conservative	0	Mismatches 956	Indels 60
				Gaps 9
QY	53 caaagctcgatgtaaaaaatcttactctggcgtatccccaaagt-----tatgattccgc	106		
Db	29 CAAAACACGTGGGGCAAAAAAATTATTCCTCTATATTTCCCAAAATTACCATGTGATACG	88		
QY	107 aaaaagtgggagctttaagtatttataaagctgctgataaattagttatgctcgt	166		
Db	89 AACAGAGTATGTGTTTACAGGATTTAGTCAAAAGCCGGCAAGAGTGGGGATTTGAGTAC	148		
QY	167 tagcgaagagcctatcacactgaagaacgacgaaaaaatctgtacacagtaaatcagt	226		
Db	149 AAAGAGAGAACGCGCATATATTTGCAACAGCTCAAAACCAGTTTAAAGCAGATTCAAACCG	208		
QY	227 ttctctctctacacaaaactggtatgtctattcttcgcaacaaattagaanaagttctac	286		
Db	209 CTATTTGGCTTAATCTGAGCGGTGGCATTTGTGTATTCGCGCTCCACAAATTTGATAATTGCTAC	268		
QY	287 aaaaacattctaccataagttagcgcaaaaggtttgacagtgtagaanaaatattgatcgta	346		
Db	269 AGAAA-----ACTTAAAGCAGGCCACAGCATTTAGGTTCTGCCAAGAACATTTGACAAA	319		
QY	347 aattagtgtaaaagcaagtaattgtatatacaacataagctctttcttgggcaactgcatag	406		
Db	320 ATGCAAAATTAAGCCCAAAACTGTATTTATCTGGCATTCATCTATTTTAAAGCTCAGATTTGG	379		
QY	407 cgggtatagaaactggtatcttctaatacaaaaaaagtgatgctgacactgtagtcttgcta	466		
	380 CTGGAATATGATTTTATGATAGGCTCTTACAGAA---TTAAAGCAACCAACATGCTCTTGGCA	436		

OY	467	aagctagatgacttgatbtaabgaagtaattgtaatctatctcgtgagtaacccaaga	526
Db	437	AAGCTGGCTTGGACCTAAACAATTCATTAAATTTGAAATATATGCTAAATTCAGTAAACAC	496
OY	527	ctgaagcaattctctcaacagctagcaagctagatcttactatatacgcaagctaaagct	586
Db	497	TTGACGAATTTGGTGACCAATTTGTCATTTTGGTTCCAAAACATCAAAATATCCAAAGCT	556
OY	587	tcctabaatagaacaagaattgcaaaactbaat---tttccbaaacaacatctggt	643
Db	557	TAGGACTTTTGGAGACAAACTCAAAATATCGGTGACCTTGATTAAGCTGGCCCTGGTT	616
OY	644	tggaaataattacacggtttgctatcaagcaatcttcgaagctttgctttagcggtaaaa	703
Db	617	TAGATGTTATCTCAGGGCTATTATTCGGGCCACAGCTGCACCTTGTACTTGCGAATAAAA	676
OY	704	atgcatacgcactgycacaaaagattgctgcaggttttgaaatlaagcaatcaagttatgta	753
Db	677	ATGCTTCAACAGCTAAAAAAGTGGGTGGGTGTTGAATTGGCAACCAAGTTGTTGGTA	726
OY	764	atgtaacaaaagcaattctctcatatgttttagcacaaagtgctgctgcgtctatcaa	823
Db	737	ATATTACCAAGCCGCTTCTTCTTCAATTTTAAAGCCCAACGTTGTGCGAGGTTTATCTT	796
OY	824	ctactgycgtctgctgcgtcttaacttaacttcatcgtatactgctggaacttagtccttgg	883
Db	797	CAACTGGGCCCTGTGGCTGCTTTATGTGCTTCTACTGTTTCTCTTGCGATTAGGCCATTAG	856
OY	884	cattatagaatgacagataaattcaatcaatgctaatgctctctgtagagtttgcaaac	943
Db	857	CATTTCGCCGTAATTCGCCGTAATTAATTCATGCAAAAACGTTTAAAGAGTATAGCCGAC	916
OY	944	aattccgaaaatttggcgtcatgacatgggagatcaattatgctgcgtgaatacgaacgtgagtg	100
Db	917	GCTTTAAAAAATTAGGCTATGACCGAAGTAAATTTATTAGAGAAATATCACGGGGAAACAG	976
OY	1004	gtactatgaagcttcatcttaactaaattagtagcagcataggctgcagttctctggtg	106
Db	977	GGACATATTGATGCATTCGGTTCCTCAATTAATACCGCATTTGGCCGCTATTGCTGAGTGTC	1033
OY	1064	tttcgcgtgcgtcgttagagatctgctgtttgttggtagcaagattgaactatgctgcaagtg	112
Db	1037	TGTCGTGCTGTCAGACCGCGCTGCTTATGTGCTTACCGGATTTGCCCTTAATTAATGATCTGGGA	109
OY	1124	ttcaaggaattcatctcgtgaattcttgaagaagctcctaaacagcgaattcttgaagaagtg	118
Db	1097	TTACCGGTAATTTCTACGATCTCTGCATTAATCTCAACAACGAACTGTTGAGACAGGTTG	115
OY	1184	ctaacgcttccaaagttaaaattctttagagtgaggaaaagcaaatgycgtcgaactatc	124
Db	1157	CAAAATAAATTCATTAACAAAATTTGTAAATGGGAAAAAATATATCACGGTAACACTACT	121
OY	1244	ctgataaagcgtcatgatactcgtcatgctcgttactttagcctaataactaaatttgt	130
Db	1217	TTGAAAATGGTTAGAGATGCCCGTTATCTCTGCGAATTTTACAGAAATTAATGAATTTCTTAC	127
OY	1304	ctgagctaaataaagaagcttgaagctggaacgctgtctatctgcaatcaaccaaccaacgcttgg	136
Db	1277	TGAACCTTAAACAAGAGCTTACGCAACAACGTGTCAATTCGCTATTACTACACCAATATGGG	133
OY	1364	ataataatatgggtgagtgtagcaggtttaccaaattgggttgaagcatctaaagagggaa	142
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OY	1424	aagcttatacgcagatgctcttgaagaatgctgcaagaagaagcttgaagctgcttccaatatact	148
Db	1397	AAGCTATGTGTGATGCGCTTGAAGCAACGCAAAACACATTAAAGCCGATTAATTTAGTACAGT	145
OY	1484	tgtatgtctaaacctgtgatcatagacattgtaattccaatlyggaaaaaacycaagcgt	154
Db	1457	TGGATTTTCGGCAACGGTAATTTATGATGATGAGTAAATTTGGGTTAAAGCAAGCATTCACAGTA	151

OY	1544	tgaatltcaactcgcccttgtltaacagaaagaaactgtaacatcagtgaacgttttaactaatg	1603
Db	1517	TCTTATTGGAAGCGCCATTTATTGACGGCGGAAAGAGCATGTGAACGGGTCAACAAG	1576
OY	1604	gtaaataaccttatattiaaagttaaatccggagcgtgaataaacactgccaagttaacg	1663
Db	1577	GTAATAATGAAATATATATTACCAAGCTTCATATTTAACCGTGATGATAGCTGGAAAATTACAG	1636
OY	1664	atggaagagcftagttcctaantagaatttcctaangtaltcaagcgttagacgagacag	1723
Db	1637	ATGGTCACACAAAGTTCTACTCTTGGATTTAACTAACGTGTGCACGCTATTGGTAATGAAT	1696
OY	1724	aaggccacaagagatigtgtcctaaglaaalgcaaaa-----g	1762
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OY	1763	ctgcgaactacgataltcttgttgltcaaggtlaaataatgaatatgatlbgatlgagc	1822
Db	1757	AAGTGATATGACAAACGATTTGTGTGGTTCTGTGACGCGAAATTGATGGCGGTGAAGTT	1816
OY	1823	acgactcgtgctctataglaaagaacgagagatitgtglaatalatcaatcgtlagaigtga	1882
Db	1817	ACGACCGAGTTCACGTATAC---CCGTGGAAACATATAGTGCTTTAACTAATGATCCAACA	1873
OY	1883	gttcaacagaagaagcagatlaaagttaaatcgtgaagtgtgccgagglgatatcac	1942
Db	1874	AAGAGACCAGACAGGTATGTTATACCGTAATATCCTTTGTGAGAAACCGGTGAAGCACTAC	1933
OY	1943	atgaadtgtgtaagcgtcaagaacaacaaagtlbggtlaaaacytaactgnaaactaccagatc	2002
Db	1934	ACGAAGGACTTCAACCCCATTACCGCATTAGTGGCGCACCGTAAGAAAAATATCAATATTC	1993
OY	2003	gtgatattaagatlaaanaaagtgttgtaagttacagttacagttacogataatltgaaacag	2062
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OY	2063	tagaagaagaatigtgttctcaatthaatgaatgtaattcaaaagtcthaatltcaacagaca	2122
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OY	2123	tattccaatgtgtgaagtgatgattacttcgatagtggtgtggtgtgacgcgcgtgtg	2182
Db	2111	CTTTAAACGGTGTGTGATGGTGTGATATATTTGACGGTGTGACGCGCAATACACGCTTAT	2170
OY	2183	tttgtgtlaaagcaacagatcgaacttctcgagatgaagaagcgaatbatlttaactgabtgcg	2242
Db	2171	TTGGTGTGTAAAGCGATGATATTTCTCGATGGTGAAGTGTGATGATTTTATCGATGCGG	2230
OY	2243	gttcctgtgtgatgtatataatagtgtgtgtcgtgtlaaigaatgtcatatclttcggaag	2302
Db	2231	GTAAGGCAACGACCTATTACACGGGTGGCAAGGGCGATGATTTTTCTTCACCGTAAAG	2290
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Db	2468	TGCTTAATTTAAAGCAACTAAAGATGAGAAAATCGAAGAAATCAATCGGTCAAAATGCGC	2527
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Db	2528	AGCGATCACCTCAAAAGCAAGTTGATGATCTAT	2561

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Db	380	CTGGAAAGGATTATAGATAGAGGCGCTTACAA--TAAACGCAACCAACATCTTGGCTA	436
QY	467	aagcgtatcttgcttgatctaagagaataatgtgaatctatctcaagtaactcaaga	526
Db	437	AACTGGCTTGGAGCTAACAAATTCATTATATGAAATAATTGCTAATTACGTAATAAAC	496
QY	527	ctgaagcattcttcacagcttagcaagcttgatgtctctactacacgcgctaaggct	586
Db	497	TTGACGAATTTGGTGAAGCAAAATAGTCATTTGGTTCAAAACTACAAATATCAAAAGCT	556
QY	587	ctcttaataaggaaacagcttgcaaaccttaat---ttcttaaaacaacttgct	643
Db	557	TAGGAGATTAGAGACAAACCTCAAAAATATGCGTGAGCTTATTAAGCTGGCGTTGGTT	616
QY	644	tggaaataatctagcttgcttagcaagcattctgcagcttgctcttagcgataaa	703
Db	617	TAGATGTATCTAGGGCTATTTATCGGGCGCAACAGCTGCACTTTACTTGACAGATATAA	676
QY	704	atgcacgcacgtgcacaaaaagctgcgcgcagtgcttgaattaaagcaatcaatttgta	763
Db	677	ATGCTTCAACAGCTAAAAAGTGGGGGCTTTGAATTTGCAAAACCAAGTTGTTGTA	736
QY	764	atgtacaacaagcaattctctcatatgcttttagcacacaagctgcgcgtgctataca	823
Db	737	ATATTACCAAGCGCTTCTCTTACATTTTATGCCCCAACGTGTTCCACAGATTATCTT	796
QY	824	ctactgtgtgtgtgcttgcttaacttaacttaagatagtgtgcaattgctcttg	883
Db	797	CAACTGGCGCTGGCGCTTATATGCTTACTGTTTCTTCCGATTAAGCCATTAG	856
QY	884	catttaagaaatgcagagataaatacaactcagctacgtctctgatatgcttcaaac	943
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QY	944	aattccgaaaaattggtctatgatlbgggatcattatlgctcgtgaatacaagcgtggtg	1003
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QY	1004	gtactatagaagcttcaataacaaataagaagcaatagtcagttcgtctgctg	1063
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QY	1064	tttcgcgtcgtcgtctgtaggatactgcgtctgttggcgacagatlcacatcttagctga	1123
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QY	1124	ctacagatgatactctctgtaatttagaagcgtctaacaagcaatglttgaaagtgtg	1183
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QY	1184	ctaacgcttacaagtaaaatttttagagtgggaaaaagcaaaatggtgcgttcgaactat	1243
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QY	1244	ctgaataagcctatgatactcgttatgcgtctatcttagctaactaaattttgt	1303
Db	1217	TTGAAAAATGGTTATGATGCCCGCTTATCTTGGCAATTTACAGATTAATTAATTAATCTTAC	1276
QY	1304	ctgaagtaaaataaagcttggaaagctgaaagcgttatcttgcaactcaaccaacaagcttg	1363
Db	1277	TGAACCTTAACAAGAAGTTATACAGCGAAGCGATGTCATTTACTCAGCAGCAATGGG	1336
QY	1364	ataataatcttggttggttagcaggtatactcaaatctgggtgaacgcataagacgga	1423
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QY	1424	aagcttaagcagctgcttcttgaaagatgtaagaagaagcttgaagctgtgtccaatatact	1483
Db	1397	AAAGCTATGTGATGCGCTTTGAAGAAAGGCAACACATTAAGCCCATTAATTAATAGACGT	1456
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Db	1517	TCTTATTGAGAACGCCATTATTATGACGCCGGGACACGACATCTGTAAACGCGTACAAACAG	1576
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Db	1577	GTAATATGAAATATATATTATCCAAAGCTCAATATTAAACCGTGTAGATAGCTGAAAAATTACAG	1636
Oy	1664	atggaagagcttaagttcttaaatagaattctcttaaaagttatccagcgtgtlagccgaagcaag	1723
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Oy	1734	aaggcacgaacgagatctgtctctaactagtaaatgtcaaa-----g	1762
Db	1637	TAGACAAATGCTGTGAATATTACTTAACCAACCAAGAAACAAAATTTTGTCCAAACTTGGTG	1756
Oy	1753	ctygcaatgacgatactcttctgttgcgaaggtlaaaatgaatatltga.tggtggagatgagac	1822
Db	1757	AAGGATGATGACAAACGTATTGTGTGGTCTCGTACACGCAAAATGATGTGGCGTGAAGGTT	1816
Oy	1823	acgatacgttgtctctatagttaagaacggaagatttggtcaatatcttcgttagatgtgtaaga	1882
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Oy	1943	atgaagttctgtgaagcgttcaagaacacaaggttgggtlaaacgctaactgaaactaccgatac	2002
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Oy	2183	tttgtgtgttaaaagcgaacgatacgaacttctctgagatgaagggatatacttcgatgagcg	2242
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Oy	2243	gttctcgttga.tgatagtttaaaagtgtgttgcgttgaatga.tgctc.tatatacttcttggaaag	2302
Db	2231	GTAAGGCAACGACCTATTACACGGGTGGCAAGGGGATGATATTTTTCGTTACCGCTTAAG	2290
Oy	2303	gtgatgtgaatgatacttctgttaacgattggaacgagcgaatgaataatlaagcatttgcagatg	2362
Db	2291	GCGATGGTAAATGATTTATTATACCGATTCTGAACGGCAATGATTAATTTATCATTTCTCTGATT	2350
Oy	2363	caaatatcttga.tatltga.ttgaa.cgttlaccaagaaggttat.tagt.tlaaa.cga.aatg	2422
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Db	1277	TGAAGTAAACAAAGAACTTACAGGACAGAAAGCTGTCTGCTTTACTGACAGCAATGGG	1336
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Oy	1424	aagcttatgcagatgaccttltgaagaatggcagaagaagtltgaagctggtlccaatactact	1483
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Oy	1604	gtaaatcacttataataaataaglttaaatltcgagcgtgtlaaaaaacttgcgaagtlcacg	1653
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Oy	1664	atggagagcgctagtttctaaatltgacttctctaaagttatctgaaggtltagcgtgaacag	1723
Db	1637	ATGTGTGACGAAGTCTTCACTCTTGGATTTAACTAACCGTGTACGGCTATTGGTATTGAAT	1696
Oy	1724	aagcagaagcagagatltggtctlaatagtaatgtcaaaa-----tg	1762
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Oy	1763	ctggcaatgcagatatcttgtgtgtgtcaagtgtaaaatgaataatgtatgtgtgaatgtgac	1822
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Db	1817	ACGACCCAGATTCACTATATG---CCGTGTGAACATGTGTGCTTTAACTATTGTATGCAACA	1873
Oy	1883	gtgcaacagaagcaggagatctataagttaaatcgttaaggtltgctgagtgatctaac	1942
Db	1874	AAGAGACCGACAGATGATTTATACCGTAAATTCGTTCTGTAACAAACCGGTAAAGACATAC	1933
Oy	1943	atgaagttgtgaagcgttcaagaacaaaggttgggtlaaacgttactbtaactacagatctc	2002
Db	1934	ACGAAGTGACTTCACACCCATACCGCAATTAGTGTGGCAACCGTGAGAAAATAATGAAATATC	1993
Oy	2003	gtgactatgaaatlaagaanaaglttgggtatgtgtatcagttcactacgataatltgaatcag	2062
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Oy	2063	tagaagaagtaattgtgttccaaatlaaataagatltcaaaagttcctaattcaacagca	2122
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Oy	2123	tattccatagtgtaagagtgatgtacttactcagatgtgtgtgtgtgaacgcagctgt	2182
Db	2111	CCTTTAACGGTGTGATGTGTGATATTAATTTAGCGTATACGACGCGCAATGACCGCTTAT	2170
Oy	2183	ttgggtgtaaaagcgaacgtacttcttgaagatgaatgaagcgtatgtactcgaatggcg	2242
Db	2171	TTTGTGTGAAGAAGCGGATGATATTCTCGATGTGTGAATGTGATGATTTTATCGATGGCG	2230
Oy	2243	gttctgtgtgatgtatgtataatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2302
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RESULT 10
US-08-535-837-1
; Sequence 1, Application US/08535837
; Patent No. 5985289
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: HARLAND, RICHARD J.
; TITLE OF INVENTION: HAEMOPHILUS SOMMUS OUTER MEMBRANE
; TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBERTA L. ROBINS
; STREET: 285 HAMILTON AVENUE, SUITE 200
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,837
; FILING DATE: 27-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9001-0026.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-9400
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2794 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2778
; US-08-535-837-1

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	Query Match	29.3%	Score 814.4	DB 2	Length 2794
	Best Local Similarity	60.2%	Pred. No. 2.9e-177		
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					Gaps 9
Qy	53 caaagtcgagataaanaatcttactctgacatcccaaat-----tatgatacgcg				106
Db	29 CAAAAACCTGGGGCAAAAAAATATCTCTATATTTCCCAAAATTAACAAATATGATACGG				88
Qy	107 aaaaagtggtgccttaaatgatttataaagcgcgcgaatattgatttcgcgt				166
Db	89 AACCAAGGTAATGTTTACAGGATTTAGTCAAGCGCGCCAAAGAGTTGGGGATTGAGCTAC				148

QY	167	tagaagaagcctatcaacactcigaaacgcgaanaaatcgtgtgacacgtaaatcaagt	226
Db	149	AAAGAGAAAGACCAATATATTGGCAACGCTCAACACCAAGTTTAGGCGACGATTCAAACG	208
QY	227	ttcctctccacaacaactcgtgatgtcattcccttcgcgaacaatatggaagaagcttca	286
Db	209	CTATTTGGCTTAACCTGAGCGCTGGCATTTGTGTATCCGCTCCACAAATTGATAAATTGGCTAC	268
QY	287	aaaaaatcttacaacaatgaatttagccaaagggttagaagcgttagaanaatatgatcgta	346
Db	269	AGAAA-----ACTAAAGCAGCGCAGCAAGTATGTGGTCTGCGCAAGATGTTGCACAA	319
QY	347	aattaggtaaagcaagtaatgatatctatacaacttaagctccttttttggcactcatag	406
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QY	467	aagctagtatctgacttgatataatgataataattggtacatctatcotaagtaactcaaga	526
Db	437	AACTGGCTTGAGAGTAAACAAATTCATTTATGAAATATTGCTAATTCAGTAAAAAACAC	496
QY	527	ttgaagcatttcttcaacggttagcaagttgattgcttactatcgcagcctaaggtc	586
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QY	587	tctctaataaggaaacagttgcaaatcttaat---tttcttaacaacatccttgatt	643
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QY	644	tggaaataactactggttttgcatacagcaattctgcaggtcttggcctttagcggataaa	703
Db	617	TAGATGTTATCTCAGGGCTATATATCGGGCGCAACAGCTGCATCTTACTTCACAGTAAAA	676
QY	704	atgcactgcactgcgaaaaaagttgcgcgcaggttttgaattaaagcaatcaagttatgta	763
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Db	737	ATATTACCAAAAGCCGTTTCTTCTTTACATTTTAAOCCCAACGTTTGCACAGGTTTATCTT	796
QY	824	ctactgctgctgctgctgctttaaattacttcaatcgatlatglttggcaatagtcctt	883
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QY	884	cattatgtaatgcagcagataaatcaatcaatcgaatcgaatgcgttgaatgttgcgaac	943
Db	857	CATTTTGCCGGTATTTGCCGATTAATTTAAATCATGCAAAAAAGTTTAAACAGTTATGCGCAGAC	916
QY	944	aattccgaaaatttgcgtatgcatgagggatcatttatctgcttbaatatacagtggtt	1003
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QY	1004	gtactatgtaagcttcaatcaacatattagtaacgcgacttagtgtagttctcgttggt	1063
Db	977	GGACTATTGATGCAATCGGTACTACGTAAATTAATACCGCATTTGGCCGCTATTTGCTGGTGGTG	1036
QY	1064	ttccgcgtgcgtgtagatcgtcgtgttggtagacagatgacactatgattgtaagtg	1123
Db	1037	TGTCGTGCTGCGACGCGGCTCGGTTATTTGCTTACACCGATTCCTTTATTAATCTGGGA	1096
QY	1124	ttacaagatgatctcgcgaattttagaagcgctctaaacagcgaatgtttgaagaatg	1183
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Db	1217	TTGAAATGGTTACGATGCCCGTTATCTTGGCAATTTTACAAGATTAATGTGAATCTTAC	1276
Qy	1304	ctgagctaaataaagagttggaagctgaaacgltgltatgtcaatcaccacaacglttgg	1363
Db	1277	TGACCTTAACAAAGAGTTTACACGACGAACGCTCATGCTATTACACAGCAATGGG	1336
Qy	1364	ataataattgtgtgagtttagcaggtatlaaccaaatvtgtgtgaacgcatlaagcgga	1423
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Qy	1424	aagcttgcgaagtgcttttgaagaatggaagaagttgaagctgtgttccaattactt	1483
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Qy	1544	tgcattcacttcgcttgttataacagcagaactgtaacgtaacglttaactatgt	1603
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Qy	1763	ctggcaatgcagatattcttgtgtgcgaagttaaataatgaatgtatgtgtgaatgtac	1822
Db	1757	AAGTGATGACAAACGTTTGTGTGTGTTCTGTGTAACGAGAAATTTATGTGGCGTGAAGTT	1816
Qy	1823	acgaatgtcttcttatagtaagaacgagagatttgttaattactgttagatgttaca	1882
Db	1817	ACGACCGAGTTCACTACTATAG---CCGTAAGAACTATGCTCTTAACTATTGATGCAACGA	1873
Qy	1883	gtgcaacagaagcagcaggtatcatcaagttaatcgttaagttgtcagagtgatatctacc	1942
Db	1874	AAGAGACCGAGCAAGGTAGTTATTAACCGTAAATCGTTTCTGTAACAAACCGTAAACACATAC	1933
Qy	1943	atgaagtgtgaagcgtfcaagaacaagaagtggttaaaagttacttaactccagatc	2002
Db	1934	ACGAAGTCACTTCAACCCATACCGCAATTATGTGGGCAACCGTAAACAAAATTAAGATATTC	1993
Qy	2003	gtgatattgaatlaagaanaagttgggtatgtgttatcaagtciaacgataatttgaatcag	2062
Db	1994	GTCATAGCAATTAACACACACCACATG---CCGTTATTACACCAAAATATCTTGAAGCTG	2050
Qy	2063	tagaagaagtaattgttctcaattaaatgaatgtatctaaaggtctcaattcaacagaqa	2122
Db	2051	TTGAAGAAATTAATCGGTACATCATTAACAGATATCTTTAAAGTGTAGTAACTCAATGATG	2110
Qy	2123	tattccatagtgtggaagtgatgattactcgaatgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2182
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Qy	2183	tgtgtgttaagaagaaacgtacgacttcttggaagatgaagaagatgaattactcgaatgcg	2242
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Qy	2243	gtctcgtgtatgataatlaaatgtgtgtgtgtgtatgtatgtctatactcttcggaag	2302
Db	2231	GTAAGGCAACGACCTATTACAGGTGGCAAGGGCAGTATATTTCGTACCGGTAAAG	2290
Qy	2303	gtgatgtaatgataacttgtacgatgtgaacggtgaatgaataattagcatlttgcaatgt	2362

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Qy	2534	gttatatacacttccgatccaattgataaaatttt	25677
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RESULT 11
US-09-124-491-5
: Sequence 5, Application US/09124491
: Patent No. 6022960
: GENERAL INFORMATION:
: APPLICANT: POTTER, ANDREW A.
: APPLICANT: MANN, JOHN G.
: TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: REED & ROBINS LLP
: STREET: 285 HAMILTON AVENUE, SUITE 200
: CITY: PALO ALTO
: STATE: CA
: COUNTRY: USA
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/124,491
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/694,865
: FILING DATE: 09-AUG-1996
: APPLICATION NUMBER: US 08/387,156
: FILING DATE: 10-FEB-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/960,932
: FILING DATE: 14-OCT-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/779,171
: FILING DATE: 16-OCT-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: MCCracken, THOMAS P.
: REGISTRATION NUMBER: 38,548
: REFERENCE/DOCKET NUMBER: 9001-0016.22
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415)327-3400
: TELEFAX: (415)327-3231
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2794 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..2778
: US-09-124-491-5

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Query Match	29.3%;	Score 814.4;	DB 3;	Length 2794;
Best Local Similarity	60.2%;	Pred. No. 2.9e-177;		
Matches 1538;	Conservative	0;	Mismatches 956;	Indels 60; Gaps 9

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OY	467	aagcttatgtacttgatttaataagataaataatgtgatatactcagaagtaactacaaga	526
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OY	587	tctctaataagaaacaagltgcaaaactlaaat--tcttctaanaacaactcttgct	643
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Db	617	TAGATGTTATCTCAGGGCTTTATCGGGCGCAACACCTCAGCTTGTACTTGGACGATTA	676
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OY	824	ctactgtgcgtgtgcgtcgtcttaacttaactcaacgatagtcttgccaattagctcttcg	883
Db	797	CAACTGGGCGCTGGCGCTTAAATTGCTTACACTGTTTCTCTTGCGATTACCCCATTAG	856
OY	884	cattatgaatgcagcagataaatacaatcatatgctaaigtctctgtatgagtttgcanaac	943
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Db	917	GCTTTAAAAAATTAGGCTATGACGAGGATTAATTAATTAAGCAATAATATCACGCGGAACAG	976
OY	1004	gtactatagaagcttcaataactacaataatgtaacgcatltagtgagacttctcgtgtg	1063
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QY	1883	gttgcacaagaagcggaggaattttaaagtttaactgttaaggtgtcgtgagtgatatacc	1942
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RESULT 12			
5476657-2			
Patent No. 5476657			
APPLICANT: POTTER, ANDREW A.			
TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA LEUKOTOXIN			
COMPOSITIONS AND USES THEREOF			
NUMBER OF SEQUENCES: 8			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/15,537			
FILING DATE: 09-FEB-1993			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: 504,850			
FILING DATE: 05-APR-1990			
APPLICATION NUMBER: 335,018			
FILING DATE: 07-APR-1989			
SEQ ID NO.:2			
LENGTH: 2794			
5476657-2			
Query Match			
Best Local Similarity 29.3%; Score 814.4; DB 6; Length 2794;			
Matches 1538; Conservative 0; Mismatches 956; Indels 60; Gaps 9;			

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Db	269	agaaa-----actbaaagcagcgccagacgatlaagttcttcgcgaagcattgtcaaa	319
Oy	347	aattaggctaaagcagaatagtgatctacacattaaagcctcttttggccattgattag	406
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Oy	467	aagctagttatctgacttgatataatgtagaataatgtgaactctatctcagagtactcaacga	526
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Db	497	tttgcgaaatttggtgagcgaattatgctcaaatcttggtctcaaacacatacgaagtc	556
Oy	587	tcctaaataaggaanaaagttgcanaacttaaat---tttctcaanaaactgttgt	643
Db	557	taggagactttagagacaaaactcaaaaataatcggtgacttgataaagcttgcttgct	616
Oy	644	tggaaataactcgtgtgttcatacagcattctgcaggtcttgctttaagcgaataaa	703
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Oy	704	atgcatacagctgcgaanaaagttgtcgcgaggttttgaaattaaagcatacgaattatgta	763
Db	677	atgcttcaacagccttaaaaaggtggggtgcgggttttgaaattgcaaaccaagtttgttga	736
Oy	764	atgcaacaagaagaacttctctcaatctgttttagacaacagttgtcgtgtctatcaa	823
Db	737	atataccagaagcgtttctctctcaacttttagccaaagtggtgcagcaggttatctt	796
Oy	824	ctactggtcgtgtcgtcgtcttaattactcatcagatattgttggcaattagtccttgg	883
Db	797	caactggtcgtgtcgtcgtcttaattgctctctacgtttctctcttgagattagccattag	856
Oy	884	catttatgaatgcagcagaataatccaatccaatgctaatgctcttgatgattgcgaaac	943
Db	857	catttgcggtatctgcgataaatttaactatgcgaanaagtttagagaatttagtcgcgaac	916
Oy	944	aattcggaaaattctgctgatgcagggatgcgaatttatctgtgaatatacgcgtgttgg	1003
Db	917	gctttaaataaatttagcgtatgcagcggagataatttattagcagaataatcagcggggaaag	976
Oy	1004	gtactatttgaaagcttcaattactacaatagtagtcgcatatagtgcaattctcgtgtgg	1063
Db	977	ggaactattgcatcgtgattactgaatccaatccaatcattggtgcgtatgtcgtgtgg	1036
Oy	1064	tttcgcgtgctgctgtcgtagatcctgcgtgtgtgcgaacgttcgactatagttcaggtg	1123
Db	1037	tgctgtgctgtcgtcgaacggtgcgtgtatgtgtcttcacaggtatgctctatagatctggga	1096
Oy	1124	ttacagagattgcatctcgtgaattttagaagcgtctcaaacagcgaattgtttagaagtgtg	1183
Db	1097	ttaccggtgtcaattcttcaagatctcgtcaatatcttcaacaagcaatgttttgacagcttg	1156
Oy	1184	ctaacggttctacaaggtlaaatttttaggtgtgggaaagcgaatgtgcgttcgagaactt	1243
Db	1157	caaatlaaactcttaacaanaattgttagaattggggaaaaaaataatcaggttaagaactact	1216
Oy	1244	ttgttaagaagctatgattctcgtttatgcgtctattttagctataactaaatttttgt	1303
Db	1217	ttgaaatgtgttcgaatcccggtctatctctgcgaatttcaagaatataatgaaattcttacc	1276
Oy	1304	ctgagcgaataaagaatttgaaagctgcgaacggtttatgttcaatcccaacgaagtttgg	1363
Db	1277	tgaacttaaaccaagaagtttaccggtcgaacgctgtcatcgtctattctcagcgaatggg	1336
Oy	1364	ataataatcttggtaggttttagcgggtattaccanaatttgggttgaacgcattaaagcggaa	1423

[illegible]

Db 2231 GTAAAGCAGACGACTATTAACAGCGTGGCAAGGCGATGATATTTGCTACCGSTAAG 2290
Qy 2303 gtagatgtaactgactcttgagatgacgggcaatgataatgacattgcaatg 2332
Db 2291 GCGATGGTAAATGATATTAACGCTCTGACGCAATGATTAATATCTCTCATAT 2350
Qy 2263 caataatctgatatgattgattgaacgtaaccaagaggatattatgattgaacgaatg 2422
Db 2351 CGAAGTTAAAGATTTAACATTGTAAGAAAGTTAAACA----TAATCTTGTCATCAGATA 2407
Qy 2423 atcatcaggtagtattatcaaccaagatgtaacatacaatcttaacaa----- 2477
Db 2408 GCAAAAAGAGAAAGTACCATTCGATTCGAGAGGCGTATTTGCTTAAGAG 2467
Qy 2478 -----tatcaagaataaacaagatcataaattgagcaactatgtaagaatgta 2533
Db 2468 TGCCTAATTAAAGCACTTAAGATGAGAAATCGAAGAATCATGCTCAAAATGCGC 2527
Qy 2534 gtatactactcgatcgatcaatgataaatttt 2567
Db 2528 AGCGGATCACCCTCAAGCAAGTTGATGATCTTAT 2561

RESULT 15
US-07-960-932-8
Sequence 8, Application US/07960932
Patent No. 542210
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUM P.A.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L. ROBINSON
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/960,932
FILING DATE: 19921014
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000-0016, 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2838 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2829
US-07-960-932-8

Query Match 29.3%; Score 814.4; DB 1; Length 2838;
Best Local Similarity 60.2%; Pred. No. 2,9e-177;

Matches 1538; Conservative 0; Mismatches 956; Indels 60; Gaps 9;
Qy 53 caaatcttgatttaaaatccttacttgctatcccaaat-----tatgacgc 106
Db 29 CAAAACCTGGGGCAAAAATAATTAATTCCTATATATCCCAAAATTAACCAATATGATCTG 88
Qy 107 aaaaagtgaggacttaaatgattttaaagctgtgtgaattagtaattcgtc 166
Db 89 AACAGGTAATGCTTACAGAGATTAGTCAAGGCGCCGAAGAGTGGGATTAAGTAC 148
Qy 167 tagcagaagagcctaactacacatgaaacagcaaaaaatcgtgtgacagtaaatcagt 226
Db 149 AAAGAGAAGAACCGCAATATATTCACAGCTCAACAGATTGAGCAAGTTCGAACCG 208
Qy 227 ttctctctccacaacactggtatgctatcttcgaacaaaaattgaaagtcttac 286
Db 209 CTATTTGGCTTAACAGACCGTGGCATTTGTATTCGCTCCACAAATGATTAATTTGCTAC 268
Qy 287 aaaaactctacaatgaattagcgaaggttagcagtgtagaataatgatcgta 346
Db 269 AGAAA-----ACTAAAGCAGGCCAAGCATTTAGTTCTGCCGAAGCATTTACAAA 319
Qy 347 aataggtaaagcaagtaatgtaatacaaatgaactctcttttgggcaatgtag 406
Db 320 ATGCAATTAAGCCCAAAACGTATTAATCTGGCATTAATTAATTTAGGCTCACTATTGG 379
Qy 407 cgggtatagaacttgatcttcaatacaaaaagtgatgctgcaactgattgctta 466
Db 380 CTGGAATGAGATTGATGAGAGCCCTTACAGAA--TAACAGCAACCAACATGCTCTGCTA 436
Qy 467 aagtagtattgacttgattgaatgagatattgtaattctatctacagagtaactcaaga 526
Db 437 AAGCTGCTTGAGCTTAACAATTCATTAAATTAATGTAATTCAGTAAACAC 496
Qy 527 ttgaagcattctctcacagcttagcaagttagttctactatacgcaggtcaagct 586
Db 497 TTGACGAATTTGCTGACCAATATAGTCAATTTGTTCAAAACATCAAAATTCAGAGCT 556
Qy 587 tctctaataagaagaagttgcaaatcttaact--tttctaaacaaatcttgct 643
Db 557 TAGGACTTTAGGAGCAACAACTCAAAATATCGCTGACCTGATTAAGCTGGCTTGCTT 616
Qy 644 tggaaataattactggttgctacagcattcttgaggttgcttgcttgaggtataaa 703
Db 617 TAGATGTTATCTCAAGGCTATTATCGGCGCAACAGCTGCACTTGCTGACATATAA 676
Qy 704 atgacatgcactgcaaaaaagctgctgcaagtttgaaatgaagaatcaagttatgta 763
Db 677 ATGCTTCAACAGCTAAAAAAGTGGGTGGGCTTTGAATTGGCAAAACCAACTGTTGTA 736
Qy 764 atgtaaacaaaagcaattcttcaatgltttagacaacagtgctgctggtctatcaa 823
Db 737 ATATTACCAAGCCGTTCTTCAATTTTAAAGCCCAACGGTTGACGACAGTTATCTT 796
Qy 824 ctactggtgctgctgctttaaacttaactcaatgattgttgcaattgctctctg 883
Db 797 CAACGTGGCGCTGTGCTGCTTATATGCTTCTACTGTTCTCTGCGCATTAAGCCATTAG 856
Qy 884 cattatgaatgcaagcaataaaltcaatcagtaatgctctgtagagttgcaaac 943
Db 857 CATTTGCCGTAATGCGGATTAATTAATCAAGAAAAGTTTGAAGAGTTATGCCAAC 916
Qy 944 aatccgaaaaatttgctatgagtgaggaatcaattatgctgtaatacagcggtgtg 1003
Db 917 GCTTTAAAAAATTAAGCTATGACGAGATTAATTAATTAAGCAATATCAAGCGGGAACAG 976
Qy 1004 gtactattgaagcttcaactaactgaattagtagcagcattgaggtttctgctg 1063
Db 977 GGACTATTGATGATCGCTTACTGATTAATTAATTAATTAATTAATTAATTAATTAATTA 1036
Qy 1064 ttccgctgctgctgtagatctgctgctgctgctgctgctgctgctgctgctgctgctg 1123
Db 1037 TGCTGCTGCTGCAAGCGGCTGCTTATTTGCTTACCGATGCTTATTTAGTATCTGGA 1096

QY 1124 ttacagatgatctctcgtgaattttaagaagcgtcttaacagcgcaatgtttgaagtggtt 1183
Db 1097 ttacggcggttaattttacgattctgcaattcttaaaacgaacgattgtttgacacgttg 1156
QY 1184 ctacacggtttacaggttaaatlttaagtggaagaacgaacatgagcggtcagaactatt 1243
Db 1157 CAATTAATTCATACAAAATTTGTAGAAATGGGAAAAAATATACCGGTAAAGAACTACT 1216
QY 1244 ttgataaagcgtatgatctcgtttatgctgtctattttagactaaactaaattttgt 1303
Db 1217 TTGAAAAATGTTAGCATCCCGTTATCTTGGCAATTTACAAATATATATGAAATTTCTTAC 1276
QY 1304 ctgagctaaataaagaagttggaagcgtgagcgtgtattgtcaatcccaacaaacgttgg 1363
Db 1277 TGAATTTAAACAAAGATTACAGGAGACGTCATGCTATTACTACAGCAATGGG 1356
QY 1364 ataataatltgttgatgaagcaggtatcacaatltggttgaaacgcataagaacgga 1423
Db 1337 ATTAACAACATTGGTATTAGCTGTATTAGCCGTTTGGTAAAGTAAAGTCCCTTGTGGTA 1396
QY 1424 aagcttaagcagatgcttttgaagtgcaagaagaattgaagcgtgtccaatattactt 1483
Db 1397 AAGCTTATGTGATGCGTTTGAAGAGCAACACATTAAAGCGATTAAATTAGTACAGT 1456
QY 1484 tgaatgtcaaaactgtgtatcatagacattgaatltcaaatlbggaaaaaaacgcagcgt 1543
Db 1457 TGGATTTCGGCAAAAGGTATTATTATGATGTGATTAATTCGGGTAAACGAAACTCGACATA 1516
QY 1544 tgcattcaatcgccttctgtttaaagcagcagacgtgaatcagtgtaagtttaactatg 1603
Db 1517 TCTTATTCGAACGCCATTATTATGACGGCGGACAGACAGCANTGTGACGGTACCAACAG 1576
QY 1604 gtaaatcactctatatiaaagttaaatltcgagcgtgtlaaaaaacgtgcagattacag 1663
Db 1577 GTAATATATATATATTACCAAGCTCAATTTAACCGTGTATAGTGTGAAATTTACAG 1636
QY 1664 atgagaaggttagttcttaaatatagatttctctaagttatcagcgtgtgacgcagacag 1723
Db 1637 ATGGTGCACAGATTCTTACTCTTGTATTAACTAACGTTGTTCAAGCGTATTGGTATTGAAT 1696
QY 1724 aagggcaagaagatgtgtctaatagtaaatgcaaaa-----g 1762
Db 1697 TAGACATGCTGGAAATGTAACTAAACCAAAAGAAACAAATAATTATGCCAAACTTTGGTG 1756
QY 1763 ctggcaatgacatatcttctgtgtcaaggttaaatgtaatatltgatgtgtgagatgagc 1822
Db 1757 AAGGTATGACAAAGTATTGTGTGTCTGTACGACGAAATGTGATGCGGTGAAGGTT 1816
QY 1823 aagatcgtgtctctctaatgaagcagaggttggtaatatattactgtatagatgtacga 1882
Db 1817 ACGACCGAGTTTCACTATAG---CCGTGGAACATATGTGCTTTAACTATTGATGCAACCA 1873
QY 1883 gttgcaagaagaagcagattatagcagtttaacgttaagttgtcgtgagttatctacc 1942
Db 1874 AAGAGACCGGACAGGTAGTTATACCGTAAATCGTTTGTAGAAACCGGTAAAGCACTAC 1933
QY 1943 atgaagtttgaagcgtlcaagaacaaggttgggtlaaacgttactgaactatccaglatc 2002
Db 1934 ACGAATGTGACTTCAACCAATACCGCAATGTAGTGGCAACCGTGAAGAAAAATGAAATATC 1993
QY 2003 gtgattatgaatlaaagaagaattgggtatgtatcaagttcaccgataatttgaatcag 2062
Db 1994 GTCATGACATTAACGACGACCATG---CCGTTATTACACCAAAAGATACCTTGAAGGTG 2050
QY 2063 taagaagaagaatgtgttctcaattaaatgaatltcaaaagttcnaaatlcaacagaca 2122
Db 2051 TTGAAGAAATTTATCGTACTATCATATACGATATCTTTAAAGGTAGTAAGTCAATGATG 2110
QY 2123 taltcataatgttgaaggtgatgatattactcgaatgtgtgtgtgtgacacgcgttgt 2182
Db 2111 CTTTAAAGGTGTGATGATGTGATATCATATGACGTTAAGCGCAATGACCGCTTAT 2170

QY 2183 ttgtgttlaaaggcaacgatacgcattcttggagatgaaggcgatgtattactgatgcg 2242
Db 2171 TTGTTGTTAAAGCGATGATATTTCTCGATGTGGAATGGTATGATTTTATGATGCGCG 2230
QY 2243 gttcgtgtatgatgtatlaaagtggtgtgtgtgtatgtatgtctatcttccggaag 2302
Db 2231 GTAAAGCAACGACCTATTTACCGGTGGCAAGGCGGATGATTTTGTTCACCGTAAAG 2290
QY 2303 gtaatgttaatgaatttctgtacgataggcagggcaatgaataatlaacatttgcagatg 2362
Db 2291 GCGATGATATGATATTTATTTACCGATTTCGACGCAATGATTAATATATCTCTCGATT 2350
QY 2363 caaatatactgataatgaattgaacgtaccaaagaggtatattatagttaaagaatg 2422
Db 2351 GCAACTTAAAGATTTTAACTTTGAAAAAGTTAAACA---TAAATCTGTATCAGCAATA 2407
QY 2423 atcattgaatgaatlaacatacacaagatggtatcacaatacaaatlttaacaaa----- 2477
Db 2408 GCAAAAAAGAGAAAGTACCATTTCAAAACTGTTCCGAGAGGCTGATTTGCTAAAGAA 2467
QY 2478 ----tataaagaataaacaagatcataaataatltgagcaactaatltgtlaagatgtga 2533
Db 2468 TGCTTAATTTAAAGCAACTTAAAGATGAGAAATCGAAGAAATCATGTCAAAATGGCG 2527
QY 2534 gttatcaacttccgatacaaatltgataaatltt 2567
Db 2528 AGCGATCACCTCAAGCAAGTTGATGATCTTAT 2561

Search completed: September 15, 2002, 11:17:13
Job time: 15360 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 11, 2002, 08:56:42 ; Search time 65.81 seconds
(without alignments)
2436.807 Million cell updates/sec

Title: US-09-884-696-2
Perfect score: 4646
Sequence: 1 MSNINVIKSNIOAGLNTSKS.....SSNALQPIPTQGLAPSV 927

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

1: SP_TREMBL_19:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rv1rus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4646	100.0	927	2	093G12
2	2358.5	50.8	946	2	09EV24
3	2356	50.7	953	2	09EV23
4	2355	50.7	953	2	09EVX2
5	2355	50.7	953	2	09EV25
6	2345	50.5	953	2	09EV26
7	2338.5	50.3	953	2	09EV32
8	2336.5	50.3	953	2	09EV33
9	2332.5	50.2	953	2	09EV28
10	2332	50.1	953	2	09EV25
11	2329.5	50.1	953	2	09EV31
12	2329	50.1	953	2	09EV27
13	2329	50.1	953	2	09EV29
14	2326	49.9	953	2	09EV34
15	2320	49.9	954	2	09EUE1
16	2307	49.7	953	2	09EV30

17	2286	49.2	955	2	09EV22	09ev22 pasteurella
18	2274	48.9	955	2	09EUD4	09evd4 pasteurella
19	2233.5	48.1	956	2	093NP1	093np1 actinobacil
20	2008.5	43.2	1049	2	09RCG8	09rcg8 pasteurella
21	1960.5	42.2	1052	2	093NP0	093np0 actinobacil
22	1820	39.2	1055	2	043892	043892 actinobacil
23	1766	38.0	998	2	085101	085101 escherichia
24	1764	38.0	998	2	09LC58	09lc58 escherichia
25	1760	37.9	998	2	P71223	P71223 escherichia
26	1752	37.7	998	2	046716	046716 escherichia
27	1740	37.5	1022	2	093NP2	093np2 actinobacil
28	1738	37.4	998	2	047461	047461 escherichia
29	1733	37.3	998	2	047262	047262 escherichia
30	803	17.3	1706	2	09L469	09l469 bordetella
31	482	10.4	233	2	051865	051865 pasteurella
32	411	8.8	1208	16	09PE19	09pe19 xyella fas
33	410	8.8	1636	16	09PE17	09pe17 xyella fas
34	391	8.4	2064	16	09PAT8	09pat8 xyella fas
35	383	8.2	208	2	051868	051868 pasteurella
36	367	7.9	850	2	0937V6	0937v6 bordetella
37	365	7.9	697	16	09JTM8	09jtm8 nelsseria m
38	365	7.9	850	2	0937M0	0937m0 bordetella
39	364	7.8	850	2	0937W1	0937w1 bordetella
40	364	7.8	850	2	0932Y7	0932y7 bordetella
41	363	7.8	850	2	0937V9	0937v9 bordetella
42	363	7.8	850	2	0937V5	0937v5 bordetella
43	363	7.8	850	2	0937V4	0937v4 bordetella
44	362	7.8	850	2	0937V8	0937v8 bordetella
45	360	7.7	850	2	0937V7	0937v7 bordetella

ALIGNMENTS

RESULT 1
ID 093G12 PRELIMINARY; PRT; 927 AA.
AC 093G12:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE RTX TOXIN.
GN MBXA.
OS Moraxella bovis.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
OX NCBI_TaxID=476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TIFTON I;
RX MEDLINE=2138402; PubMed=11497442;
RA Angelos J.A., Hess J.F., George L.W.;
RT "Cloning and characterization of a Moraxella bovis cytotoxin gene.";
RL Am. J. Vet. Res. 62:1222-1228(2001).
DR EMBL; AF205359; AAK84651.1; -
SQ SEQUENCE 927 AA; 98845 MW; F4B703577E10A96D CRC64;

Query Match 100.0%; Score 4646; DB 2; Length 927;
Best local similarity 100.0%; Pred. No. 7.8e-199;
Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSNINVIKSNIOAGLNTSKGKRLYLAIKPDYPOKGGTLNDPIKADELGIARLAEPP 60
DB 1 MSNINVIKSNIOAGLNTSKGKRLYLAIKPDYPOKGGTLNDPIKADELGIARLAEPP 60
QY 61 NHETAKSVDTVNOQFSLTQTGAISATKLEKFLQKHSNKLAKGLDSVENIDRLGKA 120
DB 61 NHETAKSVDTVNOQFSLTQTGAISATKLEKFLQKHSNKLAKGLDSVENIDRLGKA 120
QY 121 SNVLSTLSSFLGALAGIELDSLKKGDAPDALAKASIDLINETIGNLSOSTOTTEAFS 180
DB 121 SNVLSTLSSFLGALAGIELDSLKKGDAPDALAKASIDLINETIGNLSOSTOTTEAFS 180

Oy	820	-ITSLNQYGNKRDHKTEQLGDKGSITTSDDDKLIDQKKDGVITTSOELKLADENK	878
Dd	838	DFANEAVNYKATK-DEKIEETIGONGERITSKOVDDL--AKNGKITODELSKVVDNE	894
Oy	879	SOKISASDIASSLNKVLGSMALFGANVSVAANOPIPTPROGI	922
Dd	895	LKHHS-KWNTNSLDKLSSASAFITSSNDNRVLAFTSMDOSL	937
 RESULT 3 O9EV23 PRELIMITARY; PRT; 953 AA.			
ID	O9EV23	PRELIMITARY;	PRT; 953 AA.
AC	O9EV23		
DT	01-MAR-2001	(TREMBLrel. 16, Created)	
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)	
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)	
DE	LEUKOTOXIN.		
CN	LkTA.		
OC	Mannheimia glucosida.		
OC	Bacteria; Proteobacteria; gamma subdivision: Pasteurellaceae;		
CC	Mannheimia.		
OX	NCBI_Taxid=85401;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-PH290.		
RX	MEDLINE=21101823; PubMed=11157953;		
RA	Davies R.L., Whitlam T.S., Selandar R.K.;		
RT	"Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)		
RT	Gene In Bovine and Ovine Strains of Mannheimia (Pasteurella)		
RT	haemolytica.";		
RL	J. Bacteriol. 183:1394-1404(2001).		
DL	EMBL; AF314522; AAC40306.1;		
DR	InterPro: IPR001753; Enoyl_CoA_hydrtse.		
DR	InterPro: IPR001343; Hemlysn_Ca_bnd.		
DR	InterPro: IPR003355; RTX_N.		
DR	Pfam; PF00335; hemolysinCbind; 1.		
DR	Pfam; PF02382; RTX; 1.		
DR	PRINTS; PR00313; CABDNRGPT.		
DR	PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.		
SO	SEQUENCE 953 AA; 102150 MW; D99C36DA595B1624 CRC64;		
 Query Match 50.7%; Score 2356; DB 2; Length 953; Best Local Similarity 49.5%; Pred. No. 5,4e-97; Matches 471; Conservative 182; Mismatches 258; Indels 40; Gaps 15;			
Oy	1	MSNIIV-IKSN---IQAGINST-----KGLKNLYAIAPKD--YPDQKGSTLND	43
Dd	5	LTNISTNKSSWLPAKSGSLNRTGOSLAKAGOSLKTKARKIILYIPKYDYDTEKGGNLDD	64
Oy	44	FIRKADELGIARLAEPEPHHTETAKKSVDPVNQFSLTQTGIAISATKLEKFLQKSHTNKL	103
Dd	65	LVKAAEELEGIEYQKEGDIAKAQYISLGTTIGNVLELTGERGYLSAPOLDKLQK---IKV	121
Oy	104	AKGLDSVENIDRKLGKASNVLSTLSSFGLTAGIELDSLRIKKGAAPDALAKASIDLIN	163
Dd	122	GQAISASAMLRKGFSENMATVTLSIGQSILGSYVALGMDUDEALQK-MSNELTLAKAGDELIN	180
Oy	164	EICGLWSOTGTITEAFSSQLAKLGSTISQAKGFSNIGKNKLQN-N-FSKTNLGEITITGL	222
Dd	181	SLIEIANSVYTLDAFDGOINDGSKLQNVKLSLIGDKLKLSGFDKTSILDIDVSSGL	240
Oy	223	SGISGFLALPKMASTGRKVAAGFELSNOVGNTKATISSYVLAAQVAAAGSTTGVAVAL	282
Dd	241	SGATIALVALDKMASTSRKVAGGFEFLAMOVGNITKAAVSSYLLAORVAAGLSTGPVAL	300
Oy	283	ITSSIMLASPLAFNAADKFHNHAALDEFKQFRFFGYDGDDHLAEXORGVGITIASLT	342
Dd	301	IASYSLAISPLAFGIADKRFHNASLSDSYAERFKKLGVDGNNLLAEYRGRTGTDASYT	360
Oy	343	TISTRALGAVSGVSAAYGAVGAPIALLVAGVTGLISILEPASKQAMFESVANRLOGKI	402
Dd	361	AINTPLAIIAGVGSAAAGSVYASTIALVSGITVISTIILOSQAMENEHANIKNKI	420

QY	403	LEWENQNGGCVFQDQXSRVAAYLANNLKFLSELNKELEBRVATITQOHRMDNIGELA	40
Db	421	WEWENNNNGKNTFENGXYATRLANTQDMKFLNLNKLQERVATITITQOQMDNNIGDLA	48
QY	463	GITKRGKIKSGKAADAFEDQGVKQVACSNITLDAKTIITDINSNGKATQALHTSPLL	52
Db	481	GISRLGEVLSGKAAYVDAFEECKHLKAKLKVQDLSANGIDIVSNSGAKQTQIILFRTLPL	54
QY	523	TAGTESRRLTLNGKSYITNKLFGKRVKMWQVTDGEASSKLDFSKVIQVY-----AETE	57
Db	541	TPGTGHRERIRIQGKXEYITKLININRVDSMKITDGAASFPLDTLTVVQRIGIELDAGNVT	60
QY	576	GTDDELGLLVNNAKAGNDLTFVQGGKNNIDGCGSHDDVVFQSKQCGFQNTIVDTGSATEAGSY	63
Db	601	KTKERKIVAKLGAGDQNVFVSGTTEIDGEGEYDVRVSR-GNYALTYIDAKTEHQGSY	65
QY	636	TVNRKRVAGDLYHEVYVKKQETQVKGKRTETIQYRDYELKRVGYGYOSTNLKAVEEVISQ	69
Db	660	TVNRREVVEGKALHEVTSHTLTALVGNREKIEYR-HSNQNHAGYTTKTKLAVEELIGTS	71
QY	696	FNDVFKGSKFNDIFHSGEDDLDDGAGDRLFGSKGNDRLSGDEGDDLDDGSGSDVYLN	75
Db	719	.HNDIFKSGSKFNDAFNGGQVDITIDGNDGNDRFLFGKGCDDIIDDGNGDGFIDGSKGNDLH	77
QY	756	GGAGNDVYIFPRGCGNDPLTYOSTGNDKTLAFADANISDIMEERTKGGITVYKRNDHSGSINI	81
Db	779	GKGDDITFVHRGDDNDITTDSDGNDKLSFSDSNLKDITFEFVYKHNLVY-TSRKREKVTI	83
QY	816	PRWY----ITSNLQVNSQKTDHKEIQLGKQSGSYTTSQDILKLDQKKDGTIVITSQELK	87
Db	838	QDMFEADPAFKRVRYKATVK-DEKIEIILQNGERTSKQVDDLL-AKNGKKTIDQELS	89
QY	872	KLADENKSKQKLSASDIASLKLKLVGSMALFGTANSVSNALOPTIQTPTGCI	922
Db	895	KVVDVYELLKHS-KNVTNSLDKLISASAFSTNSDSRNVLVAPMTLQDSL	944
RESULT 4			
Q9ETX2	1D	Q9ETX2 PRELIMINARY: PRT: 953 AA.	
AC	Q9ETX2:		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	LEUKOTOXIN.		
GN	LKTA.		
OS	Mannheimia glucosida.		
OC	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;		
OC	Mannheimia.		
OX	NCBI_TaxID=85401,		
RM	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=PH49, AND PH344;		
RA	Davies R.L., Whitlam T.S., Selander R.K.;		
RT	"Sequence diversity and molecular evolution of the leukotoxin (Lkta)		
RT	gene in bovine and ovine strains of Mannheimia (Pasteurella)		
RT	hemolytica."		
RL	J. Bacteriol. 0:0-0(2001).		
DR	EMBL; AF314518; AAC40302.1; -		
DR	EMBL; AF314517; AAG40301.1; -		
DR	InterPro: IPR001473; Enoyl_CoA_hydrtase.		
DR	InterPro: IPR001433; Hemolysin_Ca_bind.		
DR	InterPro: IPR003355; RTX_N		
DR	Pfam; PF00353; HemolysinCbind; 1.		
DR	Pfam; PF02382; RTX; 1.		
DR	PRINTS; PR00313; CABDNCRPT.		
DR	PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.		
SEQ	SEQUENCE 953 AA: 102133 MW: 70DB354157F5881E CRC64;		
Query Match 50.7%; Score 2355; DB 2: Length 953;			
Best Local Similarity 49.5%; Pred. NO. 6e-97;			


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Db 601 KTKETKIYAKLAGADDNVEVSGCTEIDGEGYDRVHYSR-GNYGALITIDATKETEGSQ 659
Qy 636 TYNRKARADIDYHEVYKROETKYKRTETIQYRDYELRKVGYGYOSTDNKSYEEVIGSQ 695
Db 660 TYNRFETSKALHEVSTHTALVGNREEKIEYR-HSNQNHAGYTRYKDTLKAEEIIGTS 718
Qy 696 FNDVFGSKFNDIFHSGEDDLIDGAGDRLFGKGNDRLSGDEGDDLLDGGSGDDVYN 755
Db 719 HNDIFGSKFNDAFNAGDDVDITDGDNDRLFGKGGDDIIDGNDDDPFDGSGKNDLH 778
Qy 756 GGAGNDVYIFRKGDNDTLYDGTGNDKLAFPADANISDIMIERTKEGIYKRNHSGSINI 815
Db 779 GGGGDDIFVHRQGDNDIITDSGNDKLSFSDSNLKDLPFEKYKHNLYI-TNSKREKVTI 837
Qy 816 PRMY-----ITSNLYNQNSKKTDEKIEQLGKDSYITTSQIDKIIDKDKDGYITSOEL 871
Db 838 QDMFREADFAKEVRNRYKARK-DEKIEIIGQNGERTSKOYDOLI--ANGNGKITODELS 894
Qy 872 KLADEKRSOKLSASDIASSLNLKLVGSMALFGTANSVSNALOPITPOTOGI 922
Db 895 KYVDNELLAKHS-KNYTNSLIDKLISASAFSTSSNDSRNVLVAFTHMLDOSTL 944

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RESULT 6
Q9EV26 PRELIMINARY: PRT: 953 AA.
AC Q9EV26: 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LEUKOTOXIN.
GN LKTA.
OS Mannheimia glucosida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=85401;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PH240;
RX MEDLINE=21101823; PubMed=1157953;
RA Davies R.L., Whitlam T.S., Selander R.K.;
RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (lktA)
RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
RT haemolytica."
RT J. Bacteriol. 183:1394-1404(2001).
DR EMBL: AF314519; AAG40303.1.-;
DR InterPro: IPR001753; Enoyl_COA_hydrtase.
DR InterPro: IPR001343; Hemolysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PF00353; hemolysinCbind; 1.
DR Pfam: PF02382; RTX_1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN.1.
SQ SEQUENCE 953 AA; 102236 MW; AC5874B3B75D1C98 CRC64;

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Query Match 50.5%; Score 2345; DB 2; Length 953;
 Best Local Similarity 48.9%; Pred. No. 1.7e-96;
 Matches 468; Conservative 186; Mismatches 250; Indels 54; Gaps 16;

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Qy 1 MSNINY-IKSN---IOAGINST-----KSGLKNLYLAIPKD--YDPQKGGTND 43
Db 5 LTNISTNLKSSWLTAKSGLNRTGQSLAKAGQSLTKGAKKILILIPKDYDTDEKGGNLOD 64
Qy 44 FTKADELCIARLAEPNHTETAKKSVDPVNOFLSTQTGIAISATKLEKFLQKHSNTKL 103
Db 65 LVKAARELGIYVQKEEGNDIAKQTSLTGTLQNVGLTBERGIVLASAQDOKLQK---TKY 121
Qy 104 AAGLDSEVINDIKRLKASAVNLSTLSFGLTALAGIELDSLTKGDAAPDALAKASIDLIN 163
Db 122 GGAISAEMLTKGFNSNAKTVLSGIIOSIILSGISVLAGMDLDELQK--NSNETLAKAGLELTN 180
Qy 164 EIIIGNISQSTQRTIEARSSQLAKGSIISQAKGFSNIGNKLQNLN-PSKTNLGLIEITGLL 222

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Db 181 SLENIANSKYTIDAFGDDQINQSGKIQNKYGLSSLDKLAGSGDKTSGLGDVYSGLL 240
Qy 223 SGISAGFALADKNASTGKKVYAAGFELSNOYIGNVTRAISSYVLAQRYAAGLSTTGAAAL 282
Db 241 SGATLAVLADKNASTRKAGAGFELANQVYGNITRAVSSYILAQRVAAAGLSTGPVVAL 300
Qy 283 ITSSIMLATSPLAFMAAKDFFNANALDEFARPKFRFGYGDHLLAEYQGVGTIASLT 342
Db 301 IASTVLSAISPFAGIADFNNAKLSLEYAEFFKRLGVDGMDLAEYQGTSTIASVT 360
Qy 343 TISTALGAVSAGVAAVAGAPATALLAVAGTGLISGLISLEASKQAFESVANRLQGI 402
Db 361 AINTALALAGVSAAAGVINSPIALLVSGITGVISTILOYSKQAFEHVANKIHNKI 420
Qy 403 LEWEKONGVYFDKGYDSRYAAYLANNLKFLSELNKELEAEVIAITQORMDNIGELA 462
Db 421 VEMEKNNHGNYPENGYDARYLANLDNMKFLNLNKELOAERVIAITQOQMDNIGDLA 480
Qy 463 GIKKLEGRISKARAYADAFEDGKKVEAGSNITTDARTGIIDISNSKKTQALHTSPIL 522
Db 481 GISRLGEKYLISKAAYDAFEEGKHLKADKLVDLSANGIIVDSNSGAKTOHILFTPPL 540
Qy 523 TACTESRERLTNGKYSYINKLKFGRVKNMOVTDGEASSKIDFSGKIORY-----AETE 575
Db 541 TPCTEHRERQYQTKYEITKLTNLNRYDSWKITDGAASSTDTDLNVORYGIELDNAGNVT 600
Qy 576 GTDELILYNAKAGNDIFVGGKMNIDGGDGHDRVFSKDGFGNTVDGTATAGSY 635
Db 601 KTKETKIYAKLAGADDNVEVSGCTEIDGEGYDRVHYSR-GNYGALITIDATKETEGSY 659
Qy 636 TYNRKARADIDYHEVYKROETKYKRTETIQYRDYELRKVGYGYOSTDNKSYEEVIGSQ 695
Db 660 TYNRFETSKALHEVSTHTALVGNREEKIEYR-HSNQNHAGYTRYKDTLKAEEIIGTS 718
Qy 696 FNDVFGSKFNDIFHSGEDDLIDGAGDRLFGKGNDRLSGDEGDDLLDGGSGDDVYN 755
Db 719 HNDIFGSKFNDAFNAGDDVDITDGDNDRLFGKGGDDIIDGNDDDPFDGSGKNDLH 778
Qy 756 GGAGNDVYIFRKGDNDTLYDGTGNDKLAFPADANISDIMIERTKEGIYKRNHSGSINI 815
Db 779 GGGGDDIFVHRQGDNDIITDSGNDKLSFSDSNLKDLPFEKYKHNLYI-TNSKREKVTI 837
Qy 816 PRMY-----ITSNLYNQNSKKTDEKIEQLGKDSYITTSQIDKIIDKDKDGYITSOEL 871
Db 838 QDMFREADFAKEVRNRYKARK-DEKIEIIGQNGERTSKOYDOLI--ANGNGKITODELS 894
Qy 872 KLADEKRSOKLSASDIASSLNLKLVGSMALFGTANSVSNALOPITPOTOGI 922
Db 897 VQVYELLK-----HSKNYTNSLIDKLISASAFSTSSNDSRNVLVAFTHMLDOSTL 944

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RESULT 7
Q9EV32 PRELIMINARY: PRT: 953 AA.
AC Q9EV32: 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LEUKOTOXIN.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PH706;
RX MEDLINE=21101823; PubMed=1157953;
RA Davies R.L., Whitlam T.S., Selander R.K.;
RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (lktA)
RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
RT haemolytica."

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RESULT 10
OQETG5 ID OQETG5 PRELIMINARY; PRT: 953 AA.
AC OQETG5;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE LEUKOTOXIN.
GN LKTA.
OC Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_Taxid=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PH284, PH388, AND PH8;
RA Davies R.L., Whittam T.S., Selander R.K.;
RT "Sequence diversity and molecular evolution of the leukotoxin (lktA)
RT gene in bovine and ovine strains of Mannheimia (Pasteurella)
RT haemolytica.";
RL J. Bacteriol. 0.0-0(2001).
DR EMBL; AF314507; AAC40291.1; -
DR EMBL; AF314504; AAC40288.1; -
DR EMBL; AF314506; AAC40290.1; -
DR InterPro: IPR001753; Enoyl_CoA_hydrtse.
DR InterPro: IPR001343; Hemolysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PF00353; hemolysinCbind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS; PR00313; CABNDNGRPT.
DR PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 101997 MW; D593D6A577C3ADE9 CRC64;

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Query Match 50.2%; Score 2332; DB 2; Length 953;
Best Local Similarity 50.1%; Pred. No. 6.3e-96;
Matches 465; Conservative 175; Mismatches 263; Indels 26; Gaps 13;

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OY 8 KSNTOAGINSTKSGKNTLYAIIPKD--YDPOKGGTLNDFIKADELGARLAEEPHHET 65
DB 28 QSLTQAG-SLKTGAKKTIILYIPQNYDTDEQNGLODIVRAEELGLEVOREEHNNIAT 86
OY 66 AKKSVDTVNOPLSTOTGIAISATKLEFLOKHSSTNKLAKGLDSVENIDRLGKASNYLS 125
DB 87 AQTSLGTIQTALGTERGIVLASPIDKLQK--TKAGQALGSAESIYONAKKATYLS 143
OY 126 TLSSFLGALAGTIELDSLTKKDDAAPDALAKASIDLINEIIGNSQSTQITAFESSQLAK 185
DB 144 GIQSTILGSLVAGMDLDEAL-QNNSNQHALAKAGLELTNSLENIANSVKTIDDEFGEQISQ 202
OY 186 LGSTTSQAKGFSNIGNKTONL-NFSKTNLGLIEITGLSGISAGPALDKNASTKRYVA 244
DB 203 FEGSLQNTKIGLCTLDGDKLNTGGLDKAGIGLDVIGSLSGATAALVLADKNASTKRYGA 262
OY 245 GPELSNOYIGNVTKAISSVYLAQRYAAGLSTGAAVALITSSIMALISPLAFMAADKFN 304
DB 263 GPELANQYVGNITTKAVSVYLAQRYAAGLSTGPAVALIASVLSALISPLAFAGIADKFN 322
OY 305 HANALDEFAPKRFKRGYDGDHLLAEYQKRGVTEASLTITISALCAVSAAGVAAVGSAY 364
DB 323 HAKSLESYAERFKLGYDGDNLAEYQKRGVTEASLTITISALCAVSAAGVAAVGSAY 382
OY 365 GAPILLAVAGVTGLSGITLSEASKQAMFESVANRLQGTILEMKGNGGONYFPKGYDSRYA 424
DB 383 ASPILLVSGITGVISTIIQYSKQAMFESVANRLQGTILEMKGNGGONYFPKGYDSRYA 442
OY 425 ATLANKLFLSELNKELEAEVYATITQORWNNIGELAGITLGRINSGKAYADAFEDG 484
DB 443 ANLQNMKFLNLNKELEAEVYATITQOQWNNIGELAGISRLGKAYADAFEDG 502
OY 465 KVEVGSNTTLDKAGTIIDISNSNGKTOALHFTSPLLTAGTESRRLTNGKRYTIINKLK 544

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DB 503 KHKRADKLVOYDLSANGIIVDSNSGKAKTOHILFETPLLTGTEHREHRYQTKYEYIKLN 562
OY 545 FGRYKNNQVTDGEASSKLDSKVIORY-----AETEGDELGLYNNAAGNDIPVQ 597
DB 563 INRVDSMKITDGAASFEDLITNVQIRIGIELDNNAGNVTKRETKLAKLCEGDNNFVGS 622
OY 598 GKMMIDGDDGHDVRYFSKDGFGNITVDGTSATEAGSYTVNRKVARGDIVHEVYKROETK 657
DB 623 GTTEIDGEGEDRYHYSR-GNYGALTIDATKETFGQSYTVNRFVETGKALHEVYSTRHAL 681
OY 658 VGRTEITQYRDYELRKVGVGYOSTDMLKSYEYIGSQFNDVFRGSGFNDFHSGEDDL 717
DB 682 VGNREEKIEYR-HSNNOHHAGYTKYKDLKAVEELIGSHNDIFRGSKFNDFNGDDVDT 740
OY 718 LDGAGDDRLFEGKGNDRLSGEGDDLLDGGSGDVLNGAGNDVYIFRRKGNDTLTYD 777
DB 741 IDGNDGNDRLEFGKGGDDLLDGGNDDEFLDGGKNDLHKGDDIFVHRGDDNDITDS 800
OY 778 TGNDKLAEPADANISDMIERTKEGIYVRNDHSGSINIPWY---ITSNLQNYQSKTD 833
DB 801 DGNDKLSPSDSNLKDITFEKYNHLYI-TNSKREKVTIDWFREADPAKEVPYKATK-D 858
OY 834 HKIQQLGKDSYTTSDQIDKILQDKDGYITTSQELKLADENKSKLASDLSAASLTK 893
DB 859 EKIEELIGQNEERTSKQVDDL--AKGNKKITQDELKSVYDNYELKHS-KVNTSLDK 915
OY 894 LVGSMALFETANSVSSNALOPITQPTQGI 922
DB 916 LISSVAFSTSSNDSRNVLVAFSTMLDQSL 944

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RESULT 11
OQEV31 ID OQEV31 PRELIMINARY; PRT: 953 AA.
AC OQEV31;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE LEUKOTOXIN.
GN LKTA.
OC Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_Taxid=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PH588;
RA MEDLINE=21101823; PubMed=11157953;
RA Davies R.L., Whittam T.S., Selander R.K.;
RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (lktA)
RT gene in bovine and ovine strains of Mannheimia (Pasteurella)
RT haemolytica.";
RL J. Bacteriol. 183:1394-1404(2001).
DR EMBL; AF314510; AAC40294.1; -
DR InterPro: IPR001753; Enoyl_CoA_hydrtse.
DR InterPro: IPR001343; Hemolysn_Ca_bind.
DR Pfam: PF00353; hemolysinCbind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS; PR00313; CABNDNGRPT.
DR PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 102160 MW; A189BF80754A7907 CRC64;

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Query Match 50.1%; Score 2329.5; DB 2; Length 953;
Best Local Similarity 50.1%; Pred. No. 8.1e-96;
Matches 469; Conservative 178; Mismatches 259; Indels 31; Gaps 16;

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OY 5 NVKSNIOAGINSTKSGKNTLYAIIPKD--YDPOKGGTLNDFIKADELGARLAEEPHNH 62
DB 25 NAGQSLAKAG-QSLKTGAKKTIILYIPQNYDTDEKNGLODIVRAEELGLEVOREEGND 83

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OY      696 FNDVFKSGKFNDFHSEGGDILLDGAGGDRIFRGKRKNDBLSDEGEDDLLDGSSGDVYN 755
Db      719 HNFIFKGSKRFMDAENGSDGVFTIDGNNGNRLFEFGKGDDLLIDGNGDDEFIDGKRGNDLH 778
OY      756 GGACNDVYIFPKGGNDPLVDGTGDNKLAFADANISIMIERTEKEGIIVRNHGSGSINI 815
Db      779 GKKRQDLIFVHHGONGNSITFESBCKDLSTDSNLKLTFFEKVNHLHY-TNKQEKVTI 837
OY      816 PRWY----TTSLNANYOSNKTDRKHIEOLICKDGSYITSDOIIDLQDKKDGYVTSOELK 871
Db      838 QNMWFREAEFKATIONNYATR-DDKIEEIIIGONGERITSKOVELITE--KNGKIAOSELT 894
OY      872 KLAENASQKIASADIASSLKUKLGVSMALETASVSNNLPOTPTOGGLIPSV 927
Db      895 KVVDNYQLHKYS-RDASNLDKLLISSASAFTSSND-SRWLV---ASFY-SMLDSPSL 944

RESULT   13
09EVZ9          PRELIMINARY;             PRT;           953 AA.
AC    09EVZ9;
DT    01-MAR-2001 (TREMBrel, 16, Created)
DT    01-MAR-2001 (TREMBrel, 16, Last sequence update)
DT    01-DEC-2001 (TREMBrel, 19, Last annotation update)
DE    LEUKOTOXIN.
GN    LkTA.
OS    Pasteurella haemolytica.
OC    Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
CC    Mannheimia.
OX    NCBI_Taxid=75985;
RN    [1]
RP    SEQUENCE FROM N.A..
RC    STRAIN=PR278;
RX    MEDLINE=21101823; PubMed=11157953;
RA    Davies R.L., Whittam T.S., Selaender R.K.;
RT    "Sequence Diversity and Molecular Evolution of the leukotoxin (lktA) gene in Bovine and Ovine Strains of Mannheimia (Pasteurella) haemolytica.";
RL    J. Bacteriol. 183:1394-1404(2001).
DR    EMBL, AF314514; AACG40298.1;-
DR    InterPro; IPR001753; Enoyl-CoA_hydrtse.
DR    InterPro; IPR001343; Hemilysin_Co_bind.
DR    Pfam; PF003355; RTX_N.
DR    Pfam; PF00353; hemolysincabind; 1.
DR    PRINTS; PRO0313; CAENDNGRPT.
DR    PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ    SEQUENCE 953 AA; 102147 MW; 11600FDA7849AICA CRC64;
```

[illegible]

QY	302	KFNHANA	LDEFAKOFKRFYGDGHLAEYRGVGTTEASLTTTSTALGAVSAGVSAAG	361
Db	320	KFNHAKS	IEAEEFKFKIGYDGNLLAEYRGVGTIDASTATINTALAAIAGVSAAG	379
QY	362	SAVAPAIL	VAGTGTGIGLEASRCAMEEVSANRLOGKILTEMKONGONFEDKGYDS	421
Db	380	SVASIPALL	VSITGTITLLOYSKRAMERHANRKHNVEMKNNHKKNFENGYDA	439
QY	422	RYAAVLANN	KFUSELKELEAEERVAITQORMDNIGELATTKLGERIKSGAYADAF	481
Db	440	RYLANLOD	NMFELTNLKKELDAEERVAITQOOWDNNIGLAGISRLGEKLSGKAVDAF	499
QY	482	EDGKRV	EGSITTDATGTIIDSNSKGTQALHFTSPLLTAGTSREHRTMGKYSYN	541
Db	500	EEGHKIKAD	KLVQDSSANGIIDSNSKATQHTLFTPTLFTGTEHREHVOTGTEYIT	559
QY	542	KLKFGRYK	NQVVTGDEASSKLDEFSKYIQRY-----AETEGTDEIGLIYNARAGNDIP	594
Db	560	KLININR	VDMSKITTGGAASFEDLLINVQRIIGIELDNAGNVTKTKETKILAKLEGDDNVF	619
QY	595	VGGCKM	INDGSDGHDRAVYFSKDGEGFNITVDGTSATFAGSYTNRRKARADYHVEYKRQ	654
Db	620	VGSETTEI	DGEDEGDRVHYSR-KGVNGALITDATETEGOSGYTVNRFETKALHEVYSTH	678
QY	655	ETVYKGR	ETETVYDEYELERKGVGYGSDNKLKSEEVYISOFDNFVFKSFNDIFHSGEQ	714
Db	679	TALVGNR	REBEKTEYR-HSNQNHAGIYTKDTLKAVEELITGISHNDIFGSKRFNDAFNAGDG	737
QY	715	DDLDDG	AGADRRLEFGKGNDRLSGDEBDDLDDGGSGDVLNKGAGNDVYIFRKGDNLT	774
Db	738	VDITID	NGNDRLEFGKGDIDLDDGNGDIFDGKGNDDLHGKGDIDFVHRKGDNDII	797
QY	775	YDGGND	KLAADANISDIMIERKKEGIYKRNHSSINPRKY-----ITSNLQNVQSN	830
Db	798	TJDSOD	NDLSESDSNLKLTFEKKYHNLVY-TNSKKERVTIQDFRADFAKEVPNKAT	856
QY	831	KTDHKEI	EDLKDGSYISDIDKLDKKGVTYSQELKLKLADENKKSOKLASDIASS	890
Db	857	K-DEKIEI	TIQNGERITRSKYVDLI--AKNGKTIITDELISKVYDNEILKHS-KVNTNS	912
QY	891	LNLIVG	SMALFGTANSSNALOPITOPTGTI	922
Db	913	LDKLIS	SAFTSSNDSRHVLAPFTSMIDSL	944
RESULT 14				
ID	Q9EV34	PRELIMINARY;	PRT;	953 AA.
AC	O9EV34;			
DT	01-MAR-2001 (Tremblrel. 16, Created)			
DT	01-MAR-2001 (Tremblrel. 16, Last sequence update)			
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)			
DE	LEUKOTOXIN.			
GN	LKTA.			
OS	Pasteurella haemolytica.			
OC	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;			
CC	Mannheimia.			
OX	NCBI_TaxID=75985;			
RN	SEQUENCE FROM N.A.			
RP	STRAIN-PH56;			
RC	MEDLINE=21101823; PubMed=11157953;			
RX	Davies R.L., Whitlam T.S., Selander R.K.;			
RT	"Sequence Diversity and Molecular Evolution of the Leukotoxin (lktA)			
RT	Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)			
RL	haemolytica.";			
DR	J. Bacteriol. 183:1394-1404(2001).			
DR	EMBL: AF314505: AAG40289.1: -			
DR	InterPro: IPR001473; Enoyl_CoA_hydrtse.			
DR	InterPro: IPR001443; Hemolysin_CoA_hind.			
DR	InterPro: IPR003355; RTX_N.			
DR	Pfam: PF00353; hemolysinCbind; 1.			


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Db 500 EEEKHLKADKLVLQDSANGILIVDSNGKAKTOHILFRPLTPGTERKERVOTGKYEYIT 559
QY 542 KLRGCRVNMWQVOTDGEASSKIDFSKVIQRY-----AETEGTDEIGLIYAKAGNDIDIF 594
    || :||:||||||| :||:| :||:| :||:|
Db 560 KLINIRVDSMKITDGEASTDILTINVOXIGIELDNAGNVTKTETKIIAKLGEGDDNVF 619
    || :||:||||||| :||:| :||:| :||:|
QY 595 VGGKMNIDGGDGHDRVYFSKDGEGNITVDGTSATENGASYTNRKVARGDIYHEVYKRQ 654
    || :||:||||||| :||:| :||:| :||:|
Db 620 VSGTTEIDGEGEYDRVHYSR-GNYGALITIDATKETEGSYTVNRFEVETGKALHEVSTH 678
    || :||:||||||| :||:| :||:| :||:|
QY 655 ETKVGKRTETIQYRDYELRAVGYGQSTDNLKSYEEVIGSQPNDFKSGKFNDFHSGEG 714
    || :||:||||||| :||:| :||:| :||:|
Db 679 TALVGSREKTEYRHSNNROHA-GYTKDTLTSIEIIGTSHNDIFKGSQFNDAFNGGDG 737
    || :||:||||||| :||:| :||:| :||:|
QY 715 DDLDDGGAGDDRLFGGKGNDRLSGDEDDLLDGGSGDDVNLNGAGANDVYIFRKGDDNDL 774
    || :||:||||||| :||:| :||:| :||:|
Db 738 VDTIDGNGNDRLFGGKGDIIIDGGDDFDIDGKGNDLHGKRGDDIFVHRGDDGNDISI 797
    || :||:||||||| :||:| :||:| :||:|
QY 775 YDGTGNDRKLAADANISDIMIERTEKEGIIIVKRNHSGSINIPRWY---ITSNLQNYQSN 830
    || :||:||||||| :||:| :||:| :||:|
Db 798 TEAGGHDRLSPFSDSNLKDLPFEKVNHLYI-TNTKQEKVTIONMFRREEFAKTVKNYVAT 856
    || :||:||||||| :||:| :||:| :||:|
QY 831 KTDHKIEOLIGKDGSTYTSQIDKTLQDKD-----GTYITSQELKKLADENKKSQKL 882
    || :||:||||||| :||:| :||:| :||:|
Db 857 R-DEKIEEIIIGONGERITSQYDELIAKDKNDKIDKNDLANVANSYELLK----- 905
    || :||:||||||| :||:| :||:| :||:|
QY 883 SASDIASSLNKLVGSMALFGTANSVSSNAL 912
    || :||:||||||| :||:| :||:| :||:|
Db 906 NSRNVNLSLKLISVSFTSSND-SRNVL 934
    || :||:||||||| :||:| :||:| :||:|

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Search completed: September 11, 2002, 09:01:25
 Job time: 283 sec


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Db      173 QSLTQAG-SSLKTGAKKIIILYIPQNYQVTEQNGCIQDILVKAEEIGIEVQREERNINAT 231
QY      66 AKKSVTVNOFLSLTQTGIALSATKLEKFLQKHSSTNKLAKGLDSEVNDIKLKASNVLS 125
Db      232 AOTSIGTQTAIGTLERGIYLSAPQIDKLQK---TKAGALGSASISIVONANKAKTVLS 288
QY      126 TLSSFLGTALAGIELDSLKKGAPADALAKASIDLINETIGNLSOSTQTIIEFSSQOLAK 185
Db      289 GIOSIIGSVLAGMDLDEAL-ONNSNOHALAKAGLEITNSLIENIANSVKTLDEFGQISQ 347
QY      186 LGSTISQAKGFSNIGNKLOML-NFSKTNLGLEITIGLISISAGFALADKNASTGKVVAA 244
Db      348 FGSKLQNIKGLTIGDMLKKNIGGLDRAGLGLDVIYSGLLSATAIYALADKNASTAKVGA 407
QY      245 GFELSNQVIGNVTKAISVYLAQRYAAGLSTGVAALITSSIMLAISPLAFMNAADKEN 304
Db      408 GFELANQVGNITKAVSSYIIAQRYAAGLSTGVAALITSSIMLAISPLAFGIADKEN 467
QY      305 HANALDEFAKQFRKFGYDGHLLAEYORGVTIEASTITSTALGAVSAGVSAAGSAY 364
Db      468 HAKLSLEYAEERFKLGYDGNLLAEYORGVTIDASVTAINTALALAGVSAAGSAYI 527
QY      365 GAPILALVAGVTGLISGLEASKOAMFESVANRLQGLKLEMEKONGONTYFDKYSRYA 424
Db      528 ASPIALLVSGITGYISTIIQYSKQAMFEHVANKIHKKIYEMEKNNHKKNYFENGADARYL 587
QY      425 AYLANNLKFLSELNKELEAEVYIAITQORNDNINIGELAGITKGERIKSKAYADAFEDG 484
Db      588 ANLQDNMKFELNLNKELOAEVYIAITQOQWNNIGDLAGISRLGEKVLGSKAYVDAFEEG 647
QY      485 KKVAGSNITIDAKTGITIDISNSNGKQOALHFTSPILTACTESRETRNGKSYINKLK 544
Db      648 KHTRADKLVQDSANGIIVDSNSGKAKTOHILFTPLTPTREHRENVQIKYETIKLN 707
QY      545 FGKYNMOVTDGEASSKLDFSKYQVYR-----AETEGTDEIGLIVNAKANDDIYEQ 597
Db      708 INRVDSMKITDGAASSTFDLTNYVQRIEILDNAGNVTKETKIKIILAGSGDDNVFVS 767
QY      598 GKMNIDGSDGHDVRYFSKDGSGFNTVYGTSTAFEGSYTVARKVARGIYHEVYKROQTK 657
Db      768 GTTELDGEGYDRIYHYSR-GNMGALTIDATKETEGSGSYTVNREYETGALHEVYSTHIAL 826
QY      658 VGRFTETIYQDYELRKRYGYQYSTDNLSKSYEEVIGSQFNVFKSGKPNDFHSGEGDDL 717
Db      827 VGNREKTEIYR-HSNNOHAGIYGTDTLKAYEETIGTSHNDFKSGKPNDAFNGSDGYDT 885
QY      718 LDGAGDDBLFGGKGNDRILSGDEGDDLLDGGSDGVYVNGAGNDVYIFRKGGNDTLYDG 777
Db      886 IDGNGDNRLFLFGKGGDDLLDGGNGDDFLDGGKGNLHGGKGGDILFVHKKGGNDIITDS 945
QY      778 TGNDKLAFADANISDIEMIERTEKGIITVRNDSGSINIPRWY---ITSNLQNYOSNKT 833
Db      946 DGNLDLSDSNKLKDLTEPKYKHNLYI-TNSKKEVYTIQNMFPREADPKAYVNYKATK-D 1003
QY      834 HKIEQLIGKDSYITSDQIDKILQDKDGTVITSQPLKKLADENKSQKLSASDIASLNLK 893
Db      1004 EKIEEIIQNGBRITSKYVDLLI--AKGNGKITODELSKYVDNYVELLKH-S-KNVTNSIDK 1060
QY      894 LVGSNALFETANSVSNMLQPTQPTQGI 922
Db      1061 LISSVAFITSSNDSRNVLVAFTSMLDQSL 1089

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RESULT 2

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US-08-170-126-2
; Sequence 2, Application US/08170126
; Patent No. 5594107

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GENERAL INFORMATION:

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; APPLICANT: POTTER, ANDREW
; APPLICANT: CAMPOS, MANUEL
; APPLICANT: HUGHES, HDM P.A.
; TITLE OF INVENTION: CYTOKINE-CYTOTOXIN GENE FUSIONS AND USES
;
;
;

```

```

;
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 635 BRYANT STREET
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,126
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/777,715
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/571,301
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9000-0013.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ. ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1098 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-170-126-2

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Query Match 50.28; Score 2334; DB 1; Length 1098;

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Best Local Similarity 50.18; Pred. No. 8, 8e-175;
Matches 465; Conservative 175; Mismatches 263; Indels 26; Gaps 13;

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QY      8 KSNQAGINSRKSGLKMLYLAIPKD--YDPQKGTLDNDFKADDELGIABAEPNHTEY 65
Db      173 QSLTQAG-SSLKTGAKKIIILYIPQNYQVTEQNGCIQDILVKAEEIGIEVQREERNINAT 231
QY      66 AKKSVTVNOFLSLTQTGIALSATKLEKFLQKHSSTNKLAKGLDSEVNDIKLKASNVLS 125
Db      232 AOTSIGTQTAIGTLERGIYLSAPQIDKLQK---TKAGALGSASISIVONANKAKTVLS 288
QY      126 TLSSFLGTALAGIELDSLKKGAPADALAKASIDLINETIGNLSOSTQTIIEFSSQOLAK 185
Db      289 GIOSIIGSVLAGMDLDEAL-ONNSNOHALAKAGLEITNSLIENIANSVKTLDEFGQISQ 347
QY      186 LGSTISQAKGFSNIGNKLOML-NFSKTNLGLEITIGLISISAGFALADKNASTGKVVAA 244
Db      348 FGSKLQNIKGLTIGDMLKKNIGGLDRAGLGLDVIYSGLLSATAIYALADKNASTAKVGA 407
QY      245 GFELSNQVIGNVTKAISVYLAQRYAAGLSTGVAALITSSIMLAISPLAFMNAADKEN 304
Db      408 GFELANQVGNITKAVSSYIIAQRYAAGLSTGVAALITSSIMLAISPLAFGIADKEN 467
QY      305 HANALDEFAKQFRKFGYDGHLLAEYORGVTIEASTITSTALGAVSAGVSAAGSAY 364
Db      468 HAKLSLEYAEERFKLGYDGNLLAEYORGVTIDASVTAINTALALAGVSAAGSAYI 527
QY      365 GAPILALVAGVTGLISGLEASKOAMFESVANRLQGLKLEMEKONGONTYFDKYSRYA 424
Db      528 ASPIALLVSGITGYISTIIQYSKQAMFEHVANKIHKKIYEMEKNNHKKNYFENGADARYL 587
QY      425 AYLANNLKFLSELNKELEAEVYIAITQORNDNINIGELAGITKGERIKSKAYADAFEDG 484
Db      588 ANLQDNMKFELNLNKELOAEVYIAITQOQWNNIGDLAGISRLGEKVLGSKAYVDAFEEG 647

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01 485 KKVAGSNTLLDAAKTGTTTIDISNSGKKTQALHTPSTLLTQAGNESRPLNCKYSVINKL 544
02 648 KHIADKLVQDASANGTIIDVSSNGAKKATHTLPRPLLPGTIEHREVRQGTGETYITKLN 707
03 545 FGVRKNOVQVTDGEASSKLDFSSKVIQRY-----AETEGTDEIGLIVNAKAGNDIDFVGQ 597
04 708 INRVDSKRTIDGAASSYFDLLTNVQRIHGLELDAGAVYTKRETKIIAKGEGDDNVFVGS 767
05 598 GKMIIDGGDGHDRVYFSKDGFCGNITVDGTSATAGSYTVNRKVARGDYIHEVYKROETK 657
06 768 GTTIDIDGEGEDRVHYSR-GNYGALTIIDATKETEQGSYTVNRFVEFGALHEVSTHTAL 826
07 658 VGRKTEIYQRYDVELKRVGVGYSTQDNLSVEYVIGSQNDVFKGSKPRNDFIHSEGGDL 717
08 827 VGNNEEKIEYR-ISHNQHHAAGYTTKTLAAVEEIIIGTSHNDLFKGSKFDAANGSDGVDY 885
09 718 LDGAGAGDRFRFGGKGNDRLSGDEGDDLLDGGSGDDVYLNAGAGNDVYIFPKGPGNDLTVDG 777
10 886 IDGNDGNDRLFGGKGGDIIIDGNGNDPFIQGGKNDLHGGKRDLLFVHRKGDGNDIITDS 945
11 778 TGNDKLPADANISDIMIERTKEGIIYKRNDSGSINIPRWY-----ITSNLOQSNKTD 833
12 946 DGNCKLSFSDSNLKDILFEKVKHNLVI-TNSKKEKVTIGNMFRADFAKEVPNYKATR-D 1003
13 834 HKIQGLGKGGSYTTSQIDKTIQDKKDGCVITISQELKKLADENKSQKLSASDIASSLNK 893
14 1004 EKIEIILGNGERTSSQVODLI--AKGNGKTIQDELKSVYDNYELKHS-KNYVNSIDK 1060
15 894 LVGSMALFGTANSVSSNALDPIOTPOGI 922
16 1061 LISSVSAFTSSNDSRNVYLAFTSMLOSL 1089
17
18 RESULT 3
19 US-08-954-418-2
20 Sequence 2, Application US/08954418
21 Patent No. 6096320
22
23 GENERAL INFORMATION:
24 APPLICANT: POTTER, ANDREW
25 APPLICANT: CAMPOS, MANUEL
26 APPLICANT: HUGHES, HUM P.A.
27 TITLE OF INVENTION: CYTOKINE-CYTOTOXIN GENE FUSIONS AND USES
28 NUMBER OF INVENTION: THEREOF
29 NUMBER OF SEQUENCES: 6
30 CORRESPONDENCE ADDRESS:
31 ADDRESSEE: REED & ROBINS
32 STREET: 635 BRYANT STREET
33 CITY: PALO ALTO
34 STATE: CALIFORNIA
35 COUNTRY: UNITED STATES OF AMERICA
36 ZIP: 94301
37
38 COMPUTER READABLE FORM:
39 MEDIUM TYPE: Floppy disk
40 COMPUTER: IBM PC compatible
41 OPERATING SYSTEM: PC-DOS/MS-DOS
42 SOFTWARE: PatentIn Release #1.0, Version #1.25
43 CURRENT APPLICATION DATA:
44 APPLICATION NUMBER: US/08/954,418
45 FILING DATE:
46
47 CLASSIFICATION:
48 PRIOR APPLICATION DATA:
49 APPLICATION NUMBER: 08/170,126
50 PRIOR APPLICATION DATA:
51 APPLICATION NUMBER: US 07/571,301
52 ATTORNEY/AGENT INFORMATION:
53 NAME: ROBINS, ROBERTA L.
54 REGISTRATION NUMBER: 33,208
55 REFERENCE/DOCKET NUMBER: 9000-0013.21
56 TELECOMMUNICATION INFORMATION:
57 TELEPHONE: (415) 617-8999
58 TELEFAX: (415) 327-3211
59 INFORMATION FOR SEQ ID NO: 2:
60 SEQUENCE CHARACTERISTICS:

```

[illegible]

Db 1061 LISSVSAFTSSNDSRNLVAPTSMLOSL 1089

RESULT 4

US-08-619-812-8
Sequence 8, Application US/08619812
Patent No. 6100066

GENERAL INFORMATION:

APPLICANT: POTTER, ANDREW A.
APPLICANT: THEISEN, MICHAEL
APPLICANT: HARLAND, RICHARD J.

APPLICANT: RHOX, CLEMENT R.
TITLE OF INVENTION: VACCINES FOR HAEMOPHILUS SOMNUS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: REED & ROBINS

STREET: 635 BRYANT STREET

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/619,812

FILING DATE: 15-MAR-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/038,719

FILING DATE: 29-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 9000-0019,20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 617-8999

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ. ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 924 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-619-812-8

Query Match 50.1%; Score 2326.5; DB 3; Length 924;

Best local similarity 50.0%; Pred. No. 2.6e-174; Indels 25; Gaps 12;

Matches 461; Conservative 174; Mismatches 262;

Db 15 LNSTKSGKLKLYLAIPKRD-YDPQKGTLDNDFIKADELGIAHAEPNHTEAKRSVDT 72
Db 7 LSPPKTGAKKIIYIPQNYDYDEQNGLDLYKAAHELGIEVQREERNINIAAQSLGT 66
Db 73 VNOFLSLTGTGIAISATKLEKFLQKSTNKLANGLDSVENIDRKLKASNVLTSLSLG 132
Db 67 IQTAIGLTERGIVLSAPQIDKLQK--TKAGQALGSAESIYONANKAKVLSLGISILG 123
Db 133 TALAGITLDSLIKKGAAPALAKASIDLINEIIGNSOSTOTTEAFSSOLALGSLTSG 192
Db 124 SVLAGMDLDEL-ONNSNQHAKLAGELTNSLLENANSVKTLDEGEQISQFGSKLON 182
Db 193 AKGFSNIGNKLOML-NFSKTNLGLLEITITGLLSGISAGFALADRNASTGKRVAAAGFELSNO 251
Db 183 IKGIGTGDKLKNIGLDKRAGLDVISGLLSGATATVADKNASTAKKVGAGFELANQ 242
Db 252 VIGNVTKAIISSVYLAQVAAAGLSTGCAVALLITSSIMLAISPLAFMAAKKFHANLDE 311
Db 243 VVGNIITRAVSSYIIAQVAAAGLSTGCAVALLITSSIMLAISPLAFIADKFNHAALES 302

QY 312 FAKOPFRFGYGDGDLHAEYQGVGTTEASTLTITSTALGAVSAGVSAVAAVGAAPIAL 371
Db 303 YAEFRKKLGIDGNLAEYQGVGTTEASTLTITSTALGAVSAGVSAVAAVGAAPIAL 362
QY 372 VAGVGTGILGILKASQAMFESVANRLQKILEMEKONGQNTFPGYRSRAAYLANL 431
Db 363 VSGITGVISTIIQSKQAMFEHVAANKIHNKIYMEKNNHGNKTFENGYPARLAYLANLQDM 422
QY 432 KFLSELNKELEAEVAVIAITQQRMDNNILAGITIKGERIKSGKAYADAFEDGKVEAGS 491
Db 423 KFLNLNKELEAEVAVIAITQQRMDNNILAGITIKGERIKSGKAYADAFEDGKVEAGS 482
QY 492 NITLDAKTGIIDISNSNGKQALHFTSPLLTAGTESRERLTKGYINKLKFQVKKW 551
Db 483 LVQDSANGIITDVNSNGKQALHFTSPLLTAGTESRERLTKGYINKLKFQVKKW 542
QY 552 QVTDGEASSKLDPFSKYQVY-----AETGDEIGLIYNAKAGNDIPFGGKKNIDG 604
Db 543 KITDGAASSTFEDLTNVVQRIEILDNAGNVTKETKTIKALGEGDNNVFGSGTTEIDG 602
QY 605 GDGHDVYFYSKDGSGFNITVDGTSATEAGSYTVNRKVARQDIYHEVVKROETVYKRTET 664
Db 603 GEGYDRVHYSR-GNYGALTITDATKETEGSYTVNRFVETGKALHEVYSTHTALVGNREEK 661
QY 665 IQYRDYELRKVGYGYOSTDNLSKVEEYIGSFQNFVEFGSKFNDIFHSGEGDLDLGGAGD 724
Db 662 IEYR-HSNNOHHAAYYKDTLKAEEIIGTSHNDFGSGFNDAFNGGDDVDTIDGNDGN 720
QY 725 DRLFGKGNDRLSGDEGDDLDGSGGDDVNLGAGNDVYTFRKQDNDLTLYDGTGNDKLA 784
Db 721 DRLFGKGNDRLSGDEGDDLDGSGGDDVNLGAGNDVYTFRKQDNDLTLYDGTGNDKLA 780
QY 785 FADANISDIMEIKTEKIGIYVNRNDSHSSINIPRY-----ITSNLONSQKTHKIEOLI 840
Db 781 FDSNKLKDLFEKVKHNLVI-TNSKKERVTQNFREADPAKEVPNTKAK-DKIEI 838
QY 841 GKDSYITSDQIDKILQDKDGYITTSQELKLADENKSOQLDIASSLNKLVGSMAL 900
Db 839 GONGRITRSKYVDLLI-AKNGKITQDELISKYVDNELLKHS-KVNTNSDLKLISSVSA 895
QY 901 FGTANSSVSNALQPTQPTGCI 922
Db 896 FTSSNDSRNLVAPTSMLOSL 917

RESULT 5

US-07-908-253-2
Sequence 2, Application US/07908253
Patent No. 5534256

GENERAL INFORMATION:

APPLICANT: POTTER, ANDREW A.

APPLICANT: HARLAND, RICHARD J.

TITLE OF INVENTION: HAEMOPHILUS SOMNUS OUTER MEMBRANE
PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: ROBERTA L. ROBINS

STREET: 635 BRYANT STREET

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/908,253

FILING DATE: 19920702

CLASSIFICATION: 420

ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA L.


```

:      REGISTRATION NUMBER: 33,208
:      REFERENCE/DOCKET NUMBER: 9000-0026
:      TELECOMMUNICATION INFORMATION:
:      TELEPHONE: (415) 617-8999
:      TELEFAX: (415) 327-3231
:      INFORMATION FOR SEQ ID NO: 2:
:      SEQUENCE CHARACTERISTICS:
:      LENGTH: 926 amino acids
:      TYPE: AMINO ACID
:      TOPOLOGY: linear
:      MOLECULE TYPE: protein
:      US-07-908-253-2

```

Query Match	50.1%	Score 2326.5	DB 1	Length 926
Best Local Similarity	50.0%	Pred. No.2.6e-174		
Matches 461	Conservative 174	Mismatches 263	Indels 25	Gaps 12
QY 15	LNSTSGKLNLYLAIPKD--YDPQKGTLLNDFIKADELGIALRAEENHETAKSVDT	72		
Db 7	LSFPTGQKIIILYIPQVNYQYDEQNGNLDQIVLQKAAEEIGVEQREERNINLATAQTSIGT	66		
QY 73	VNQFLSTPOTGAIASATLEKFLQKHSNKNLAKGDSVENIDRKLGKASNVLTSLSPFG	132		
Db 67	IQTALGELERGVLSAPIDIKLQK--TKGQALGSASESTYQNNAKKATVLSGIQSTIG	123		
QY 133	TALAGIELDSLTKKQADAPDALAKASIDLINELINLQSTQSTIAPFASQOLAKLSTISQ	192		
Db 124	SVLGMDDLEAL-QUNSNQHLAKAGLELTNSLIENIANSVKTIDFEGQISQFSQKIQN	182		
QY 193	AKGFSNIGNKIQNL-NFESKTNIGLEITITGLISGISAGRALADKNASTGKVAAGFELSQ	251		
Db 183	IKGLTQTDKCKLNKIGGLDKAGIGDIVISGLISGAFAALVLDKNASTAKKVAAGFELANQ	242		
QY 252	VIGNATKAISSVYLAKQRAAGLSTGVAVALITSSIMLAISPLAEMNAADKFNHNADE	311		
Db 243	VGNNTTKAVSSYIIAQRAAGISSTGCPAALASTVSLAISPALAGIADKRNHAKSLES	302		
QY 312	FAKQFRKFGYDHDHLLAEYQRQGVTEIASLTTTISTALGAVSAGVSAAGVAVGAPIAL	371		
Db 303	YAEERKKLGYGDGNLLAEYQRGTGIDASVTAIINPALAAIGVSAAGVSAAGVSIAPIAL	362		
QY 372	VAGVGLISGLIEASKQAFESVARNRLODKITLMEKQNGQVPEPKYDSRAALANL	431		
Db 363	VSGITGVISTLQYKSKMFHEVNAKINKLIEWKNNHMKGFYFNGDARLALNIDNM	422		
QY 432	KFLSELNKELEAERYIATQORMDNNIELAGITLGERIKSGKAYAAAFEDGKRVFVAGS	491		
Db 423	KFLNLNKELEAERYIATQOQMDNIDDIAGISLGERKYLSGKAYVDAFEGCKRIHKKDX	482		
QY 492	NITLDAKTIIDISNSGKKTQALHFTSPDLTLAGTESRBLTNGKYSYINKLKEGRVKN	551		
Db 483	LVLQDSAGCIIDVNSGCAKTOHILFRRPLLTPEGHEHREVRQYTGKYEYITKINIRVDSW	542		
QY 552	QVTDQEASSKIDSEKVIQYR-----AETGETDIEIGLIVAKAANDIDFVQOGKMNIDG	604		
Db 543	KITDCAASSTEDTLNVVQRIGIELDNAGNAVTKTKETKIIAKIGEBDDNVFVSGTTEIDG	602		
QY 605	GDGHQVDFYSKDQFGNITVDQTSATEAGSYTVNRKVARGDYIEHVAKROETKVGKRTET	664		
Db 603	GEGYRVHYRVS-GNYGALTLIDATKETEGQSYTVNRFVETGKALHEVSTHTALVGNREEK	661		
QY 665	IQYRYELKRYGYQOSQNDNLKSVFVYVGSQFNDVFKFSKFNDFPHSEGDLLDGGAGD	724		
Db 662	IETRY-HSNQNHAGIYTKDLTAAVEEIIIGTSHINDLFEKSFEDADANGSDGVDTIDGNGCN	720		
QY 725	DRLFFGKGNDRLSGDEGDDLLDGGSGDDVNLVAGGAGNDVYIFPKAGGNTLXYDGTGNKLA	784		
Db 721	DRLFFGKGDIDLGGNGDDFDIDGCKGNLDLHGKGDIDFVHRKGGGNDIITDSDGNDKLS	780		
QY 785	FADANISDIMEKTEGELIVKRNHSSGINIPRWY----ITSNLQNSYNSKTDHKEIQLI	840		
Db 781	FSDSLKQLEKTEKYHNHNLV-TNSKREKVTQOMNREADFAKVEYVNTATK-DEKIEELI	838		

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Oy 841 GRDSEYIRSPDIDKLODKRGVITTSOELKTLADENKSOKLSDIASJINKYVSMAL 900
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 839 GONGRITRSKQVDDLI--AKNGCKITQDELSKVVDNYELLKHS-KVNTNSLDKRLISSVA 895
Oy 901 FGTANSVSNAKQIPTOPTGCI 922
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 896 FTSSNDSRNVLAPVMTLDOSL 917
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1      RESULT      6
2      US-08-455-970A-2
3      ; Sequence 2, Application US/084555970A
4      ; Patent No. 5708155
5      ;
6      ; GENERAL INFORMATION:
7      ;
8      APPLICANT: POTTER, ANDREW A.
9      APPLICANT: REDMOND, MARK J.
10     APPLICANT: HUGHES, HOW P. A.
11     TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
12     TITLE OF INVENTION: CHIMERAS
13     NUMBER OF SEQUENCES: 15
14     CORRESPONDENCE ADDRESS:
15     ADDRESSEE: REED & ROBINS
16     STREET: 285 HAMILTON AVENUE, SUITE 200
17     CITY: PALO ALTO
18     STATE: CALIFORNIA
19     COUNTRY: UNITED STATES OF AMERICA
20     ZIP: 94301
21
22     COMPUTER READABLE FORM:
23     MEDIUM TYPE: floppy disk
24     COMPUTER: IBM PC compatible
25     OPERATING SYSTEM: PC-DOS/MS-DOS
26     SOFTWARE: PatentIn Release #1.0, Version #1.25
27     CURRENT APPLICATION DATA:
28     APPLICATION NUMBER: US/08/455,970A
29     FILING DATE: 31-MAY-1995
30
31     CLASSIFICATION: 424
32
33     PRIOR APPLICATION DATA:
34     APPLICATION NUMBER: US 07/960,932
35     FILING DATE: 14-OCT-1992
36     ATTORNEY/AGENT INFORMATION:
37     NAME: ROBINS, ROBERTA L.
38     REGISTRATION NUMBER: 33,208
39     REFERENCE/DOCKET NUMBER: 9001-0016.10
40     TELECOMMUNICATION INFORMATION:
41     TELEPHONE: (415) 327-3400
42     TELEFAX: (415) 327-3231
43     INFORMATION FOR SEQ ID NO: 2:
44     SEQUENCE CHARACTERISTICS:
45     LENGTH: 926 amino acids
46     TYPE: amino acid
47     TOPOLOGY: linear
48     MOLECULE TYPE: protein
49
50     US-08-455-970A-2

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	Query March	50.13;	Score 2326.5;	DB 1;	length 926;
	Bates Local Similarity	50.08;	Pred. No. 2.6e-174;		
	Match 461; Conservative	174;	Mismatches 262;	Indels 25;	Gaps
Oy	15 LNSTSGGLKNLYLAIPKD--YDPQGGTLNDFIKAADELGIARLAEENPHETAKKSDVT	72			
Dd	7 LSPFTGAKKKIILYPQWGYDTEEGNGLDLPVKAAEELGEYGRERENNATATQTSLSGT	66			
Oy	73 VNQLSLTQTGLAISATKLKEFKFLQKHSTNKLAQLDSVENIDRKLGAASVNLSTLSFLL	132			
Dd	67 IQTALGERGIVISAPIDRLKLR--TKAGQALGSAESIVONANKAKTVLSGISILIG	123			
Oy	133 TALAGIELDSLIRKGDAADPLAKASTIDLINELIIIGNLSOSTORTFEARSSOLAGISTIQ	132			
Dd	124 SYLGMDIDEAL-QNNSQHALLAAGLELNSLIENTIANYSVKITLDEGEBOISQGSKLQN	182			
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183 IKGGTIGDGLKNGIDKAGLGDVTSGLSGATLALVADKNAKSTAKKVGAGFELANQ 242
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252 VIGNVTKAISSYVLAORVAAGLSTTGAVAAALITSSIMLAISPLAFMNAADKFNHANALDE 311
Db VIGNVTKAISSYVLAORVAAGLSTTGAVAAALITSSIMLAISPLAFMNAADKFNHANALDE 311
OY 312 FAKOFKRGYDGDHLLAEYQGVGTIEASLTITSTALGAVSAGVSAAGVAVGAPATL 371
312 FAKOFKRGYDGDHLLAEYQGVGTIEASLTITSTALGAVSAGVSAAGVAVGAPATL 371
Db 303 YAEFRKLLGYDGDHLLAEYQGVGTIEASLTITSTALGAVSAGVSAAGVAVGAPATL 362
OY 372 VAGVTGLISGLTEASKOAFESVANRLQKILEWEKONGQVDFKDSRYAAYLANL 431
372 VAGVTGLISGLTEASKOAFESVANRLQKILEWEKONGQVDFKDSRYAAYLANL 431
Db 363 VSGITGVISTILQYSKQAMFEHVANKIHNNKVEWEKNNHGNKNTYENGDAYLANLQDM 422
OY 432 KFLSELNKELEAEVIAITQOQWNNIGELAGITKLGRIKSGKAYVDAFEDGKVEAGS 491
432 KFLSELNKELEAEVIAITQOQWNNIGELAGITKLGRIKSGKAYVDAFEDGKVEAGS 491
Db 423 KFLNLNKELEAEVIAITQOQWNNIGELAGISRLGKVEKAYVDAFEGKHAKADK 482
OY 492 NITDAKGTIIDISNSNCKTQALHFTSPLLTACTESERLTNGKYSYINKLFGRYKNW 551
492 NITDAKGTIIDISNSNCKTQALHFTSPLLTACTESERLTNGKYSYINKLFGRYKNW 551
Db 483 LVQLDANGIIDVNSNGAKTQHLFRLPLTPGTEHREKQVOTKYEYITKLNINRDSW 542
OY 552 QVTDEASKLDFSKVIOQV-----AETEGTEIGLIVAKAGNDIFVGOGKMNDG 604
552 QVTDEASKLDFSKVIOQV-----AETEGTEIGLIVAKAGNDIFVGOGKMNDG 604
Db 543 KITDAASSTFDLTNVVQRIEIDMAGNVTKTKETKLIAGLGDDNVFVSGSTTEIDG 602
OY 605 GDGHDVFEYSKDGFGNTVDGTSATEAGSTVNRKVARCGIIEHVYKROETKYGKRET 664
605 GDGHDVFEYSKDGFGNTVDGTSATEAGSTVNRKVARCGIIEHVYKROETKYGKRET 664
Db 603 GEGYDRVHYSR-GNYGALTIDATKTEEGSYTVNFEVTEGALHEVSTHVALGNREK 661
OY 665 IOYRDELKRYGYGYOSTDNLKSYEEVIGSOFNDVFKSGKNDIFHSGEGDLDLGGAGD 724
665 IOYRDELKRYGYGYOSTDNLKSYEEVIGSOFNDVFKSGKNDIFHSGEGDLDLGGAGD 724
Db 662 IEYR-HSNQNHAGYTYDITLKAWEIITGSHNDIFKSGKNDIANGDDVDTIDGNGN 720
OY 725 DRLFGKGNDRISGDEGDDLDGSGDDVNLGAGNDVYITRKQDGNITLDGIGNDKLA 784
725 DRLFGKGNDRISGDEGDDLDGSGDDVNLGAGNDVYITRKQDGNITLDGIGNDKLA 784
Db 721 DRLFGKGGDDLDGNGGDDFDIDGKGNLDLHGKGGDIFVHRKGGNDITIDSDGNDLS 780
OY 785 FADANISDIEMERTKEGIIIVKRNDSGSIINPRV----ITSNLONGYOSNKTDKTEOLI 840
785 FADANISDIEMERTKEGIIIVKRNDSGSIINPRV----ITSNLONGYOSNKTDKTEOLI 840
Db 781 FDSNMKIDITLFEKVAHNLYI-INSKKEKVTIONMFRADFAKEVYNYATK-DEKIEELI 838
OY 841 GKDGYSITSDOIKLIDOKKDGTVITSELKKLADENKSQKTSASDIASLKLKLVGSAL 900
841 GKDGYSITSDOIKLIDOKKDGTVITSELKKLADENKSQKTSASDIASLKLKLVGSAL 900
Db 839 GQNGRITSKYVDLI--AKNGKITODELSKYVDNYELLKHS-KNVNISIDKLISVSA 895
OY 901 EGTANSVSSNALQITOPTQGI 922
901 EGTANSVSSNALQITOPTQGI 922
Db 896 FTSSNDSRNVLVAPTSMDOSL 917
896 FTSSNDSRNVLVAPTSMDOSL 917

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RESULT 7
US-08-387-156-6
; Sequence 6, Application US/08387156
; Patent No. 5723129
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: REDMOND, MARK J.
; APPLICANT: HUGHES, HOW P.A.
; TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 635 BRYANT STREET
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patentia Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,156
FILING DATE: 10-FEB-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016.21
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-387-156-6

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Query Match 50.1%; Score 2326.5; DB 1; Length 926;
Best Local Similarity 50.0%; Pred. No. 2,6e-174;
Matches 461; Conservative 174; Mismatches 262; Indels 25; Gaps 12;

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OY 15 LNSTKSLKLNLYAIPD--YDPQKGTINDPFIKADELGIALAEPPNTERAKKSVDP 72
Db 7 LSPKTKAKKILYIPONYQVDTQNGLDLVKAAEELIEVORENNIATQTSLSGT 66
OY 73 VNGSLTQNGIAISATKLEKFLQKHSNTKLANGLDSVENIDRKLGASVNLSTLSFLG 132
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Db 243 VIGNVTKAISSYVLAORVAAGLSTTGAVAAALITSSIMLAISPLAFMNAADKFNHANALDE 311
OY 312 FAKOFKRGYDGDHLLAEYQGVGTIEASLTITSTALGAVSAGVSAAGVAVGAPATL 371
Db 303 YAEFRKLLGYDGDHLLAEYQGVGTIEASLTITSTALGAVSAGVSAAGVAVGAPATL 362
OY 372 VAGVTGLISGLTEASKOAFESVANRLQKILEWEKONGQVDFKDSRYAAYLANL 431
Db 363 VSGITGVISTILQYSKQAMFEHVANKIHNNKVEWEKNNHGNKNTYENGDAYLANLQDM 422
OY 432 KFLSELNKELEAEVIAITQOQWNNIGELAGITKLGRIKSGKAYVDAFEDGKVEAGS 491
Db 423 KFLNLNKELEAEVIAITQOQWNNIGELAGISRLGKVEKAYVDAFEGKHAKADK 482
OY 492 NITDAKGTIIDISNSNCKTQALHFTSPLLTACTESERLTNGKYSYINKLFGRYKNW 551
Db 483 LVQLDANGIIDVNSNGAKTQHLFRLPLTPGTEHREKQVOTKYEYITKLNINRDSW 542
OY 552 QVTDEASKLDFSKVIOQV-----AETEGTEIGLIVAKAGNDIFVGOGKMNDG 604
Db 543 KITDAASSTFDLTNVVQRIEIDMAGNVTKTKETKLIAGLGDDNVFVSGSTTEIDG 602
OY 605 GDGHDVFEYSKDGFGNTVDGTSATEAGSTVNRKVARCGIIEHVYKROETKYGKRET 664
Db 603 GEGYDRVHYSR-GNYGALTIDATKTEEGSYTVNFEVTEGALHEVSTHVALGNREK 661

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Db 603 GEGYDRVHYSR-GNYGALTIDATKETEGSGSYTVNREVEFGKALHEVYTHFTALVGNREK 661
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Db 662 IEHR-HSNNOHAGYTYKTOLKAVEEIICTSHDIFKSGFNDFAFGDGVDTIDGNDGN 720
Qy 725 DRLFSGKGNRLSGDEGDDLLDGGSGDDVYLVNGAGNDVYFRKGGDNDLTLDGTGNDKLA 794
Db 721 DRLFSGKGGDILLDGGNDGDFIDGGKGNLDLHGKGGDIFVHRKGGDNDITDSDGNDKLS 780
Qy 785 FADANISDIMEKTEGIIIVKRNDSGSINIPRY---ITSNLOVYQSNKTDHKEIOLI 840
Db 781 FDSNKLKDLTFEYKHNHLY-TNSKKKEVYIQWFRADFAKEVPYKATK-DEKIEEII 838
Qy 841 GNDGSIYTSQIDKILQDKKDGTVITSQELKLADENKSKLSASDIASLNLVGSML 900
Db 839 GQNGERTITSQVDDLI-AKNGKITQDELKVDVYELLKHS-KVNTNSLDKLSSVSA 895
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Db 896 FTSSNDSRNVLAFTSMLDQSL 917
RESULT 8
US-08-694-865-6
; Sequence 6, Application US/08694865
; Patent No. 5837268
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: MANN, JOHN G.
; TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS LLP
; STREET: 285 HAMILTON AVENUE, SUITE 200
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/694, 865
; FILING DATE: 09-AUG-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REFERENCE/DOCKET NUMBER: 9001-0016, 22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)327-3400
; TELEFAX: (415)327-3231
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-694-865-6
Query Match 50.1%; Score 2326.5; DB 2; Length 926;
Best Local Similarity 50.0%; Pred. No. 2,6e-174;
Matches 461; Conservative 174; Mismatches 262; Indels 25; Gaps 12;
Qy 15 LNSTKSGKMLYLAIPKRD--YDPQKGTLLNDFIKADDELGIALAEPPNTEFAKSVDT 72
Db 7 LSPFKTGAKKIILYIPQNYDTEGSGDGLDVKAEEIGLEIWEQREERNIAAQAQSLGT 66
Qy 73 VNOFLSTGTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLKASNVSLTSSFLG 132

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Qy 133 TALAGIELDSLKKGDAAPALAKASIDLINELIGNLSOSTOTTIEAFSSOLAKGISTQ 192
Db 124 SVLAGMDLEAL-QNNSNQHLAKAGLELNTSLENIANVSKVTLDEGGEIOSFGSKLQ 182
Qy 193 AKGFNSNGKLOUL-NESKTNLLEITITGLSGISAGFALADKNASGKRVAGFELSNO 251
Db 183 IKGLTGLDKLKNIGGLDKGLGLDVYISGLSATLAALVYADNASTAKRVAGFELANO 242
Qy 252 VIGNVTKAISSYVLAQVAVAGLSTGAVAAALITSSIMLAISPLAFMAADKFNHANAIDE 311
Db 243 VVGNITKAVSYLLAQVAVAGLSTGAVAAALITSSYLSAISPLAFMAADKFNHAKLES 302
Qy 312 FAKQFRKFGYDGHLLAEYORGVTIASLTITSTALGAVSAGVSAAGVAVGAPIAL 371
Db 303 YAEFRFKLGYDGNLLAEYORGVTIDASYTAINTALAAAGVSAAGVSAAGVIAPIALL 362
Qy 372 VAGVTGLSGILFASQAMFESVANRLQKILMEKONGONGYEDGYSRYAAYLANNL 431
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Qy 432 KFLSELNKELEAEERVAITITQORMDNNGELAGITKLGERIKSGKAYADAFEDCKYVAGS 491
Db 423 KFLNLNKELEQAEERVAITITQORMDNNGELAGISRLGEKLSKAYADAFEDCKHIKADK 482
Qy 492 NITLDAKTGIIIDISNSNGKKTQALHFTSPLTJAGTESREBLJNGKSYINKLFGRYKNW 551
Db 483 LVQDSANGIIDVNSGSKATQHLFPTPLTGTETHEHREYQNGKYEYITKLNINRVDW 542
Qy 552 QVTDGEASSKLDPSKYIQRV-----AETGEDEGLYNAAGNDIVGCGKNMIDG 604
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Qy 605 GDGHDVRYFSKDGFGNITVDTSATFAGSYTVNRKVARADIVHEVYKROETKAKRTET 664
Db 603 GEGYDRVHYSR-GNYGALTIDATKETEGSGSYTVNREVEFGKALHEVYTHFTALVGNREK 661
Qy 665 IOYRDVELRKVGYGYOSTNLKVEEYVIGSQFNDVFKSGFNDIFHSGBDDLLDGGAGD 724
Db 662 IEHR-HSNNOHAGYTYKTOLKAVEEIICTSHDIFKSGFNDFAFGDGVDTIDGNDGN 720
Qy 725 DRLFSGKGNRLSGDEGDDLLDGGSGDDVYLVNGAGNDVYFRKGGDNDLTLDGTGNDKLA 784
Db 721 DRLFSGKGGDILLDGGNDGDFIDGGKGNLDLHGKGGDIFVHRKGGDNDITDSDGNDKLS 780
Qy 785 FADANISDIMEKTEGIIIVKRNDSGSINIPRY---ITSNLOVYQSNKTDHKEIOLI 840
Db 781 FDSNKLKDLTFEYKHNHLY-TNSKKKEVYIQWFRADFAKEVPYKATK-DEKIEEII 838
Qy 841 GNDGSIYTSQIDKILQDKKDGTVITSQELKLADENKSKLSASDIASLNLVGSML 900
Db 839 GQNGERTITSQVDDLI-AKNGKITQDELKVDVYELLKHS-KVNTNSLDKLSSVSA 895
Qy 901 FGTANSVSSNALOPTPOPTOGI 922
Db 896 FTSSNDSRNVLAFTSMLDQSL 917
RESULT 9
US-08-878-748-6
; Sequence 6, Application US/08878748
; Patent No. 5969126
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: REDMOND, MARK J.
; APPLICANT: HUGHES, HUM P.A.
; TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 635 BRYANT STREET

```

CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,748
FILING DATE: 19-JUN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3231
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-878-748-6

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Query Match      50.1%; Score 2326.5; DB 2; Length 926;
Best Local Similarity 50.0%; Pred. No. 2,6e-174;
Matches 461; Conservative 174; Mismatches 262; Indels 25; Gaps 12;

QY 15 LNSTSGKLNLYLAIKPD--YDPQGGTILNDIKADELIGARLKEEPNHTTAKSVDT 72
DB 7 LSPPTGAKKILLYIPQNYDTEQNGQIDVKAEEGLIVQREERNNTAQTSLGT 66
QY 73 VNQFSLPDTQTAISATKLEFKLQKSTNKLAKGLDSVENIDRLKASNYLSTLSFGL 132
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QY 133 TALAGIELDSLIRKGDADAPDALAKASIDLINEITGNLSOSTQITAFSSQLAKGSTISQ 192
DB 124 SVIAGMDLEAL-QNNNSQHALAKAGLELTNLSINIANSVKTLDEFGEOLISQFGSKION 182
QY 193 AAGFSNIGKLNLT-NFSNTNIGLEITIGLISGAFGLADKNASTGKVAAGFELSNO 251
DB 183 IKGGLTGLGKLNIGGLDAGJGLDVTISGLSGATRAVLADKNASTAKKVAAGFELANQ 242
QY 252 VIGNVTAKISSYVLAQRVAAGLSTTGAVVALITSSIMLAISP LAPMNAADKENHANALDE 311
DB 243 VVGNITKAVSYIILAQRVAAGLSTTGAVVALITSSIMLAISP LAPMNAADKENHANALDE 302
QY 312 FAKQFKKFGYDGDHLAEIQRGVGCTIEASLTIITRGLGAVSAGVSAANAVGAPIAL 371
DB 303 YAEERFKKLYDGDNLAEIQRGVGCTIEASLTIITRGLGAVSAGVSAANAVGAPIAL 362
QY 372 VAGVTGLISGLEASKQAFESYANRLQKLTLEMEKONGQVYFDPKGYDSRAAYLANNL 431
DB 363 VSGIITVISTIIQYKQAFENHAKVINKKIYEMENNNKGYFENGYIARLANIQDM 422
QY 432 KFLSELNKELEAERYIAITQORNDNIGELAGITKLGRIKSGKAYADA FEDGKVEAGS 491
DB 423 KFLLNKTELQARVIAITQOQNDNIGLGLAGISRLGEKIVLSGKAVDAFEEGKHAKDK 482

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QY 492 NITLDAKTGILDISNSNGKQTALHFTSPLLTAGTESRERLTNGKYSYINKLKFGYKMW 551
DB 483 LVQIDANGILIDVNSNGKAKTQHILFRTPLLTGTGTEHREVRVQTKYEYITKLININW 542
QY 552 QYTDGEASSKLDFSKYIQV-----AETEGDELGLYNAAGNDLFFVGQKNNING 604
DB 543 KITDGAASSTFDLTNNVQRIQIELDNAGVNTKTKETKILAKLGEQDNVYVSGTTEIDG 602
QY 605 GDGHDVRYEAKDGFENITVDGTSATEAGSYTVNRKVARDIYEVYKROETKVGKRTET 664
DB 603 GEGYDRHYER-GNYGALITIDATKETEGSYTVNRFVETKALHEVTSFTHALVGNREEK 661
QY 665 IQRYDYLKRVYGYQSTDNMUKSVEEYTGSEFNDYRGKGFENDIPIHSGEEDLLDGGAD 724
DB 662 IEYR-HSNNOHHAGYTKDILKAVEELITGSHDIFGSKFNDAFNGDGVDPIDNDGN 720
QY 725 DRLFGKGNRLSGDEGDDLLDGGSGDDVANGANDVYIFRRKGDNDLTLDGTGNDKILA 784
DB 721 DRLFGKGDLDLDGNGDDLTLDGKGNDLHGKGDIDIFVHRKGDNDLITDSDGNDKLS 780
QY 785 FADANISDIMERTREGIIVKRDHSGSINIPRWY---ITSMLQNYOSNKTQHKTEQLI 840
DB 781 FSDSNLKDLPFEKVKHNLVI-TNSKREKVTIOWMFREADFAKEVPYKATK-DEKIEEII 838
QY 841 CKDSYITTSQIDKILDDKKDGYITSOELKTLADENKSKLASDIASSLNKLTVGSMAL 900
DB 839 GONGERITTSQVDDLI--AKNGKITODELSKVVDNYELKLHS-KVNTSLDKLISVSA 895
QY 901 FGTAHSVSNALQPIPTQTOGI 922
DB 896 FTSSNDSRNVLVAPTSLMDQSL 917

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```

RESULT 10
US-08-535-837-2
Sequence 2, Application US/08535837
Patent No. 5985289
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: HARLAND, RICHARD J.
TITLE OF INVENTION: HAEMOPHILUS SOMNUS OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L. ROBINS
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,837
FILING DATE: 27-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0026.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-535-837-2

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Query Match 50.1%; Score 2326.5; DB 2; Length 926;
Best Local Similarity 50.0%; Pred. No. 2,6e-174;
Matches 461; Conservative 174; Mismatches 262; Indels 25; Gaps 12;

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15 LNSTSGKLNLYAIPKD--YDPQGGTLNDFIKADELGIAFLAEPNTEFAKSSVDT 72
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7 LSPFKTGAKKIILYIPQNYQYDTEQNGLDLVKAAEELGIEVQREERNINATQTSLSGT 66
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
73 VNQFLSLTQTGIAISATKLEKFLQKHSNTKLNKAGLDSVENIDRKLKASVNLSTLSSFLG 132
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
67 IQTAIGLTERGIYLSAPQIDKLLQK---TKAGQALGSAESIVQANNAKAKTVLSGIGSIILG 123
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
133 TALAGLELDSLKKGDAAPALAKASIDLINETIGNLSOSTQTTEAFSSQLAKGSTISQ 192
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
124 SVLAGMDLEAL--QNNNSQHLAKAGLELNSLEINANSVKTLDEGEQISQFGSKLQN 182
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
193 AKGFSNIGNKLNQNL-NFSKTNLGLIETITGLSGISAGFALADKNASTGKVVAGFELSNO 251
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
183 IKGLGTLGDKLNKINGLDKAGLDIVISGLSGLSATAALVADKNASTAKKVVAGFELANQ 242
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
252 VIGNVTKAISSVYLAQVAAGLSTTGVAVALITSSIMLAISPLAFNNAADKFNHANAALDE 311
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
243 VVGNITKAVSSYLLAQVAAGLSTGVPVALLASTVSLAISPLAFAGIADKFNHAKSLES 302
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
312 FAKQFKKFGYDGDHLLAEVQRGVGTTEASTTTSTALGAVSAGVSAANAASVAGAPLALL 371
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
303 YARERFKKLGIDGNLLAEVQRGVGTITDASVJALNTALAAAGVSAANAASVLAASPLALL 362
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
372 VAGVITGLSIGLLEASKQAMFESVANRLOGKILEMEKONGONGFEDKGYVAAYLANNL 431
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
363 VSGITGVISITILQYKQAMFEHANKIHNKIVEMKNNHKNKFENCYDRIYLANLQDNM 422
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
432 KFLSELNKELEAEVJALITQORMDNNGELAGITTKLGERIKSGAYADAEDCKKVEAGS 491
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
423 KFLNLINKLEQAEVJALITQOQMDNNGELAGISRLGEKVLGKAYVADAECECHKIRADK 482
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
492 NITLDAKTGIDISNSNGKKTQALHFTSPLLTGTESREPLTNGKSYINKLFGKPKNM 551
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
483 LVQLDASANGIIVDSNGKATQHIERTPLLTGTETHEKREVQTKYEYITKLININRDSW 542
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
552 QVNDGEASSKLDKFSKYIQRV-----AETEGTDEIGLVNNAKAGNDIVFGGKKNIDG 604
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
543 KIIDGAASSTFDLTNVVQRIEILDNAGNVTKTKETKIILAKLGEQDNVAVGSGTTEIDG 602
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
605 GDGHDRVFYSKDGSGFNITVDTGSATFAGSYTVNRKVARGDIVHEVKKROETVVGKRTET 664
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
603 GEGYDRVHVSR--GNYGALITDATKETEGSGSYTVNRFEVETGKALHEVYSTHTALVGNREK 661
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
665 IOVRDVELKRVGCGYSTDLKASVEEYIGSQFNDVFKGSKFNDIFHSGBEDDLDDGACD 724
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
662 IETR-HSNNOHAGVYTKDLKAVEELIGTSHNDIRKSGSKFNDAFNGCGDVPDITIDGDN 720
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
725 DRIFGKGNDRLSGDEGDDLLDDGSGDDVYLNAGANDVYFFRKGGDNDTLTYDGTGNDKLA 784
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
721 DRIFGKGGDIIIDGNGDDEIDGKGNDDLHGKGGDIIFFHRRKGGDNDITDSDGNDKLS 780
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
785 FADANISDIMEKTEKGGIIVKRNDSGSGINIPRWY----ITSNLDQNYQSKRTDHKEQLT 840
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
781 FSDSNLKLDFEFKVKHNLVY--TNSKREKVTIOMWFEADPAKBPVPYKATK--DEKITEEII 838
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
841 GKQGSYITTSQIDKIIQDKKDKGVITISQELKLADENKSKLSASPDASSLANLVGSMAL 900
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
839 GQNGERTITSQVODLI--AKGNGKITQDELISKVVDVYELLKHS--KNVTNLDKLISVSA 895
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
901 FGTANSVSSNALQPTOPTQGI 922
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
896 FTSSNDSRNVLVAPTSMLOSL 917
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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RESULT 11
US-09-124-491-6

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Sequence 6, Application US/09124491
: Patent No. 6022960
: GENERAL INFORMATION:
: APPLICANT: POTTER, ANDREW A.
: APPLICANT: MANNIS, JOHN G.
: TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: REED & ROBINS LLP
: STREET: 285 HAMILTON AVENUE, SUITE 200
: CITY: PALO ALTO
: STATE: CA
: COUNTRY: USA
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/124,491
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/694,865
: FILING DATE: 09-AUG-1996
: APPLICATION NUMBER: US 08/387,156
: FILING DATE: 10-FEB-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/960,932
: FILING DATE: 14-OCT-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/779,171
: FILING DATE: 16-OCT-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: MCCracken, THOMAS P.
: REGISTRATION NUMBER: 38,548
: REFERENCE/DOCKET NUMBER: 9001-0016.22
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415)327-3400
: TELEFAX: (415)327-3231
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 926 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-124-491-6

Query Match 50.1%; Score 2326.5; DB 3; Length 926;
Best Local Similarity 50.0%; Pred. No. 2,6e-174;
Matches 461; Conservative 174; Mismatches 262; Indels 25; Gaps 12;
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;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: REED & ROBINS
;; STREET: 285 HAMILTON AVENUE, SUITE 200
;; CITY: PALO ALTO
;; STATE: CALIFORNIA
;; COUNTRY: UNITED STATES OF AMERICA
;; ZIP: 94301
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/455,970A
;; FILING DATE: 31-MAY-1995
;; CLASSIFICATION: 424
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 07/960,932
;; FILING DATE: 14-OCT-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: ROBINS, ROBERTA L.
;; REGISTRATION NUMBER: 33,208
;; REFERENCE/DOCKET NUMBER: 9001-0016,10
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 327-3400
;; TELEFAX: (415) 327-3231
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 936 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-455-970A-12

Query Match 50.1%; Score 2326.5; DB 1; Length 936;
Best Local Similarity 50.0%; Pred. No. 2,6e-174;
Matches 461; Conservative 174; Mismatches 262; Indels 25; Gaps 12;

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QY 73 VNQFLSLTGTGIAISATKLEKFLQKSTNKLAGLDSVENIDRRILKASVNLSTLSFLG 132
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QY 133 TALAGIELDSLIRKGDAAPADLAKASIDLINELIGLNSOSTQTIEAFSSOLAKGSTISO 192
DB 124 SYLAGMDLDEAL-QNNSNQHAKLAGLELNSLIENIANSVKTLDEGEQISQFGSKLN 182
QY 193 AKGFNSINQKLNQ-LNFSKTNLGLLEITIGLSISAGFALADKNASTGKVAAGFELISQ 251
DB 183 IKGLTGLDKLKNIGGLDKRGLDIVISGLSGATLALYLDKNASTAKKVGAGFELANQ 242
QY 252 VICNVTKAISVYLAQVAAVAGLSTGTGVAALITSSIMLAISPLAFNNAADKFNHANA 311
DB 243 VGNITKAAVSYTLAQVAAVAGLSTGTGVAALITSSIMLAISPLAFNNAADKFNHANS 302
QY 312 FAKQFRFGYDGHLLAEYORGVTTEASLTITSTALGAASAGVSAANAASAVCAPITAL 371
DB 303 YAEFRKKLGYDGNLLAEYORGVTITDASVTALNTALAAIAGVSAANAASAVSAPITAL 362
QY 372 VAGVTGLSILEASKQAMEESYANRLQKILEMERKONGONTFDKGYDSRYAAYLANNL 431
DB 363 VSGITGVITIIQYSKQAMEEHVANKIHKIVEMERKNHKGKFNENGYDARYLANLQDM 422
QY 432 KETSELNKELAEARVATITQQRBDNNINGELAGITKIGERIKSKAYADAEDKKYVAGS 491
DB 423 KFLNLNKKELQAEARVATITQQRBDNNINGELAGISRLGEKVLASKAAYADAEESKHIA 482
QY 492 NITLDAKGTIIDISNSNGKATQALHFTSPLTGTGTSRETRTNGKYSYIKRLKFGRYKN 551
DB 483 LVQDSANGCIIDVSNNGKATQHILFRTPLTGTGTEREHERVQIGKYEYITKLNINRYDSW 542
QY 552 QVTDGEASSKLDPSKYIQRV-----AETGDEIGLIYNAAAGNDIVGGCKNMIDG 604
DB 543 KITDGAASSTFDLNNVQIRIGIELDNAGNVTKRKETKIILAKLBGDDNVVSGSTTEIDG 602
QY 605 GDCHDRFVYSKDGCGFNITVDTGTSATPAGSVYTNRKVARGDIYHEVVKROETKVKRTE 664
DB 603 GEGYDRVHYSR-GNYGALTITDATKETPQGSYTNRFVETKALHEVYSTHALVGNNEEK 661
QY 665 IQYRDVELRVGYGYOSTDNLKSYVEYIGSQFNDVFKSGKFNDFHSGEGDDLIDGAGD 724
DB 662 IEYR-HSNQNHAGAYYKTKLKAVEEIICTSHNDFIKSGKFNDAFNGGDDVDTIDGNDGN 720
QY 725 DRLPGCKGNDRLSGDEDDDLIDGSGGDDVYNGAGNDVYIFRRGGDDTLTYDGNCKLA 784
DB 721 DRLPGCKGDDILDGNGDDPFDGCKGDDLLHGGKDDIFVHRKGGDDIITDSDGNKLS 780
QY 785 FADANISDIMEIERTKEGIIYKRNDSGSINIPRY----ITSNLQYQSKTKDKIPIQL 840
DB 781 FSDSNLKLDFEYKYNHLVI-TNSKKREKVTIQNNFRADPAKEVPYKATK-DEKIEEII 838
QY 841 GKDSYITSDQIDKILODKKDGTVITSOELKKLADENKSKQLASDIASSLNKLKYSMAL 900
DB 839 GQNGERITSKQVDDL--AKNGKITODELSKYVDYELLKHS-KVNTNSLDKLSSVSA 895
QY 901 FGTAANSVSNALQPIPTQPGI 922
DB 896 FTSSNDSRNVLVAFTSMLDQSL 917

RESULT 14
US-08-455-970A-10
; Sequence 10, Application US/08455970A
; Patent No. 5708155
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: REDMOND, MARK J.
; APPLICANT: HUGHES, HOW P.A.
; TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 285 HAMILTON AVENUE, SUITE 200
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,970A
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,932
; FILING DATE: 14-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9001-0016,10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-3400
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 943 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 11, 2002, 08:55:36 ; Search time 75.59 Seconds
(without alignments)
1362.156 Million cell updates/sec

Title: US-09-884-696-2

Perfect score: 4646

Sequence: 1 MSNINVTKSNTQAGLNSTKS.....SSNALQPTPTPGGILAPSV 927

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq.032802:*

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2: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
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21: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4642	99.9	927	22	AAB62110
2	2334	50.2	1098	18	AAW13866
3	2334	50.2	1098	21	AAW21073
4	2332	50.2	1098	13	AAW22103
5	2329	50.1	953	14	AAW3865
6	2327	50.1	1098	15	AAW52747
7	2326.5	50.1	924	14	AAW42385
8	2326.5	50.1	924	14	AAW42380
9	2326.5	50.1	924	14	AAW42378
10	2326.5	50.1	926	12	AAW14482
11	2326.5	50.1	926	14	AAW34545

12	2326.5	50.1	926	15	AAW50291	Recombinant leukot
13	2326.5	50.1	926	15	AAW79568	Leukotoxin 352 pol
14	2326.5	50.1	977	17	AAW03942	LKT-GnRH protein f
15	2326.5	50.1	977	19	AAW79569	LKT-GnRH chimeric
16	2326.5	50.1	1069	15	AAW52748	Bovine IFNgamma/LK
17	2326.5	50.1	1069	18	AAW13867	Chimeric protein #
18	2326.5	50.1	1069	21	AAW21074	Bovine gamma-IFN/P
19	2325	50.0	953	11	AAW07167	105KD PTX protein
20	2325	50.0	953	15	AAW60072	PTX protein of Pa
21	2325	50.0	953	22	AAW04638	Pasteurella haemol
22	2323.5	50.0	943	14	AAW34546	Somatostatin-leuko
23	2318.5	49.9	936	14	AAW34547	GnRH-leukotoxin ge
24	2317.5	49.9	924	12	AAW10889	Leukotoxin 352 enc
25	2317.5	49.9	926	17	AAW03945	P. haemolytica tru
26	2313	49.8	953	12	AAW15159	Leukotoxin from P.
27	2312.5	49.8	951	14	AAW34548	Leukotoxin VP4-Leuk
28	2301.5	49.5	934	17	AAW07637	P. suis leukotoxin
29	2240.5	48.2	956	12	AAW12661	APPA haemolysin an
30	2240.5	48.2	956	18	AAW22156	Apptic protein. A
31	2240.5	48.2	956	21	AAW51410	A. pleuropneumonia
32	1928	41.5	1049	18	AAW22159	ApixiIB protein.
33	1928	41.5	1049	21	AAW51412	A. pleuropneumonia
34	1928	41.5	1244	15	AAW54781	Leukotoxin AppiIIA
35	1767.5	38.0	1022	18	AAW22152	Apixia protein. Ac
36	1767.5	38.0	1022	21	AAW51406	A. pleuropneumonia
37	1731	37.3	1023	16	AAW76891	lhah (low homology
38	1464.5	31.5	608	22	AAW04636	Pasteurella haemol
39	1380.5	29.7	758	17	AAW86998	Enterohaemorrhagic
40	1159.5	25.0	450	22	AAW04637	Pasteurella haemol
41	904.5	19.5	544	19	AAW79570	LKT-GnRH chimeric
42	901	19.4	695	19	AAW79573	LKT-GnRH chimeric
43	901	19.4	695	21	AAW58361	Leukotoxin/gonadot
44	901	19.4	695	21	AAW58333	Gonadotropin relea
45	897.5	19.3	490	20	AAW39529	Leukotoxin carrier

ALIGNMENTS

RESULT 1	
AAW62110	standard: Protein: 927 AA.
ID	
XX	AAW62110:
AC	
XX	
DT	29-MAY-2001 (first entry)
XX	
DE	M. bovis Dalton 2d RTX toxin A subunit.
XX	
KW	Moraxella: antigen; immune response; infection; RTX toxin; vaccine;
KW	antibacterial; A subunit.
XX	
OS	Moraxella bovis.
XX	
PN	MO200116172-A1.
XX	
PD	08-MAR-2001.
XX	
XX	31-AUG-2000: 2000MO-AU01048.
XX	
PR	31-AUG-1999: 99AU-0002571.
XX	
XX	(CSIR) COMMONWEALTH SCI & IND RES ORG.
PA	(UYME) UNIV MELBOURNE.
XX	
PI	Farn J, Strugnell R, Tennent J;
XX	
DR	WPI: 2001-235092/24.
XX	
DR	N-PSDB: AAF57290.
XX	
PT	Novel Moraxella bovis antigen useful in compositions for raising immune
XX	response in an animal, has protease, lipase or hemolysin activity

PS Claim 26; Fig 5; 60pp; English.

XX The invention relates to new Moraxella bovis antigens and nucleic acid
 CC sequences encoding these antigenic polypeptides. The antigenic
 CC polypeptides and polynucleotides are useful for raising an immune
 CC response in an animal directed against Moraxella, preferably against
 CC M. bovis or M. catarrhalis, and for treating Moraxella infections. The
 CC present sequence represents the amino acid sequence of the A subunit of
 CC the RTX toxin from M. bovis Dalton 2d.

XX
 XX Sequence 927 AA;

Query Match 99.9%; Score 4642; DB 22; Length 927;
 Best Local Similarity 99.9%; Pred. No. 2.4e-294;
 Matches 926; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSNINVIKSNIOAGLNSKSGKLNLYLAIPKDYDPQKGTLDNFIKADDELGIARLAEEP 60
 |||||||
 Db 1 msnlvlnksnlglnstkslgnlknlylaipkdydpqkgtlndfikaadelgiarlaeep 60
 OY 61 NHETAKSVTVVNOFSLTGTGAIASNTKLEKFLQKHTKTKLAKGDSVENDIRKIGKA 120
 |||||||
 Db 61 nhtetaksvdtvngflstltgtgiaisaatklekflqkhtnklaagdsvendirklyga 120
 OY 121 SNVLTSSPFGTALAGIELDLSLIRKKGADPADALAKASIDLINELIGNLSOSTOTIEAFS 180
 |||||||
 Db 121 snvltsslftgltaglaeldslirkkgadpadalakasidlinelignlsostqltaefs 180
 OY 181 SOLAKGSTISQAKGFSNIGKLNQNLNFSKTNLGEITLGLSGISAGFALADKNASIGK 240
 |||||||
 Db 181 sglaklgsstisqakgfsnignklnqnlfsktnlgeitlglsgisagfaladknaasgk 240
 OY 241 KVAAGFELSNQVIGVNTKAISSYVAORVAGLSTGVAALVLTSSIMLAISPLAFMMAA 300
 |||||||
 Db 241 kvaagfelsgnqvgvntkaiissyvaagrlstgvaalvtssimlaaisplafmmaa 300
 OY 301 DFNHANAIDEFKAKFRFGYDGDHLAEYORGVGTIEASLTITSTALGAVSAGVSAAV 360
 |||||||
 Db 301 dfnhanaiddefakfrfgydgdhlleayorgvgvtieasltitstalgavsagvsaav 360
 OY 361 GSAVGAPIALLVAGYTGILSIGILEASKAMFESVANRLOKRTILEMEKNGCONVYDKGYD 420
 |||||||
 Db 361 gsaavgpiallvagytgilsgileaskamfesvanrlqkrtilemekngconvydkgyd 420
 OY 421 SRYAAYLANNNKFLSELNKELEAEKVIAITQORMDNINIGELAGITRKLERIKSGKAYADA 480
 |||||||
 Db 421 sryaaylannnkflselnkeleaeerviaitqgrwmnigelaqitkrlgeriksgkayada 480
 OY 481 FEDGKRKVEAGSNITLDAKTGIIIDISNSNGKTOALHFTSPLLTACTESREKRLTNKYSYI 540
 |||||||
 Db 481 fedgkrkveagsnitldaktgiiidnsngkttqalhfstpslltactesrerltngkyyi 540
 OY 541 NMLTKGRVKNQVDTGGEASSKIDFSKVITQORVAETEGTDEIGLITVAKKAGNDIIFVGQGM 600
 |||||||
 Db 541 nmltkgrvknqvdtggeasskidfskvitqrvaetegtdeiglityvakagnndiifvgqgm 600
 OY 601 NIDGGDHDHVRVSKDGGFNGITVDGTSATEAGSYTVNRKVARGDITHEVVRQETKYGK 660
 |||||||
 Db 601 nidggdhdhvrsvkdggfngitvdgtsateagsytlvnrkvargdityhevvrketkygk 660
 OY 661 RRETIOYRDYELRKVGYGQSTDNLKSVEVEIGSQPNVFKSKRNDIRHSEGGDLDLG 720
 |||||||
 Db 661 rretioyrdyelrkvgygqstdnlksveevigsqpndvfkskrndirhsgegdldlg 720
 OY 721 GAGDDRLFCGKGNDRLSGEGDDLLDGGSDDVVLNKGAGNDVYIFRKGNGNTILYDGTGN 780
 |||||||
 Db 721 gagddrlfcgkgndrlsggeddlddggddvvlngkagndvyifrkngntilydgtgn 780
 OY 781 DKLAFADANISDIEMERTEGIIIVKRNDSGSINIPRWYITSNLQWYOSNKTDKHTEQLI 840
 |||||||
 Db 781 dklafadanisdierteregiiivkrndsgsiniprwyitsnlqwysnktdkhiteql 840

OY 841 GKDSYITSDQIDKILQDKDKGTVITTSQELAKRLADENKSQKLSASDIASLNKLKLVSMAL 900
 |||||||
 Db 841 gkdsgyitsdqidkllqdkdkgvtvitsqelakrladenksqklsasdiasslnklklysmal 900

OY 901 EGTANSVSSNALQPTPQPGIILAPSV 927
 |||||||
 Db 901 fgtnsvssnalqptpcpgiilapsv 927

RESULT 2

AAW13866 standard; Protein; 1098 AA.

AAW13866;

12-MAY-1997 (first entry)

Chimeric protein #1.

RTX cytotoxin; cytokine; immunogen; chimeric protein; cytokine; vaccine;
 Interleukin-2; IL-2; gamma interferon; gamma IFN; leukotoxin; pneumonia;
 Pasteurella haemolytica; LKT352; respiratory disease; shipping fever;
 fibrinous pneumonia; cattle; therapy.

Synthetic.

US5594107-A.

14-JAN-1997.

22-AUG-1990; 90US-0571301.

20-DEC-1993; 93US-0170126.

22-AUG-1990; 90US-0571301.

16-OCT-1991; 91US-0777715.

(CIBA) CIBA GEIGY CANADA LTD.

(UTSA-) UNIV SASKATCHEWAN.

Campos M, Hughes HPA, Potter A;

WPI; 1997-099529/09.

N-PSDB; AAT60032.

Immunogenic chimeric proteins comprising cytokine linked to RTX

toxin - useful in vaccines, esp. against shipping fever in cattle

Claim 10; Column 25-32; 56pp; English.

AAW13866 and AAW13867 represent immunogenic chimeric proteins of the
 invention. This sequence represents a chimeric protein containing the
 bovine interleukin-2 (IL-2) sequence and a leukotoxin sequence. The
 chimeric proteins of the invention comprise a cytokine, selected from
 IL-2 and gamma interferon (gamma IFN), linked to at least one RTX toxin
 epitope (preferably the sequence shown in AAW13865). The RTX toxin used
 to provide the epitope sequence is preferably a leukotoxin, especially
 the full-length Pasteurella haemolytica leukotoxin. Alternatively, the
 leukotoxin is a truncated leukotoxin lacking leukotoxic activity,
 especially LKT352. The chimeric proteins can be used for the production
 of vaccines against respiratory diseases such as pneumonia, particularly
 fibrinous pneumonia caused by P. haemolytica, including shipping fever in
 cattle.

Sequence 1098 AA;

AAW13866;

12-MAY-1997 (first entry)

Chimeric protein #1.

RTX cytotoxin; cytokine; immunogen; chimeric protein; cytokine; vaccine;
 Interleukin-2; IL-2; gamma interferon; gamma IFN; leukotoxin; pneumonia;
 Pasteurella haemolytica; LKT352; respiratory disease; shipping fever;
 fibrinous pneumonia; cattle; therapy.

Synthetic.

US5594107-A.

14-JAN-1997.

```

QY 66 AKKSVDTVNOFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLKASNVLS 125
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 232 agtslgtlctgaigttergylvsapqdkllqk---tkagqalgsaesivqnanakktvls 288
QY 126 TLSSFLGTALAGIELDSLIRKGDAPDALAKASIDLINELTIGLSOSTOTIEAFSSQLAK 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 289 gtslilgsvlaagmdleal-qmnsnqhatakgajeltlnslenlansvklidefgeqisq 347
QY 186 LGSTISQAGFSNIGKNLONL-NFSKTNLGLTITGLSGISAGFPLADKNASTGKRVAA 244
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 348 fgsqkqnllygltdklnlkgldkaglgldvlsqllsgataalyladknastakkyva 407
QY 245 GFELSNQVIGNVTKAISSVYLAQRAAGLSTTGAVAAALITSSIMLAISPLAFNNAADKFN 304
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 408 gfealangvgnltkvassylaqrvaaqlsstgvpvaallastctvslstspafagjaddkn 467
QY 305 HANALDEFAKOPRRFGYDGDHLLAEYQRGVGTIEASLTITGALGAVSAGVSAAGVSAV 364
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 468 hakslesyaerfkllgydgdnllyaeqrgtgitdasvtaintaalaagvsaaagsvyl 527
QY 365 GAPIALLVAGVGTGLSIGIEASQAMFESYANRLQCKILEMEQNGONGYTFDKYDSRA 424
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 528 asplallvsgltgvtstllqyskqamfeyanrlhnlklyewekmnhgkyfengydaryl 587
QY 425 AYLANNLKFLSELNKLLEAEERVAITQOQRMDNNIGELAGITTKGERIKSGKAYADAPEDG 484
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 588 anlqdmkflnlhnlkqgeervatqlqgqwdmnlqdlaglsrlygekvlsqkayvdfeeq 647
QY 485 KVEACSNITLDAKTGIIDISNGKKTQALHFTSPLTLAGTESRRLTNGKSYNTKLK 544
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 648 khkackllvgldsaangltdvsnsgkaktqhlfrlpilpgrtehrevqgkyeyltklk 707
QY 545 FGRVKNWQVTDGEASKLDPESKYIQRV-----AETEGDELGLVYNKAGMDLIFVQ 597
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 708 ltrvdswkltldgaasctfldlnvqrgldeldnagrvtkkckllaklqgdndvfvgs 767
QY 598 GKNNIDGGCGHDFVFSKGGFCNITVDGTSATEAGSYVNRKVAAGDIIYHEVVKQERTK 657
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 768 gteidggeggydtrvhsr-gnygaltdatketegsgsyvnrvtveqkaltnevtshlta 826
QY 658 VGRRTETIOYRDYELRKVGYSQSTDNLSVEEVISQFNDYFKSGKFPNDIFHSGEDDL 717
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 827 vgnreeklgyr-hsmnqhagyytkdtklkaeeilgtshndltfkgykfdafnaggyvdt 885
QY 718 LDGGAADDRLFGCGKNDRLSGDEGDDLGGSGDDVNLGACADYVIFRKGCGNDLTYDG 777
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 886 ldgndgndrlfsgkgddldldgngddfldgkggndllhggkgddlfrhckgqgndlltfs 945
QY 778 TGNDKLAFDANISDIMERTEKCIIVKRNDHSGSINIPRW----ITSNLOWYOSNKPD 833
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 946 dndkrlstfstdnklldlftckvknlyl-tnskkekvlqgnwrtadefakevpyrkakl-d 1003
QY 834 HKIEQLIGDGSYTSDDQIDKILQDKKDGTVITRSOELKRLADENKSOQLSASDIASLNLK 893
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1004 ektseeligngetltskqyddll--akngkltqgdelskvydnyellkhs-krvtnslck 1060
QY 894 LVGSMALFETANSVSSNALQPTOPTQ 922
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1061 llsvsafctsndsrnlvaptamlqds1 1089

```

```

RESULT 3
AAB21073
ID AAB21073 standard; Protein; 1098 AA.
XX
AC AAB21073;
XX
XX 19-DEC-2000 (first entry)
DT
XX Bovine IL-2/Pasteurella haemolytica leukotoxin fusion protein.
DE Bovine IL-2; Interleukin-2; leukotoxin; LKT; respiratory disease;
XX
KW
```

```

KW pneumonia; shipping fever; cattle; livestock; anti-Pasteurella vaccine;
KW immunogen.
XX
OS Chimeric - Bos taurus.
OS Chimeric - Pasteurella haemolytica.
XX
XX US6096320-A.
XX
PD 01-AUG-2000.
XX
XX 20-OCT-1997; 97US-0954418.
XX
XX 20-DEC-1993; 93US-0170126.
XX
XX 22-JUL-1996; 96US-0681479.
XX
XX 22-AUG-1990; 90US-0571301.
XX
XX 16-OCT-1991; 91US-0777715.
XX
XX (UYSA-) UNIV SASKATCHEWAN.
XX
XX (CIBA ) CIBA GEIGY CANADA LTD.
XX
XX Campos M, Hughes HPA, Potter A;
XX
XX WPI; 2000-531543/48.
XX
XX N-PSDB; AAA72483.
XX
XX Vaccine for stimulating immunity against pneumonia comprises chimeric
XX protein comprising gamma-interferon and leukotoxin derived from
XX Pasteurella haemolytica -
XX
XX Example 1; Column 31-38; 56pp; English.
XX
XX The invention relates to a novel vaccine composition comprising an
XX immunogenic chimeric protein that comprises gamma-interferon (gamma-IFN)
XX or an active fragment thereof, linked to an epitope of a Pasteurella
XX haemolytica leukotoxin (LKT). Pasteurella species, especially Pasteurella
XX haemolytica, are responsible for respiratory diseases in a range of
XX agricultural animals, most particularly cattle, but also sheep, pigs,
XX horses and fowl. Shipping fever is the most economically important
XX respiratory disease associated with Pasteurella species, affecting
XX 15-30% of exposed cattle and resulting in a 2-5% mortality rate in the
XX exposed population. The vaccine composition of the invention is
XX is useful for preventing or ameliorating respiratory diseases such as
XX pneumonia, particularly shipping fever pneumonia, in livestock. The
XX present sequence represents a fusion protein comprising bovine
XX interleukin-2 (IL-2) and Pasteurella haemolytica leukotoxin, which may
XX also be used as an anti-Pasteurella vaccine.
XX
XX Sequence 1098 AA:
XX
XX Query Match 50.2%; Score 2334; DB 21; Length 1098;
XX Best Local Similarity 50.1%; Pred. No. 1,1e-143;
XX Matches 465; Conservative 175; Mismatches 263; Indels 26; Gaps 13;
QY 8 KSNIOGLNSTKSGKLNLYAIPKD--YDPQKGTLPNDPFIKADDELGIARLAEPNHTT 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 173 gsltqeg-selktgakklllylpnygydteggngldvkaeeelgyevqreemnat 231
QY 66 AKKSVDTVNOFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLKASNVLS 125
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 232 agtslgtlctgaigttergylvsapqdkllqk---tkagqalgsaesivqnanakktvls 288
QY 126 TLSSFLGTALAGIELDSLIRKGDAPDALAKASIDLINELTIGLSOSTOTIEAFSSQLAK 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 289 gtslilgsvlaagmdleal-qmnsnqhatakgajeltlnslenlansvklidefgeqisq 347
QY 186 LGSTISQAGFSNIGKNLONL-NFSKTNLGLTITGLSGISAGFPLADKNASTGKRVAA 244
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 348 fgsqkqnllygltdklnlkgldkaglgldvlsqllsgataalyladknastakkyva 407
QY 245 GFELSNQVIGNVTKAISSVYLAQRAAGLSTTGAVAAALITSSIMLAISPLAFNNAADKFN 304
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 408 gfealangvgnltkvassylaqrvaaqlsstgvpvaallastctvslstspafagjaddkn 467

```


KW Bovine; Interleukin-2; IL2; P. haemolytica; leukotoxin; LTK;
 KM Ikta; chromosome walking; fusion protein; vaccine;
 KW monoclonal; polyclonal; antibody; ss.
 XX
 OS Pasteurella haemolytica - chimera.
 OS Bos taurus - chimera.
 XX
 PN US5273889-A.
 XX
 PD 28-DEC-1993.
 XX
 PF 22-AUG-1990; 90US-0571301.
 XX
 PR 22-AUG-1990; 90US-0571301.
 PR 16-OCT-1991; 91US-077715.
 XX
 PA (CIBA) CIBA GEIGY CANADA LTD.
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Campos M, Hughes HPA, Potter A;
 XX
 DR WPI; 1994-006687/01.
 DR N-PSDB; AA054212.
 XX
 PT Immunogenic fusion proteins of gamma-interferon and immunogenic
 PT leukotoxin - used in vaccines and to raise monoclonal and polyclonal
 PT antibodies
 XX
 PS Disclosure; Fig 3; 56pp; English.
 XX
 CC This sequence represents a fusion between bovine interleukin-2 (IL2)
 CC and Pasteurella haemolytica leukotoxin (LTK). The leukotoxin gene,
 CC Ikta, was isolated from a gene library of P. haemolytica by
 CC chromosome walking. Immunogenic fusion proteins such as this can be
 CC used in vaccine compositions. It can also be used to raise mono-
 CC and polyclonal antibodies.
 CC
 CC
 S0 Sequence 1098 AA;

Query Match 50.1%; Score 2327; DB 15; Length 1098;
 Best Local Similarity 49.9%; Pred. No. 3.3e-143;
 Matches 464; Conservative 175; Mismatches 264; Indels 26; Gaps 13;
 QY 8 KSNIOAGINSTSGKLNLYLAI PKD--YDPQKGGLTDFIRKADDELTA RLAEENHTET 65
 DB 173 gsltgag-sllktgakklllylpgnyqdtggnlqglvkraaelglegvgreenmat 231
 QY 66 AKRSVDYVNOFLSLTGTGTAISATKLEFLQKHSNKLAKGLDSVENIDRKLRASNVL 125
 DB 232 aqtslgtlqtaigtlerglvlsapdkllqk---tkagqalsaesivqnakakvls 288
 QY 126 TLSSFLGTALAGIELSLIKKGDAPDALAKASIDLINEIIGNSQSTQTEAFSSQLAK 185
 DB 289 gtlqslgsvlaagmdldea-qnnnqhalaqagletlmsltninsvktldfegqslq 347
 QY 186 LGSSTSOAKGFNIGNKLONL-NFSKTNLGEIITGLSGISAGFALADKNASTGKYAA 244
 DB 348 fgsklqnlkylgldgklnlgldkagjldvlsjlsagtaavl adknastakvya 407
 QY 245 GPELSNQVIGNVTKAISSVYLAQRVAAGSTGVAALITSSIMLAISPLAMNADKN 304
 DB 408 gfeiaqvvgvnltkavssyylaqryvaaglsctgpaallastvslajspatagladkfn 467
 QY 305 HANALDEFKOPRFKGYDGDHLLAEYQGVGTIEASLITTTISTALGAVSAGVSAV 364
 DB 468 hakslesyerfkkygdndllaeygrtgldasvtaintalaiaagvsaaagsvl 527
 QY 365 GADIALLVAGVGLISGILEASKQAMFESVAVNLQGLILEMEKONGGVYFPKGDSTRYA 424
 DB 528 asplallvgitgvticllqysqamfehvanklnkivewekmnhgnyfengyaryl 587
 QY 425 AYLANNUKFLSELNKELEMERVAITQQRMDNNIGELAGITKGERIKSGKAVADAFEDG 484

DB 588 anlqnmkflInlnkelgaervialtqgwdnngldaglsrlgekylskayvdafeeg 647
 QY 465 KKEVAGSNITTDAKTGIIIDINSNCKTQOALHFTSPILTFAGTERERTNKYSYINKLK 544
 DB 648 khikadklvqldasanglidsvnsqkacqhlifrppltpgtelnervetqkyeyickln 707
 QY 545 FGKRVKMOVTDGEASSKLDPSKVIQRV-----AETGTEIGLIYNAKAGNDIYVQ 597
 DB 708 lrrvsgwktldgaasstldltnvgrlgldnagnvctkckllaklgeqddnvtrvs 767
 QY 598 GKMNIDGDBGHVRVYYSKDGFGNITTVDTGTSATEGSYTVNRKARGDYHEVYKRGFTK 657
 DB 768 gtleldggegdrvhyr-gnygaltdaeketegqsyvnr fvetqalnevsthal 826
 QY 658 VGRKFTIQRDYELRKVGYQSTDNLSYEEVIGSQPNDFKSGKNDIFHSGEGDL 717
 DB 827 vnrteekieyr-hsmnqhagytkdtklaveilgsthnldfksgkfnndaifngdyvt 885
 QY 718 LDGAGDRLFGKGNDRLSGDEDDL DSGSDVYLNAGAGNDYIRRKGDGNTLDG 777
 DB 886 ldgndgndplfgkgqddldgngddldgqkgnldllyngkqyddlffvnrkqgndlctd 945
 QY 778 TGNDKIAFADANISDMIERKEGIIYKRNDSGSINIPRWY---ITSNLQYQSNKTD 833
 DB 946 dgncklisdsmkdlfckvkhnlvi-tuskkevyltqmwfreadfakevpykatk-d 1003
 QY 834 HKTEQLIKDGSYITDQIDKTLQDKKGVTSQELKRLADENKSQRLASDIASLNLK 893
 DB 1004 ekteellgngertsktyddll--ekngkltqdelskvvdnyellkhs-kvnlslidk 1060
 QY 894 LVGSMALFGTANVSNNALQPTQPRGI 922
 DB 1061 llsvsafstsdnsrnlvaptsmldqsl 1089
 RESULT 7
 ID AAR42385 standard; protein; 924 AA.
 XX
 AC AAR42385;
 XX
 DT 19-APR-1994 (first entry)
 XX
 DE Recombinant leukotoxin peptide from plasmid pCRR28.
 XX
 KW Haemophilus somnus; immunogenic; haemolysin; lppb; lppc;
 KW thromboembolic meningencephalitis; septicemia; arthritis;
 KW pneumonia; Ikta gene; haemin-binding protein; fusion protein.
 XX
 OS Pasteurella haemolytica.
 XX
 PN WO9321323-A.
 XX
 PD 28-OCT-1993.
 XX
 PF 05-APR-1993; 93WO-CA00135.
 XX
 PR 09-APR-1992; 92US-0865050.
 PR 04-JUN-1992; 92US-0893424.
 PR 04-JUN-1992; 92US-0893426.
 PR 29-MAR-1993; 93US-0038287.
 PR 29-MAR-1993; 93US-0038288.
 PR 29-MAR-1993; 93US-0038719.
 XX
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Hatland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
 PI Rioux C, Theisen M;
 XX
 DR WPI; 1993-351733/44.
 DR N-PSDB; AA051086.
 XX

PT Haemophilus somnus immunogenic proteins used in vaccines -
 PT selected from haemin-binding protein, haemolysin, LppB and LppC,
 PT and corresp. DNA
 XX
 XX Disclosure: Fig 11; 119pp; English.
 PS
 CC The lppB gene protein was expressed in *E. coli* as a fusion to the
 CC Pasteurella hemolytica leukotoxin gene lktA coded for by plasmid
 CC pAA352. The lppB gene fragment was taken from pMS11. LppB can be
 CC used in vaccines for preventing or treating *H. somnus* infections,
 CC which cause thromboembolic meningitis, septicemia, arthritis
 CC and pneumonia in vertebrates.
 CC See also AAR42370-86.
 CC
 XX
 XX Sequence 924 AA:

Query Match 50.1%; Score 2326.5; DB 14; Length 924;
 Best Local Similarity 50.0%; Pred. No. 2,8e-143;
 Matches 461; Conservative 174; Mismatches 262; Indels 25; Gaps 12;

QY 15 LNSTKSGKLNLYAIPKD--YDPQKGTLDNDFKAADELGIARLAEPNHTFAKKSVD 72
 DB 7 Lstfptgakklllylpnygydteqngldlvkaaeelgleyqreernialatqtslgt 66
 QY 73 VNQFLSUTGTGIAISATFKLEKFLQKSTNKLAKGLDSVENIDKLGKASVSTLSFLG 132
 DB 67 lgtatlgtegravisapqldklqk--tkagalgisaeelvananaktvlsqslg 123
 QY 133 TALAGIELDLKKGDAAPDALAKASIDLINELIGNLSOSTQTEAFSSQLAKGSTISO 192
 DB 124 svlagndleal-qmnsnqhalakagldetlnslentiansvktldelgeglsgfsgklqn 182
 QY 193 AKGFSNIGKNLQNL-NFSKTNLGLEIITGLSGISAKFALADKNASTGKVAANGFELSNO 251
 DB 183 lkgldgldkldlkgldkagldgldvsglsgataalvldknaastakkvagfelang 242
 QY 252 VIGNVKAISVYLAQRAVAAAGLSTGTVAALITSSIMLAISPLAPMAADKFNHANA 311
 DB 243 vvgndlkavssyllaqraavagssltgpvaalstsvlaistplafagldakfnhansles 302
 QY 312 FAKQFKFGYGDHLLAEYQGVGTIEASTLTITSTALGANVSAVSAANAAGCAPIAL 371
 DB 303 yaerfkklgydgnllaeqrgygtldasvtalntalaagvsaaagvsiasplall 362
 QY 372 VACVTGLISILEASQAFESVANRLQCKILEWEKONGQNTFDKGYDSRYAVIANNL 431
 DB 363 vsgltgvtislclqyskqamfehvanlklnklveweknngknkfengydarylanldnm 422
 QY 432 KPLSELNKELEARVIAIQOQBMNNGELAGITTKIGERIKSGKAVADAEPDGKVEAGS 491
 DB 423 klilnlnketeeravialclqgwmnldglastrlgekvlsagkayavdaleegklnkack 482
 QY 492 NITLDARTGIIDISNSNGKTKQALHFTSPLTATGESRERLTNGKSYINKLFGRYKNW 551
 DB 483 lvgldangnldvsnsgakctqhlfrtplllpgtehrervtgqkyeylklklninvdsw 542
 QY 552 QVTDEASAKLDFSKVYQVR-----AETEGDEIGLYNAKAGNDIVRGCKNNIDG 604
 DB 543 klldgaasctfdltlvvgytgieidnagnvctkckekklaklgegdndvfvsgtseidg 602
 QY 605 GDCHDRVFSKDGFGNITVDGTSATEAGSYVNRKVARDIYHEVYKRGQETVVGKRTET 664
 DB 603 gegydvvhysr-gnygalldtackteqesylvnrftvelqkhalvrlsthtalvgnreek 661
 QY 665 IQRYDELARKVGYOSTDNLKSVSEVYIGSQFNDVFKSGKFNDFHSGEGDLDLDGACD 724
 DB 662 lgyr-hsnqnhagyytktdtkaveelieshndifksgkfndafnggdvtdldgndgn 720
 QY 725 DRFGGKGNDRLSGDEGDDLDGSGDDVVLNGAGANDVYFRKGDDGNDTLTYDGTNDKLA 784
 DB 721 drlfggkddldlgnngddldfggkgnldlhggkgnldlfvhrkgdgnldltdsgndkls 780

QY 785 FADANISDIMEETKEGIIYKRNHDSGINIPRMV-----ITSMQVQSNKTDHKTIO 840
 DB 781 fsdsnlkdltefkvknlyl-tnskkevtlqmwfreaddakevpykatk-dekteell 838
 QY 841 GKDYSYITSDIDKILQDKKGTIVTSQELKLDENKSKOKLSASDIASSLANKLVGSMAL 900
 DB 839 gnggerltskqvddll--akngnkltqdelstkvndvnyellkhs-kvntslkdlssvsa 895
 QY 901 FGTANSVSSNALOPTITPOPGI 922
 DB 896 fltsndsrnylvaptslmdqsl 917

RESULT 8
 AAR42380
 ID AAR42380 standard; Protein: 924 AA.
 AC
 XX AAR42380;
 XX
 DT 19-APR-1994 (first entry)
 XX
 DE Recombinant leukotoxin peptide (split) from plasmid pCCH4.
 XX
 KW Haemophilus somnus; immunogenic; haemolysin; LppB; LppC;
 KW thromboembolic meningoenephallitis; septicemia; arthritis;
 KW pneumonia; lktA gene; haemin-binding protein; fusion protein.
 OS Pasteurella haemolytica.
 XX
 PN W09321323-A.
 XX
 PD 28-OCT-1993.
 XX
 PF 05-APR-1993; 93WO-CA00135.
 XX
 PR 09-APR-1992; 92US-0865050.
 PR 04-JUN-1992; 92US-0893424.
 PR 04-JUN-1992; 92US-0893426.
 PR 29-MAR-1993; 93US-0038287.
 PR 29-MAR-1993; 93US-0038288.
 PR 29-MAR-1993; 93US-0038719.
 XX
 PA (UYSA-) UNIV SASKATCHEWAN.
 XX
 PI Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
 PI Rioux C, Theisen M;
 DR N-PSDB; AAO51082.
 DR WPI; 1993-351733/44.
 XX
 PT Haemophilus somnus immunogenic proteins used in vaccines -
 PT selected from haemin-binding protein, haemolysin, LppB and LppC,
 PT and corresp. DNA
 XX
 XX Disclosure: Fig 6; 119pp; English.
 PS
 CC The hmb gene encoding the haemin-binding protein was expressed in
 CC *E. coli* as a fusion to the Pasteurella hemolytica leukotoxin gene
 CC lktA coded for by plasmid pAA352. The hmb gene fragment was taken
 CC from pRAp504 and starts at the codon for the 33 rd amino acid residue
 CC of ORF1. The haemin binding protein can be used in vaccines for
 CC preventing or treating *H. somnus* infections, which cause thromboembolic
 CC meningitis, septicemia, arthritis and pneumonia in
 CC vertebrates.
 CC See also AAR42370-86.
 CC
 XX
 XX Sequence 924 AA:

Query Match 50.1%; Score 2326.5; DB 14; Length 924;
 Best Local Similarity 50.0%; Pred. No. 2,8e-143;
 Matches 461; Conservative 174; Mismatches 262; Indels 25; Gaps 12;

QY	15	LNMRSGJAKNLYAIAPMD--YDPQKGTLMDFIKADELGIATLAEHPNTEFAKSSVOT	72
Db	7	ISfctqakkiIlyIpgnyqydtceqngIqdlvkaeeelIyIveqreemiaataeqIstql	66
QY	73	VNOFELSTQRTAISAARKLEKFLQKHSTNKLAAGIOSVENIDBKRLKASNVLTSLSSPFG	132
Db	67	iqtaigtatertgviIvIspaqdIltlq---tagaIqIsgaeetiIvgnankaktvIvIsgIqIlg	123
QY	133	TALAGIELDSLIRKKGDAAPALAKASIDLINIEIIGNLSSQTTTEAFSSOLAKSGTISQ	192
Db	124	svIagmdIideal-qmnsnqhalakagIeltnsIlemiansvktIIderteqIsgIqsgIqIqn	182
QY	193	AKGSSNIGNKIQLN-NSKTNMLGLEITIGLLSGISAGFALADKNASTGKKVAAQFELSNQ	251
Db	183	IkgIqIgtIdkIknIqIgdIagIqIdvIvIsgIlgIsgataaIvIadknastkktkvvgafIelqg	242
QY	252	VIGWNTAISSTVLAORVAAGLSTTGVAALITSSIMLATSPLAFMNAAKPFHNAVADL	311
Db	243	vgvniIkavssyIlaqIvvaagIstscpvaaIlaavIvIalspIafagIadkImnaksIes	302
QY	312	FAKQFRKRGYGGDHLILAEQYGVGTITIASLTTITSTALGAASVAAASAAVAGAPIALI	371
Db	303	yaerftkIyqygdnllIaeYqrgIgtIdasvIatntaIlaIagIvsaagaasvIasplall	362
QY	372	VAGVTGLISGLEAKSKQAMFSSVANNRLQGIKLEMEKONGONTFDKQYDSRYAAYIANNL	431
Db	363	vsqIgtIvIstIltIyqskqamIteIhvakIhnbIvveknbnhkyIknfyengdaryIlaaqIdm	422
QY	432	KFLSLNKLAEENVIAITQORWNNIIGELAGIKLEERIKSGAVYADAFEDSKVYAGS	491
Db	423	kflInIlnIelaeervIatIctqywdmIngdIagIstIreKxIysgIkayydaIteegkIlnIadk	482
QY	492	NITIDAKTGITDISNSNGKTOALHFTSPLLTACTESRERLTNGKSYIINKLFGHYKMW	551
Db	483	IvqIdsaangIIdvIensgaktqIhllftprIltIptIehrvetqgkyeIktIknIvrdsw	542
QY	552	QVTOGEASAKIIDEKSVIQR-----AETGCTDELIYNAKAGNDIVGOGKMMIDG	604
Db	543	kItIdgaasItdIlnvIvIrgIeIadIaagnvIbktIekIlaIkgedgdIlnvIvsgIteIdg	602
QY	605	GDGHRVRYYSKDGSGCNTVGTGTSATEAGSYTVNRKAYARGIYHEVWKRQETVVGKRTET	664
Db	603	gegydIrvIvst--gnygaItIatIaktetecgIstIvnrIftelqIkaIhevstIhtalvgnnek	661
QY	665	IQYRDYELRKVGYGYOSTDNLKSVEEVYIGSQFNDVFPKSGKFNIDIFHSBGDDLLDGAGD	724
Db	662	Ieyr-hsnqnqhaeyIyktIdIkaIveeIlgIteIhndIfkyskfndaIinggdvdtIdgndgn	720
QY	725	DRLEFGKGNDRLSGDEBGDLDLGGSSGDVYNGGAGNDVYIFRKDGNDTLYDIGNGNKLA	784
Db	721	drlIlygkdddlIdgnggdIdIdgqkgnldIhgyrgvddIvnrIkgdgnldIIdtsdgknkIs	780
QY	785	PADANISDIMEETFEPEGIIVKRNHSGSINIPRW----TTSNLOANYOSMKTDHKEBOLI	840
Db	781	fdsnIktIktIekvkhnlvI--tnskkekvIlgmwfreadIekvnykakt--dekIeelI	838
QY	841	EKDGSYITSDOIKLIDQKDKGTVYITSOELKRLADENKSOKLSASDIASSIINKLVGSMAL	900
Db	839	gnggrctIeskyvddI--akngyktIqtgelIskvvdnyellkhs--kvtnsIdkIIsIsvsa	895
QY	901	FGTANSVSNNALOPTQPTQGTI	922
Db	896	fIssndsrnvIvaptsmIdgel	917

RESULT	9
AA#42378	
ID	AA#42378 standard; Protein; 924 AA.
XX	
AC	AA#42378;
XX	
DT	19-APR-1994 (first entry)
XX	

DE	Recombinant leukotoxin peptide (splitt) from plasmid pGC45.
XX	
KW	Haemophilus somnus; immunogenic; haemolysin: lppb; lppc;
KW	thromboembolic meningencephalitis; septicemia; arthritis;
XX	pneumonia; lktA gene; haemin-binding protein; fusion protein.
XX	
OS	Pasteurella haemolytica.
XX	
PN	W09321323-A.
XX	
PD	28-OCT-1993.
XX	
PE	05-APR-1993; 93WO-CA00135.
XX	
PR	09-APR-1992; 92US-0865050.
PR	04-JUN-1992; 92US-0893424.
PR	04-JUN-1992; 92US-0893426.
PR	29-MAR-1993; 93US-0038287.
PR	29-MAR-1993; 93US-0038288.
PR	29-MAR-1993; 93US-0038719.
XX	
PA	(UYSA-) UNIV SASKATCHEWAN.
XX	
PI	Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
PI	Rioux C, Theisen M;
XX	
XX	WPI; 1993-351733/44.
DR	N-PSDB; AAQ51081.
XX	
PT	Haemophilus somnus immunogenic proteins used in vaccines -
PT	selected from haemin-binding protein, haemolysin, lppb and lppc,
PT	and corresp. DNA
XX	
PS	Disclosure; Fig 5; 11pp; English.
XX	
CC	The hmb gene encoding the haemin-binding protein was expressed in
CC	E. coli as a fusion to the pasteurella haemolytica leukotoxin gene
CC	lktA coded for by plasmid pAA352. The hmb gene fragment was taken
CC	from pPA501 and starts at the codon for the third amino acid residue
CC	of ORF1. The haemin binding protein can be used in vaccines for
CC	preventing or treating H. somnus infections, which cause thromboembolic
CC	meningo-encephalitis, septicemia, arthritis and pneumonia in
CC	vertebrates.
CC	See also AAR42370-86.
XX	
SQ	Sequence 924 AA;

[illegible]

Db 303 yaeRFkklgyddnllaeygrgtldasvtalntalaaagvsaaagsvlaaplall 362
 Qy 372 VAGVTLIGLIEASQAFESYANRLQGLIEMEKONGONTFEDGYSRVAAYLANNL 431
 Db 363 vsqllgtvstllqyskqamfenvaanklnklyeweknmngknyfengydarylaanlqdm 422
 Qy 432 KFLSELNKELEAEVRAIYQOORWNNIGELAGITTKGERIKSGAKAVADFEDCKKVEAS 491
 Db 423 kflmlnkelaeravlatlqgqwdmnlglaglsrlgekvlsqkayvdafeegkhkack 482
 Qy 492 NITLDAKGTIIDSNSNGKQTALHFTSPLTLAGTESRRLTNGKYSYNKLKFGVKKM 551
 Db 483 lvgldsaanglidsvnsqakctqhlfrtllpgrtchervgkyeyltklnlnvdsaw 542
 Qy 552 QVTDGASSKLDESKYIQRV-----AETEGDELGLVNNKAGNDLFFVGGKNNING 604
 Db 543 kltdgaasstfdltuvvgvrgldadnagvntkckekllaklgegdnnvfvsqgteidg 602
 Qy 605 GGCHDRVFYSKDGFGNITVDTGTSATEAGSYVNRKVARGDYHEVVKRQETRVGKRTET 664
 Db 603 geydvtvhystr-gnygaltdatkecegsvyvnrtfvecgkalhevtchtalvgnreek 661
 Qy 665 IOYRDYELRRVGYQSTDNLSAVEEVIQSOFNDVFKSGKFNDFHSGEGDILLDGAAD 724
 Db 662 lcyr-hsnqnhagyytktdltkaveeligtshndltfkskfndafrngdgvdtldgndgn 720
 Qy 725 DRFGKGNDRLSGDEGDDLLDGGSDVYLVNGAGNDVYIFRKGDCNDPLTGYTGDKLA 784
 Db 721 drlfggkqddllldgngddfdldgqkgnldlhqgkgnldlfvhtkqgdndlttdsgndklis 780
 Qy 785 PDANASDMMIERTEKGIIVKRNDSGSINIPRWY---ITSNLOWYOSNKTDHKTLEOLI 840
 Db 781 fedsnktldltfekvkhmlyi-tuskkevyltgnwtreadfakvpykact-dekleeel 838
 Qy 841 GKDGSYTSDDQIDKILQDKKDGTVITISOELKLADENKSOKLSASDIASSLNTLVGSMAL 900
 Db 839 gqgerltakayddll--akngkltqgdelskvvndnyellkhs-kvntslldklissvaa 895
 Qy 901 FGTANVSNNALOPTOPTQGI 922
 Db 896 ftsnsdrnvlvaptemldqsl 917
 RESULT 10
 AARI4482
 ID AARI4482 standard; Protein: 926 AA.
 AC AARI4482;
 XX
 DT 15-JAN-1992 (first entry)
 XX
 DE LKT352.
 XX
 KM Antigen: leukotoxin; vaccine; lKtA.
 XX
 OS Pasteurella haemolytica.
 XX
 PN WO9115237-A.
 XX
 PD 17-OCT-1991.
 XX
 PF 17-OCT-1991; 91WO-CA00170.
 XX
 PR 05-APR-1990; 9005-0504850.
 XX
 PA (UYSA-) UNIV SASRATCHEMAN.
 XX
 PI Acres SD, Bartluk LA, Potter AA, Lawman MJP;
 XX
 DR WPI; 1991-324967/44.
 XX
 PT Vaccines for Pasteurella haemolytica infection in cattle -

PT comprise sub-unit antigens from P haemolytica fimbrial protein,
 PT plasmin receptor, 50 k outer membrane protein and leukotoxin.
 XX
 PS Disclosure; Fig 5; 92pp; English.
 CC LKT352 is 98% homologous with authentic leukotoxin and migrates
 CC to the same position on gels.
 CC The LKT352 gene was prepd. as follows: lKtA, an MaeI fragment
 CC conrg. the gene was ligated into the SmaI site of pUC13 to form
 CC pAA179. From this, two constructs were made in the pTac-based of
 CC vector, pGH432:laci digested with SmaI. One, pAA342, consisted of
 CC the 5' AhairII fragment from lKtA while the other, pAA345, contained
 CC the entire MaeI fragment. Clone pAA342 expressed a truncated
 CC leukotoxin peptide at high levels while pAA345 expressed full
 CC length leukotoxin at very low levels. The 3' end of the lKtA gene
 CC of pAA345 was therefore ligated to StyI/BamHI digested pAA342 to
 CC yield pAA352 conrg. the LKT352 sequence. The protein expressed
 CC from the vector can be used to prepare a subunit vaccine with
 CC other P. haemolytica antigens, e.g. fimbrial protein, plasmin
 CC receptor or 50K outer membrane protein. The vaccines can be used
 CC to protect cattle from respiratory diseases such as pneumonia, esp.
 CC shipping fever pneumonia.
 CC See also AARI4481, 83, 84 and 85.
 SQ Sequence 926 AA:
 Query Match 50.1%; Score 2326.5; DB 12; Length 926;
 Best Local Similarity 50.0%; Pred. No. 2,8e-143;
 Matches 461; Conservative 174; Mismatches 262; Indels 25; Gaps 12;
 Qy 15 LNSTKSGLNLYAIPIKD--YDPQKGTLPDIFKADDELGIANLAEPNHTTAKKSVDT 72
 Db 7 lsrpkqgakklllypqnyqydeqnglqdlvkaeeelgylevqreemlaaqslqg 66
 Qy 73 VNOFLSTQGTGIAISATKLEKFLQKHSNTNKLAKGLDSVENIDRKASNVSTLSFSG 132
 Db 67 lqtaigltergvlvsapqldklqk---lkagalaesaelvgnankaktvlsqslqg 123
 Qy 133 TALAGIELDSLKKGAADPALAKASTIDLINELTGNLSOSTOTIEFSSOLAKGSTISO 192
 Db 124 svlagmldleal-qnnsnhalakagteltnslennlansvklldelfeqslsqslqgn 182
 Qy 193 AKGFNIGNKLNOL-NFSKTNLGLTITGLSGISAGPLADBNASTGKVAAGFELSNO 251
 Db 183 lkyglcldgklxlgldkaglgldvlsqslgatalvldaknaactarkvsgqfelaq 242
 Qy 252 VIGNVTKAISYVLAORVAGLSTTGAVAAALITSSIMLAISPLAFNMAADKFNHAAALDE 311
 Db 243 vgnltkavssyylaqvraaglsstgvaallastvslasplafagldkfnhakslea 302
 Qy 312 FAKQFRKFGYDGDHLAEYQRGVGTIEASTLTITSLGAVSAGVSAAGVAGAPIALLL 371
 Db 303 yaeRFkklgyddnllaeygrgtldasvtalntalaaagvsaaagsvlaaplall 362
 Qy 372 VAGVTLIGLIEASQAFESYANRLQGLIEMEKONGONTFEDGYSRVAAYLANNL 431
 Db 363 vsqllgtvstllqyskqamfenvaanklnklyeweknmngknyfengydarylaanlqdm 422
 Qy 432 KFLSELNKELEAEVRAIYQOORWNNIGELAGITTKGERIKSGAKAVADFEDCKKVEAS 491
 Db 423 kflmlnkelaeravlatlqgqwdmnlglaglsrlgekvlsqkayvdafeegkhkack 482
 Qy 492 NITLDAKGTIIDSNSNGKQTALHFTSPLTLAGTESRRLTNGKYSYNKLKFGVKKM 551
 Db 483 lvgldsaanglidsvnsqakctqhlfrtllpgrtchervgkyeyltklnlnvdsaw 542
 Qy 552 QVTDGASSKLDESKYIQRV-----AETEGDELGLVNNKAGNDLFFVGGKNNING 604
 Db 543 kltdgaasstfdltuvvgvrgldadnagvntkckekllaklgegdnnvfvsqgteidg 602
 Qy 605 GGCHDRVFYSKDGFGNITVDTGTSATEAGSYVNRKVARGDYHEVVKRQETRVGKRTET 664
 1:1:1:1 1:1:1:1 1:1:1:1 1:1:1:1 1:1:1:1 1:1:1:1 1:1:1:1 1:1:1:1


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Db      781 fdsnldkdlitfevkhnlyl-tnskkevltlgwfreaddakevpykatk-dekleeil 838
QY      841 GKGGSYITSDQIDKILQDKKKDGVITVSQELKRLADENKOKSASDIASLKLKLVGSML 900
Db      839 gqggetltskqvddll--akngkltqdeliskvndyellkhs-kvtnsldklissvaa 895
QY      901 FGTANSVSSNALOPTQPTQGI 922
Db      896 ftsndsrnvlvaptsmldqsl 917

RESULT 12
AAR50291
ID      AAR50291 standard; Protein; 926 AA.
AC      AAR50291;
XX
XX      06-OCT-1994 (first entry)
XX
XX      Recombinant leukotoxin from plasmid PAA352.
DE
XX      Vaccine: outer membrane protein; OMP; Haemophilus somnus;
KW      Iron regulated protein; leukotoxin; Pasteurella haemolytica;
KW      LKT352.
XX
XX      Pasteurella haemolytica AI (strain B122).
OS
XX      CA2099707-A.
XX
XX      03-JAN-1994.
XX
XX      29-JUN-1993; 93CA-2099707.
XX
XX      02-JUL-1992; 9205-0908253.
XX
XX      (UYSA-) UNIV SASKATCHEWAN.
XX
XX      Harland RJ, Potter AA;
XX      WPI: 1994-092909/12.
XX      N-PSDB: AAQ44760.
XX
XX      Haemophilus somnus outer membrane protein extract -
PT      enriched with iron-regulated proteins; opt. contg.
XX      Leuco:toxin antigens, for use as vaccine
XX
XX      Claim 5; Fig 5; 78pp; English.
XX
XX      A vaccine comprising an outer membrane protein (OMP) extract of
CC      Haemophilus somnus enriched with iron regulated proteins is new.
CC      The vaccine pref. further comprises an immunogenic leukotoxin
CC      polypeptide, esp. an immunogenic Pasteurella haemolytica leukotoxin
CC      homologous to LKT352. Example 1.2 describes the prodn. of
CC      P. haemolytica recombinant leukotoxin from PAA352.
CC      Two expression constructs were made. One, PAA342, contained the
CC      5'-ahat fragment of the ltkA gene, while the other, PAA345,
CC      contained the entire ltkA gene. PAA342 expressed a truncated
CC      leukotoxin peptide at high levels, while PAA345 expressed full
CC      length leukotoxin at very low levels. Therefore, the 3' end
CC      of the ltkA gene was ligated into PAA342, yielding plasmid PAA352.
CC      LKT352 or new leukotoxin is 98% homologous to authentic
CC      leukotoxin.
CC      NB: the protein sequence in Fig 5 comprises 926 amino acids,
CC      however this protein is described in the text as having
CC      931 amino acids.
XX
XX      Sequence 926 AA:
XX
Query Match      50.1%; Score 2326.5; DB 15; Length 926;
Best Local Similarity 50.0%; Pred. No. 2,8e-143;
Matches 461; Conservative 174; Mismatches 262; Indels 25; Gaps 12;
```

```

QY      15 LNSTKSLKLVLAIPKD--YDPOKCGTLNDFIKADELGIARLAEPNHTERAKKSVDT 72
Db      7 lsrptcgakklllylpqnyqydeqngldlvkaeeigleqvceernltaqslslyc 66
QY      73 VNQFSLTGTGIAISATKLEKFLQKHSTNKLAKGLDSEVENIDRKLKASNVLSSTSSFLG 132
Db      67 lqtaiglttergvlvsapqldklilqk---lkagqlgsaesivqnanakaktvlsigslg 123
QY      133 TALAGIELDSLKKGDAAPDALAKASIDLINETIGLWSQSTOTIEAFSSQLAKLGSITQ 192
Db      124 svlaemldleal-qmnsnghalakagletnslleniansvkldefeqisqfsgklqn 182
QY      193 AKGFSNIGKRLQNL-NFSKTNLGLERITIGLSIGSAGFALADKNAKNASTKVVAAFPFLSQ 251
Db      183 lkyglgtlqgklknlgldkaglgldvsgllsgataalvldkhnastakvgaqfelaq 242
QY      252 VIGNVTKAISVYLAQVAAGLSTGAVALAITSSIMLAISPLAFNMAADKFNHANALDE 311
Db      243 vvgnlckavssyllaqvraaglsstgvaallastvslaisplafagldkfnhaksles 302
QY      312 FAKQFRKFGYDGDHLAEYQKGYGTIEASLTITSTALGAVSAGVSAAVAGSAGAFIAL 371
Db      303 yaerfkklygdqnliaeyqrgtldaavtalntalaagvsaagaavslasplail 362
QY      372 VAGVTGLISGILEASKQAFESVANRLQCKLLEMEKONGONGONFEDKGYDSRYAAYLAN 431
Db      363 vsqilgvlstllqyskqamfehvanlknklywekennngknfyengydarylaanlqdm 422
QY      432 KFLSELNKELEAEVIAITQQRWNNIGELAGITTKGERISKGAADAFEDSKKVEAGS 491
Db      423 kflnlnkelqaevalatqgqwdmnlglaglsrteygekvlsqayvdafeegkhkhak 482
QY      492 NITLDAKGTGIDISNSNGKKTQALHFTSPLTAGTESREBLNGKYSYINKLKEGVKKN 551
Db      483 lvgldsaanglfdvsnsgaktqhlfrptllpqtetrevvgkyeyllklnrvds 542
QY      552 QVTDGASASKLDEPSKVIQV-----AETEGDEGLVYNKAGNDLFFVGQKNNING 604
Db      543 kltdgaastfdltlvvqrlgletldagnvntkkekckllaklggednnvfvgsqtleldg 602
QY      605 GDGHDRVYFSKDGFCNITVDDTSATEAGSYVNRKVARGDLYHEVKKQETVVGKRTET 664
Db      603 geygdtrvhystr-gnygalldatketegsyvtnrfevegkahlvetshtalvgnreek 661
QY      665 IOYRDVELRKVGYGOSTDNLKSVEEVIGSQFNDVFKSGKFNDFHSGEDDLDDGACAD 724
Db      662 lcyr-hsnngnhaqytkdtlkaveeligtshndlfkgskfndafnggdvdtldgndgn 720
QY      725 DRFLGKGRNDRLSGDEGDDLLDGGSGDDVYLVNGAGNDVYIFRKGDDNPTLYOSTGNDKLA 784
Db      721 drlfgkggddlldgngqddfdlggkgnndllhggkgddlfvhrkygdndlldtsdgrnkls 780
QY      785 FADANSDMIERTKGGIIVKRNHDHSGINIRPMY-----ITSNLOWYQSNKTDHKLEQ 840
Db      781 fdsnldkdlitfevkhnlyl-tnskkevltlgwfreaddakevpykatk-dekleeil 838
QY      841 GKGGSYITSDQIDKILQDKKKDGVITVSQELKRLADENKOKSASDIASLKLKLVGSML 900
Db      839 gqggetltskqvddll--akngkltqdeliskvndyellkhs-kvtnsldklissvaa 895
QY      901 FGTANSVSSNALOPTQPTQGI 922
Db      896 ftsndsrnvlvaptsmldqsl 917

RESULT 13
AAR79568
ID      AAR79568 standard; Protein; 926 AA.
XX
XX      AAR79568;
XX
XX      24-DEC-1998 (first entry)
```

XX Leukotoxin 352 polypeptide.
DE
XX Gonadotropin releasing hormone; GnRH; chimera; leukotoxin polypeptide;
KW multimer; vaccine; tumour; Leukotoxin 352; LKT 352; lKtA; plasmid pAA352;
KM cytotoxic.
XX
OS Synthetic.
XX
FH Key location/Qualifiers
FT Misc_feature 11..924
/note="Recombinant Leukotoxin peptide"
XX
PN W09806848-A1.
XX
PD 19-FEB-1998.
XX
PP 08-AUG-1997; 97WO-CA00559.
XX
PR 09-AUG-1996; 96US-0694865.
XX
PA (UYSA-) UNIV SASKATCHEWAN.
XX
PI Manns JG, Potter AA:
XX
DR WPI: 1998-159540/14.
DR N-PSDB: AAV61530.
XX
PT Chimeric protein of leukotoxin and gonadotropin releasing hormone -
PT useful for, e.g. preparation of vaccines for reduction of incidence
PT of mammary tumours in mammals
XX
PS Claim 7; Figure 3.1-9; 118pp; English.
XX
XX The present sequence represents a recombinantly produced or chemically
CC synthesised leukotoxin 352 (LKT 352)polypeptide, derived from the lKtA
CC gene that is present in the plasmid pAA352. This gene produces a
CC truncated protein that has an estimated molecular weight of about 99 kDa
CC and lacks the cytotoxic portion of the molecule. Thus this gene has a
CC higher expression level than that of the full-length molecule. This can
CC be used in the construction of a chimeric protein that comprises a
CC leukotoxin polypeptide, several multimers, and a GnRH sequence. The
CC chimeric protein can be used as a vaccine to help reduce the incidence of
CC mammary tumours in a mammalian individual.
XX
XX Sequence 926 AA:
XX
Query Match 50.1%; Score 2326.5; DB 19; Length 926;
Best Local Similarity 50.0%; Pred. No. 2.8e-143;
Matches 461; Conservative 174; Mismatches 262; Indels 25; Gaps 12.
OY 15 LNSTKSGKLNLYAIPKD--YDPOKGTLDNDFIKADEIGIRLAEEPHTETAKKSVDT 72
DB 7 Lstprkpgakklilylpqnyqydegnqldivkaaeelgievqreernitaaqtslyt 66
OY 73 VNQFLSTDTGTGIAISATKEKFLQKHSTNKLAKGLDVENIDRKILCKASNVLTSSFLG 132
DB 67 iqtaiglttergylslspqldklqg---tkagqalgsaesivqnaankaktvlsqslq 123
OY 133 TALAGTFLDSLIRKGDAAAPALAKASIDILNETITGNLSSTQRTIEAFSSQLKLGSTISQ 192
DB 124 svlagmldleal-qnsnqhalaqajeltuslileniansvkldeigeglsqfsglqn 182
OY 193 AKGSNITGNKLNQV-NFSKTNLGEITITGLSISAGFALADKNASTGKRVAGFELSNO 251
DB 183 ikqigltgdkiknlgldkqigldvlsqllsataalvlnadnastakkvqsgfclanq 242
OY 252 VIGNVTKAIISSYVLAQRAVAGLSTGVAVALITSSIMLAISPLAFMNADKFNHANAALDE 311
DB 243 vvgnitkavssylsqvvaaglsstgprvaalstavlslaplaafagadklnhaksles 302
OY 312 FAKQFRKFGIDGHLIAEYRGVGTIEASTITSTALGNVSAAGVAAVSAVGAFTALL 371

DB 303 yaerfkkiqygdhnlleayrgyrgtldasvralntalaalagsvsaagsvlasptall 362
OY 372 VAGVTGLISGILEASKOMAFESVANRLQKLTLEEKONGGONVYDKGDSRYAAVLANNL 431
DB 363 vsqigtvstllqyskqamfehvanklnkivewekmhngnyfemyddatyaanldgm 422
OY 432 KFLSELNKELEAEVRIATQORMDNIGELAGITKLERIKSGRAVADAEEDCKRVAGS 491
DB 423 klllnlnkelgeerviatlqgwdnldaglsarlgskvlskayadafeeghkhikadk 482
OY 492 NTTLDAKTGIIIDISNSNGKTTQALHFTSPULTAGTESERLTNKGYSYINLTKRGKRNW 551
DB 483 lvgldsaangldvsnsgakthqllfrpplltprghehervgtqkyeylftklnlnrvdsw 542
OY 552 QVYTDGASSKLDPSVVIQV-----AETEGTDEGLIVNAKAGNDIDFYGCKRMNDG 604
DB 543 kildgaastfdltnvvtqigldelnagnvltkeltkilaalgddnrvfsgtlteldg 602
OY 605 GDGHDREVFSKDGFGNITVDGTSATEAGSYTVNRKVARGDYHEVYKROETKVKRRET 664
DB 603 gegydrvhysr-gnygaltldatketegsylnrvfvelgkhalhevtshtalvgnreek 661
OY 665 IOYRDVELKRVGYGOSTDNLKSVEFVIGSOPNDVFYKSKFENDIFHSGEGDLDGAGD 724
DB 662 leyr-hsnqnhagyytkltkaveeiiytsmndlfksgkfndatnggdvtdlqndgn 720
OY 725 DRLEGGKNDRLSGDEGDDLDDGSGDYVLANGAGNDYIIFPKGNGNTLIDGTGNDKLA 784
DB 721 drifgkgddlldgngddfidgkgnndllhbgkqddlfvhhkgqndlltdsgndkls 780
OY 785 FADANISDIEMERTKGIIVKRRDHSGSINIFRW----ITSNLNYSNKTDRKIEOLI 840
DB 781 fdsnldkltfevknlmlyl-tnskkevltlgnvfreadfakevpykatk-dekleei 838
OY 841 GKDGSYTSPDIDKTIIDDKKDGTVITISOELKRLADENKSQKLSASDIASSLKLTVGSNAU 900
DB 839 gqngerltskqvddll-akngkltqdelaskvndyellkns-kvtnslcklissvsa 895
OY 901 GGTANSYSSNALQPTIPTPGCI 922
DB 896 ftsdsdrnvlvaptlmdqsl 917
RESULT 14
AAW03942
ID AAW03942 standard; Protein; 977 AA.
XX
AC AAW03942;
XX
DT 20-NOV-1996 (first entry)
XX
XX LKT-GnRH protein fusion from pCB113.
DE
XX Leukotoxin; LKT; gonadotropin-releasing hormone; GnRH;
KW fusion protein; immunogen; vaccine; fertility control;
KW contraceptive; sterilisation.
XX
OS Chimeric Pasteurella haemolytica A1 strain B122;
OS Chimeric synthetic.
XX
FH Key location/Qualifiers
FT Domain 1..929
FT Domain /label= LKT
FT Domain 927..977
FT Domain /label= GnRH_repeat_domain
PN W09624675-A1.
PD 15-AUG-1996.
XX
PF 24-JAN-1996; 96WO-CA00049.
XX

```

PR 10-FEB-1995; 950S-0387156.
XX
XX (UYSA-) UNIV SASKATCHEWAN.
XX
PI Manns JG, Potter AA:
XX
XX MPI; 1996-384447/38.
XX
XX N-PSDB; AAT37176.
XX
PT Gonadotropin-releasing hormone multimer fusion proteins - with
PT leuotoxin polypeptide for increased immunogenicity, useful in
PT antiferility vaccine prodn.
XX
XX
PS Claim 7; Fig 5A-5H; 87pp; English.
XX
XX A chimeric protein (AAW03942) is composed of a fusion between
CC a truncated leukotoxin (LKT-352) from Pasteurella haemolytica (see
CC also AAW03945) and a 4-copy gonadoliberin-releasing hormone (GnRH)
CC repeat sequence (see also AAW03944). It is the product of a
CC chimeric gene (AAT37176) produced by ligating a synthetic sequence
CC for the 4 copy GnRH into vector pAA352 (ATCC 68283), which carries
CC the LKT-352 gene. Recombinant plasmid pCB113 (LKT 352:4 copy
CC GnRH, ATCC 69749) was obtd. Escherichia coli transformants
CC produced the chimeric protein, which is useful as a vaccine for
CC fertility control, esp. immunological sterilisation of
CC domestic or farm animals.
XX
XX Sequence 977 AA:
SQ

```

```

Query Match 50.1%; Score 2326.5; DB 17; Length 977;
Best Local Similarity 50.0%; Pred. No. 3e-143;
Matches 461; Conservative 174; Mismatches 262; Indels 25; Gaps 12;

```

```

OY 15 LNSTKSGKLNLYLAIPKD--YDPQKGTLMDFTKADEGLIARLAEPNHTTAKRSVDT 72
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 7 lsfptgkakkillylpqnygteqngldlvkaaeelyevgreernmlatqslgt 66
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 73 VNPFSLTQTGIAISATKLEKFTQKSTNKLKAGLDSEVNDIKKASVNLSTLSFLG 132
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 67 lqta1gltergy1vsapqldk1lqk--tkagqalgsaes1vqnanakvt1sg1slg 123
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 133 TALAGTELDLSLKKGDAAPDAKASIDLTNETIGNLSTQRTTEAFSSOLKIGSTISQ 192
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 124 svlagndldeal-qmnsnqalatakagletnslentiansvktldelgeigisfgsklqn 182
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 193 AKGFSGNIGNKQNL-NFSKTNLGLLEITGLSGISAGFALADKNASTGKKVAAGFELSNG 251
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 183 lkg1glgldk1h1gldkag1gldv1sg1sgataalv1adknastakkvagsgfelang 242
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 252 VIGNVTKAISSYVLAORVAAGLSTGVAVALITSSIMLAISPLAFMNAADKFNHANAIDE 311
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 243 vvgnl1kavssy1laqrvaa1sg1svla1stavl1afag1adk1fhaks1les 302
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 312 FAKOPFRFGYDGHLLAEYORGVGTTEASTTSTALGAVSAGVSAAGVAGCAPATLL 371
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 303 yaef1k1lygd1la1e1y1g1g1da1sv1a1nta1aa1ag1sv1aaa1sv1a1sp1a1l 362
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 372 VAGVGTLSIGILBASKQAMFESVANRLQGLKLEMEKONGQNFEDKGYDSRYAVALANL 431
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 363 vsg1gt1v1st1l1g1ysk1gam1eh1va1nk1h1k1v1ew1ek1nh1b1k1y1f1eng1d1ery1a1n1q1dm 422
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 432 KFLSELKLEAEARVATITQQRWDNNIGELATITKLGERRKSKAKATADEFQDKKYBAGS 491
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 423 k1l1n1h1n1k1e1q1a1e1r1a1l1t1q1g1w1d1n1g1d1a1s1r1g1e1k1v1s1g1y1v1d1a1e1e1g1k1h1k1adk 482
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 492 NITLDAKGTGIDISNSNGKQTQALHFTSPLLTAGTESRELTNGKXSYIKLTFGRVKNV 551
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 483 l1v1d1a1e1a1n1g1d1v1s1n1g1k1a1k1t1q1h1l1f1r1p1l1p1g1t1e1h1r1e1v1q1g1k1y1e1i1k1l1n1t1r1v1d1w 542
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 552 QVTDGAASSKLDFSKYIQRV-----AETEGTDEIGLIVNAKAGNDIIFVGCKMNIIDG 604
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 543 k1t1d1g1a1a1s1t1f1d1t1v1q1r1g1e1l1d1n1a1g1n1v1t1k1e1k1e1k1l1a1k1g1e1g1d1n1v1f1v1g1s1g1t1e1l1d1g 602

```

```

OY 605 GGDHDFEYSKDGFGNITVDTGTSATEAGSYTVNRKVARGDVIEYVKKROETVGRKRTET 664
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 603 geygd1rv1h1sr-g1n1g1a1l1t1d1a1k1e1g1s1y1n1r1f1e1y1g1k1a1h1e1v1t1s1t1a1l1v1n1r1e1e1k 661
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 665 IOYRDYELRRKVGYOSTDNLKSEVEYIGSQFNDVFRKSKFNDIFHSGEGDLDLDGAGD 724
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 662 l1ey1r-h1sn1q1h1a1g1y1t1k1d1l1k1a1v1e1l1g1t1s1h1n1d1l1f1k1s1k1f1n1d1a1f1n1g1d1v1d1t1d1n1g1n 720
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 725 DR1FPGKGNRLSGDEGDDLDLDGSGDDVLNGAGANDVYIFRRGDGNDTLYDGTGNDKLA 784
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 721 d1r1f1g1g1k1g1d1l1d1g1n1g1d1d1g1g1k1g1n1d1l1h1g1k1g1d1l1f1v1h1r1k1g1d1n1d1l1d1s1a1d1n1k1s 780
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 785 FADANSDIMIEERTKEGIIYKRNDSGSINIPRWY----ITSN1QNYSKKTCHK1EQLI 840
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 781 f1s1d1n1k1d1l1f1e1k1v1k1h1n1v1-l1n1s1k1k1e1k1v1l1q1w1f1r1e1a1d1a1k1e1v1p1y1k1a1k1-d1e1k1l1e1l1 838
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 841 GKDGSYTSDQIDKI1DQDKKDGTVIT1SQELKRLADENK1SGLASPD1ASS1LKL1VGS1MAL 900
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 839 g1n1g1e1r1t1s1k1q1v1d1l1--a1k1n1g1k1t1g1d1e1l1s1k1v1d1n1y1e1l1k1h1s-k1v1n1s1d1k1l1s1s1v1s1a 895
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 901 FGTANSVSSNALQPTIQPTQGI 922
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 896 f1t1s1n1d1s1r1n1v1a1p1t1m1d1q1s1l 917
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
AAW79569
ID AAW79569 standard; Protein; 977 AA.
XX
XX AAW79569;
AC
XX
DT 24-DEC-1998 (first entry)
XX
XX LKT-GnRH chimeric protein.
DE
XX Chimeric; pCB113; LKT 352; GnRH; Gonadotropin releasing hormone; multimer;
KW cytotoxic activity; antigen presentation; immune response; vaccine;
KM tumour.
XX
XX Synthetic.
OS
XX
XX WO9806848-A1.
PN
XX
PD 19-FEB-1998.
XX
XX 08-AUG-1997; 97WO-CA00559.
PF
XX
PR 09-AUG-1996; 96US-0694865.
XX
XX (UYSA-) UNIV SASKATCHEWAN.
PA
XX
XX Manns JG, Potter AA:
PI
XX
XX MPI; 1998-159540/14.
DR
XX N-PSDB; AAW61531.
PT
XX Chimeric protein of leukotoxin and gonadotropin releasing hormone -
XX useful for, e.g. preparation of vaccines for reduction of incidence
XX of mammary tumours in mammals
XX
PS Disclosure: Figure 5.1-8; 118pp; English.
XX
XX The present sequence represents the LKT-GnRH chimeric protein from
XX pCB113. This plasmid contains the LKT 352 polypeptide (AAW79568) fused
XX to four copies of the GnRH peptide. This chimera lacks cytotoxic
XX activity which enables there to be an increase in antigen presentation
XX and thus an optimal immune response. The removal of this region also
XX enables the truncated LKT to be expressed at much higher levels and
XX allows the amount of antigen administered to be reduced. This chimeric
XX protein comprises a leukotoxin polypeptide, several multimers, and a GnRH
XX sequence. The chimeric protein can be used as a vaccine to help reduce
XX the incidence of mammary tumours in a mammalian individual.

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 11, 2002, 09:01:54 : Search time 22.74 Seconds
(without alignments)
20.432 Million cell updates/sec

Title: US-09-884-696-6

Perfect score: 57

Sequence: 1 FLSEUNKLEAE 12

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	75.4	953	1	LKAI_PASHA
2	43	75.4	953	1	LKAI_PASHA
3	43	75.4	953	1	LKAB_PASHA
4	43	75.4	953	1	LKAB_PASHA
5	43	75.4	956	1	HLVA_PASHA
6	43	75.4	956	1	RT2A_ACTPL
7	39	68.4	338	1	FLIG_BACSU
8	39	68.4	454	1	NFM_PIG
9	39	68.4	810	1	NFM_BOVIN
10	39	68.4	845	1	NFM_MOUSE
11	39	68.4	845	1	NFM_MOUSE
12	39	68.4	857	1	NFM_CHICK
13	39	68.4	915	1	NFM_HUMAN
14	39	68.4	947	1	LKTA_PASP
15	38	66.7	181	1	YE18_METJA
16	37	64.9	343	1	HRCA_BACSH
17	37	64.9	356	1	BASS_SALTY
18	37	64.9	363	1	BASS_ECOLI
19	37	64.9	663	1	YD58_YEAST
20	37	64.9	699	1	TOPI_FERIS
21	36.5	64.0	617	1	YE39_AQAE
22	36	63.2	378	1	HGDB_ACFE
23	36	63.2	557	1	THS2_HALVO
24	36	63.2	828	1	YF4_YEAST
25	36	63.2	3321	1	KEND_HUMAN
26	35	61.4	163	1	ATPX_OCHNE
27	35	61.4	207	1	ATPX_MYCPN
28	35	61.4	264	1	HRCA_CAMJE
29	35	61.4	445	1	PREA_BACTU
30	35	61.4	465	1	MYH6_RABIT
31	35	61.4	468	1	IFET_CRLO
32	35	61.4	579	1	G160_HUMAN
33	35	61.4	621	1	LAMC_DROME

ALIGNMENTS

RESULT	1	STANDARD	PRT	953 AA
LKAI_PASHA				
ID	LKAI_PASHA			
AC	P16535			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Leukotoxin from serotype A1.			
GN	LKTA.			
OS	Pasteurella haemolytica.			
OC	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;			
OX	NCBI_TaxID=75985;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-SEROTYPE A1 / PHL101;			
RX	MEDLINE=67306837; PubMed=3040588;			
RA	Lo R.Y.C., Strathdee C.A., Shewen P.E.;			
RT	"Nucleotide sequence of the leukotoxin genes of Pasteurella haemolytica A1.";			
RL	Infect. Immun. 55:1987-1996(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-SEROTYPE A1 / PHL101;			
RX	MEDLINE=90236888; PubMed=2185213;			
RA	Higlandner S.K., Engler M.J., Weinstein G.M.;			
RT	"Secretion and expression of the Pasteurella haemolytica leukotoxin gene cluster.";			
RL	DNA 8:15-26(1989).			
RN	[3]			
RP	SEQUENCE OF 884-953 FROM N.A.			
RC	STRAIN-SEROTYPE A1 / PHL101;			
RX	MEDLINE=90236888; PubMed=2185213;			
RA	Higlandner S.K., Engler M.J., Weinstein G.M.;			
RT	"Secretion and expression of the Pasteurella haemolytica leukotoxin.";			
RL	J. Bacteriol. 172:2343-2350(1990).			
CC	- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.			
CC	- SUBCELLULAR LOCATION: Secreted.			
CC	- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC ACTIVITY.			
CC	- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).			
CC	- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN MODIFIED (BY SIMILARITY).			
CC	- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.			
CC	THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION - THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY MODIFIED AND THIS STATEMENT IS NOT REMOVED. Usage by and for commercial entities requires a license agreement (See http://www.isb.ch/announce/ or send an email to license@isb-sib.ch).			

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CC -----
DR EMBL; M20730; AAA25529.1; -
DR EMBL; M24197; AAA25543.1; -
DR PIR; S29516; S29516.
DR HSSP; P02392; ICTF.
DR InterPro; IPR001343; Hemolysn_Ca_bind.
DR InterPro; IPR003355; RTX_N.
DR InterPro; IPR003995; RTX_A.
DR Pfam; PF00353; hemolysincabind; 1.
DR PRINTS; PR00313; CABNDNGRPT.
DR PRINTS; PR01488; RTXTOXINA.
DR PROSITE; PS00330; HEMOLYSIN_CALCITUM; 4.
KW Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
KW Transmembrane; Lipoprotein; Palmitate.
FT TRANSMEM 229 249
FT TRANSMEM 297 318
FT TRANSMEM 366 390
FT DOMAIN 734 784
FT REPEAT 734 739
FT REPEAT 743 748
FT REPEAT 752 757
FT REPEAT 761 766
FT REPEAT 770 775
FT REPEAT 779 784
FT CONFLICT 409 414
FT CONFLICT 742 742
SQ SEQUENCE 953 AA; 101996 MW; 7F93D113A118C05F CRC64;

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Query Match          75.4%; Score 43; DB 1; Length 953;
Best Local Similarity 75.0%; Pred. No. 9.1;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Oy 1 FLSELNKELEAE 12
    || |||||:|
Db 451 FLNLNKELEAE 462

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RESULT 2
ID LKAB_PASHA STANDARD; PRT; 953 AA.
AC P55116;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Leukotoxin from serotype T3.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SEROTYPE T3;
RX MEDLINE=94041617; PubMed=8225575;
RA Burrows L.L., Lo R.Y.C., Olah-Winfield E.;
RT "Molecular analysis of the leukotoxin determinants from Pasteurella
haemolytica serotypes 1 to 16."
RL Infect. Immun. 61:5001-5007(1993).
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
DEFINED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
ACTIVITY.
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -1- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
MODIFIED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----

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```

DR EMBL; U01216; AAB36691.1; -
DR HSSP; P02392; ICTF.
DR InterPro; IPR001343; Hemolysn_Ca_bind.
DR InterPro; IPR003355; RTX_N.
DR InterPro; IPR003995; RTX_A.
DR Pfam; PF00353; hemolysincabind; 1.
DR PRINTS; PR00313; CABNDNGRPT.
DR PRINTS; PR01488; RTXTOXINA.
DR PROSITE; PS00330; HEMOLYSIN_CALCITUM; 2.
KW Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
KW Transmembrane; Lipoprotein; Palmitate.
FT TRANSMEM 229 249
FT TRANSMEM 297 318
FT TRANSMEM 381 401
FT DOMAIN 734 784
FT REPEAT 734 739
FT REPEAT 743 748
FT REPEAT 752 757
FT REPEAT 761 766
FT REPEAT 770 775
FT REPEAT 779 784
FT CONFLICT 409 414
SQ SEQUENCE 953 AA; 101948 MW; FDBDC2E2FDC85FDF2 CRC64;

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Query Match          75.4%; Score 43; DB 1; Length 953;
Best Local Similarity 75.0%; Pred. No. 9.1;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Oy 1 FLSELNKELEAE 12
    || |||||:|
Db 451 FLNLNKELEAE 462

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RESULT 3
ID LKAB_PASHA STANDARD; PRT; 953 AA.
AC P55116;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Leukotoxin from serotype All.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SEROTYPE All;
RX MEDLINE=94041617; PubMed=8225575;
RA Burrows L.L., Olah-Winfield E., Lo R.Y.C.;
RT "Molecular analysis of the leukotoxin determinants from Pasteurella
haemolytica serotypes 1 to 16."
RL Infect. Immun. 61:5001-5007(1993).
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
DEFINED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
ACTIVITY.
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -1- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
MODIFIED (BY SIMILARITY).
CC -----

```

MODIFIED (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.

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CC or send an email to license@isb-sib.ch).

CC EMBL: 001215; AAB36689.1; -
CC InterPro: IPR001343; Hemlysn_Ca_bind.
CC InterPro: IPR003355; RTX_N.
CC InterPro: IPR003995; RTX_A.
CC Pfam: PF00353; hemolysinCbind; 1.
CC Pfam: PF02382; RTX; 1.
CC PRINTS: PR00313; CABDNGRPT.
CC PRINTS: PR01488; RTXTOXINA.
CC PROSITE: PS00330; HEMOLYSIN_CALCIIUM; 4.
CC Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
CC Transmembrane; Lipoprotein; Palmitate.
CC TRANSMEM 230 250 POTENTIAL.
CC TRANSMEM 297 317 POTENTIAL.
CC TRANSMEM 381 401 POTENTIAL.
CC DOMAIN 734 784 6 X REPEATS, GLY-RICH.
CC REPEAT 734 739 1.
CC REPEAT 743 748 2.
CC REPEAT 752 757 3.
CC REPEAT 761 766 4.
CC REPEAT 770 775 5.
CC REPEAT 779 784 6.
SQ SEQUENCE 953 AA: 102206 MW: 927FF56CFC884F12 CRC64:

Query Match 75.4%; Score 43; DB 1; Length 953;
Best Local Similarity 75.0%; Pred. No. 9.1;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSLNKKELEAE 12
II IIIII:II
Db 451 FLNLNKLKLEAE 462

RESULT 4
LKA_PASHA STANDARD: PRT; 955 AA.
ID LKA_PASHA
AC P55117;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Leukotoxin from serotype T10.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SEROTYPE T10;
MEDLINE=96425875; PubMed=8828217;
RA Johnson F.A., Murray J., Davies R.C., Donachie W.;
RT "Characterization of epitopes involved in the neutralization of
RT Pasteurella haemolytica serotype A1 leukotoxin.";
RL Microbiology 142:2499-2507(1996).
-1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
CC DEFINED.
-1- SUBCELLULAR LOCATION: Secreted.
-1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.
-1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE

INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
-1- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
MODIFIED (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.

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CC EMBL: 226247; CAA81206.1; -
CC InterPro: IPR001343; Hemlysn_Ca_bind.
CC InterPro: IPR003355; RTX_N.
CC InterPro: IPR003995; RTX_A.
CC Pfam: PF00353; hemolysinCbind; 1.
CC Pfam: PF02382; RTX; 1.
CC PRINTS: PR00313; CABDNGRPT.
CC PRINTS: PR01488; RTXTOXINA.
CC PROSITE: PS00330; HEMOLYSIN_CALCIIUM; 4.
CC Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
CC Transmembrane; Lipoprotein; Palmitate.
CC TRANSMEM 299 319 POTENTIAL.
CC TRANSMEM 361 381 POTENTIAL.
CC TRANSMEM 383 403 POTENTIAL.
CC DOMAIN 736 786 6 X REPEATS, GLY-RICH.
CC REPEAT 736 741 1.
CC REPEAT 745 750 2.
CC REPEAT 754 759 3.
CC REPEAT 763 768 4.
CC REPEAT 772 777 5.
CC REPEAT 781 786 6.
SQ SEQUENCE 955 AA: 102187 MW: B60F2DB8168EBCAF CRC64:

Query Match 75.4%; Score 43; DB 1; Length 955;
Best Local Similarity 75.0%; Pred. No. 9.1;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSLNKKELEAE 12
II IIIII:II
Db 453 FLNLNKLKLEAE 464

RESULT 5
HLVA_ACTSU STANDARD: PRT; 956 AA.
ID HLVA_ACTSU
AC 000951;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Hemolysin (Cytolysin II) (CLY-IIA) (CYTC) (APPA).
GN APPA OR CLYIIA OR HLVIYA OR CYTC.
OS Actinobacillus suis.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Actinobacillus.
OX NCBI_TaxID=716;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3714;
MEDLINE=92267623; PubMed=1587585;
RA Burrows L.V., Lo R.Y.;
RT "Molecular characterization of an RTX toxin determinant from
RT Actinobacillus suis.";
RL Infect. Immun. 60:2166-2173(1992).
-1- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A. SUI. MIGHT BE A
CC SECRETED CYTOTOXIN, POSSIBLY THE EXTRACELLULAR HEMOLYSIN.
-1- SUBCELLULAR LOCATION: Secreted.
-1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.

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CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -1- PFM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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CC -----
CC EMBL: M90440; AAA21918.1; -.
CC InterPro: IPR001343; Hemolysin_Ca_bind.
CC InterPro: IPR003355; RTX_N.
CC InterPro: IPR003995; RCXA.
CC Pfam: PF00353; hemolysinCaBind; 1.
CC Pfam: PF02382; RTX; 1.
CC PRINTS: PR00313; CABNDNGRPT.
CC PRINTS: PR01488; RTXTOXINA.
CC PROSITE: PS00330; HEMOLYSIN_CALCITUM; 1.
CC Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
CC Transmembrane; Lipoprotein; Palmitate.
CC TRANSMEM 238 254 POTENTIAL.
CC TRANSMEM 302 320 POTENTIAL.
CC TRANSMEM 383 406 POTENTIAL.
CC DOMAIN 719 799 9 X REPEATS, GLY-RICH.
CC REPEAT 719 724 1.
CC REPEAT 728 733 2.
CC REPEAT 737 742 3.
CC REPEAT 746 751 4.
CC REPEAT 755 760 5.
CC REPEAT 764 769 6.
CC REPEAT 773 778 7.
CC REPEAT 782 787 8.
CC REPEAT 794 799 9.
CC SEQUENCE 956 AA; 102453 MW; 3415FF1D7ADD4365 CRC64;

Query Match 75.4%; Score 43; DB 1; Length 956;
Best Local Similarity 75.0%; Pred. No. 9.1;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLISELNKELEAE 12
Db 455 FLINLNKELEAE 466

RESULT 6
RT2A_ACTPL STANDARD; PRT; 956 AA.
AC P15377;
DT 01-APR-1990 (Rel. 14, Created)
DT 30-APR-1990 (Rel. 14, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE RTX-II toxin determinant A (APX-IIA) (Hemolysin IIA) (HLV-IIA)
DE (Cytolysin IIA) (CLY-IIA).
DE APXIIA OR CLYIIA OR HLXIIA OR APPA OR CYTC.
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Actinobacillus.
OC NCBI_TaxID=715;
OX [1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=SEROTYPE 5;
RX MEDLINE=90126233; PubMed=2693022;
RA Chang Y.-F., Young R., Struck D.K.;
RT "Cloning and characterization of a hemolysin gene from Actinobacillus
RL (Haemophilus) pleuropneumoniae.";
RN [2]

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RP SEQUENCE FROM N.A.
RC STRAIN-ISOLATE CVI 13261 / SEROTYPE 9;
RX MEDLINE=92040145; PubMed=1937809;
RA Smith M.A., Britaire J., Jansen R., Smith H.E., Kamp E.M.,
RA Gielkens A.L.;
RT "Genetics of Actinobacillus pleuropneumoniae serotype 9.";
RL Infect. Immun. 59:4497-4504(1991).
CC -1- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A.PLEUROPNEUMONIAE,
CC WHICH SHOWS A WEAK HEMOLYTIC ACTIVITY AND IS MODERATELY CYTOTOXIC
CC FOR ALVEOLAR MACROPHAGES AND NEUTROPHILS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY (BY SIMILARITY).
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -1- PFM: PALMITOYLATED BY APXIC. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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CC -----
CC EMBL: M30602; AAA87232.1; -.
CC EMBL: X61111; CAA43423.1; -.
CC PIR: B33389; B33389.
CC PIR: S18853; S18853.
CC InterPro: IPR001343; Hemolysin_Ca_bind.
CC InterPro: IPR003355; RTX_N.
CC InterPro: IPR003995; RCXA.
CC Pfam: PF00353; hemolysinCaBind; 1.
CC Pfam: PF02382; RTX; 1.
CC PRINTS: PR00313; CABNDNGRPT.
CC PRINTS: PR01488; RTXTOXINA.
CC PROSITE: PS00330; HEMOLYSIN_CALCITUM; 1.
CC Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
CC Transmembrane; Lipoprotein; Palmitate.
CC TRANSMEM 233 256 POTENTIAL.
CC TRANSMEM 266 323 POTENTIAL.
CC TRANSMEM 361 406 POTENTIAL.
CC DOMAIN 719 787 8 X REPEATS, GLY-RICH.
CC REPEAT 719 724 1.
CC REPEAT 728 733 2.
CC REPEAT 737 742 3.
CC REPEAT 746 751 4.
CC REPEAT 755 760 5.
CC REPEAT 764 769 6.
CC REPEAT 773 778 7.
CC REPEAT 782 787 8.
CC SEQUENCE 956 AA; 102531 MW; BDBCABADFL14A641 CRC64;

Query Match 75.4%; Score 43; DB 1; Length 956;
Best Local Similarity 75.0%; Pred. No. 9.1;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLISELNKELEAE 12
Db 455 FLINLNKELEAE 466

RESULT 7
FLIG_BACSU STANDARD; PRT; 338 AA.
AC P23448;
DT 01-NOV-1991 (Rel. 20, Created)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

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DE Flagellar motor switch protein flig.
GN flig.
ON Bacillus subtilis.
OC Bacteria: Firmicutes; Bacillus/Clostridium group;
OX Bacillus/Staphylococcus group; Bacillus.
RN NCBL_TaxID=1423;
RP [1]
RC SEQUENCE FROM N.A.
RX STRAIN=168;
RA MEDLINE=91258343; PubMed=1828465;
RT Albertini A.M., Caramori T., Crabli W.D., Scoffone F., Galizzi A.;
RT "The fla locus of Bacillus subtilis is part of a large operon coding
RT for flagellar structures, motility functions, and an Arpase-like
RT polypeptide.";
RL J. Bacteriol. 173:3573-3579(1991).
CC -1- FUNCTION: ONE OF THE PROTEINS THAT FORM A SWITCH COMPLEX THAT IS
CC PROPOSED TO BE LOCATED AT THE BASE OF THE BASAL BODY. THIS COMPLEX
CC INTERACTS WITH CHEMOTAXIS PROTEINS (SUCH AS CHEY) IN ADDITION TO
CC CONTRACTING COMPONENTS OF THE MOTOR THAT DETERMINE THE DIRECTION OF
CC FLAGELLAR ROTATION.
CC -1- SUBCELLULAR LOCATION: Membrane-associated (by similarity).
CC -1- SIMILARITY: BELONGS TO THE FLIG FAMILY.
CC -----
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CC -----
DR EMBL: X56049; CAA39521.1; -
DR EMBL: 299112; CAB13495.1; -
DR PIR: S14495; S14495.
DR PIR: B42365; B42365.
DR HSSP: Q9MY63; 1QC7.
DR Subtilist; BG10241; flig.
DR InterPro: IPR000090; Flg_Motor_Flg.
DR Pfam: PF01706; Flig-C_1
DR PRINTS: PR00934; FLGMOTORFLIG.
DR Chemotaxis; Flagella; Flagellar rotation; Membrane; Complete proteome.
SQ SEQUENCE 338 AA; 38191 MW; 8C44193BA0ADE58E CRC64;

Query Match 68.4%; Score 39; DB 1; Length 338;
Best Local Similarity 72.7%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 LSELNKELEAE 12
||||| : : :
DB 150 LSELNPEVQAE 160

RESULT 8
ID NFM_PIG STANDARD; PRT; 454 AA.
AC P08552;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurofilament triplet M protein (160 kDa neurofilament protein)
DE (Neurofilament medium polypeptide) (NF-M) (Fragment).
DE NEF3 OR NEFM.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBL_TaxID=9823;
RN [1]
RP TISSUE=Spinal cord;
RC MEDLINE=85076594; PubMed=6439558;
RX Geisler N., Fischer S., Vandekeckhove J., Plessmann U., Weber K.;
RT "Hybrid character of a large neurofilament protein (NF-M):

RT Intermediate filament type sequence followed by a long and acidic
RT carboxy-terminal extension.";
RL EMBL J. 3:2701-2706(1984).
CC -1- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M,
CC AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
CC -1- PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P. NFM IS
CC PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS
CC THOUGHT THAT PHOSPHORYLATION OF NFM RESULTS IN THE FORMATION OF
CC INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
CC OF AXONAL CALIBER.
CC -1- PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING
CC OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE
CC LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND
CC COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
CC -1- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
DR PIR: A03075; ORFGM.
DR InterPro: IPR001664; IF.
DR Pfam: PF00038; filament; 1.
DR PROSITE: PS00226; IF; 1.
KW Intermediate filament; Coiled coil; Neurone; Acetylation;
KW Phosphorylation; Glycoprotein.
FT MOD_RES 1
FT DOMAIN 1 104
FT FT 105 412
FT DOMAIN 105 412
FT DOMAIN 413 >454
FT DOMAIN 105 136
FT DOMAIN 137 149
FT DOMAIN 150 248
FT DOMAIN 249 265
FT DOMAIN 266 287
FT DOMAIN 288 291
FT DOMAIN 292 411
FT CARBOHYD 47 47
FT CARBOHYD 432 432
FT NON_TER 454 454
SQ SEQUENCE 454 AA; 51854 MW; C809282E9C903A6B CRC64;

Query Match 68.4%; Score 39; DB 1; Length 454;
Best Local Similarity 58.3%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSLNKELEAE 12
: : : : :
DB 121 YLEQNKLEIEAE 132

RESULT 9
ID NFM_BOVIN STANDARD; PRT; 810 AA.
AC 07788;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurofilament triplet M protein (160 kDa neurofilament protein)
DE (Neurofilament medium polypeptide) (NF-M) (Fragment).
DE NEF3 OR NEFM OR NFM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
OX NCBL_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Hill W.D., Zhang L., Balin B.J., Sprinkle T.J., Splcer K.,
RA Gearhart D.A.;
RT "The bovine neurofilament M subunit has a novel set of KSP repeats
RT normally restricted to NF-H.";
RL submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M,
CC AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
CC -1- PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P. NFM IS
CC PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS

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CC      THOUGHT THAT PHOSPHORYLATION OF NEF RESULTS IN THE FORMATION OF
CC      INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
CC      OF AXONAL CALIBER (BY SIMILARITY) .
CC      -1- PPM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING
CC      OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H) , THE
CC      LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND
CC      COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION (BY
CC      SIMILARITY) .
CC      -1- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
CC      -----
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CC      or send an email to license@ebi.ac.uk) .
CC      -----
CC      DR      EMBL; AF091342; AAC36357.1; -.
CC      DR      InterPro: IPR001664; IP.
CC      DR      Pfam; PF00038; filament; 1.
CC      DR      PROSITE: PS00226; IF; 1.
CC      DR      Intermediate filament; Collid coll; Neutrone; Phosphorylation.
CC      KM      NON_TER      1
CC      FT      DOMAIN      1      296      ROD.
CC      FT      DOMAIN      297      810      TAIL.
CC      FT      DOMAIN      <1      20      COIL 1A.
CC      FT      DOMAIN      21      33      LINKER 1.
CC      FT      DOMAIN      34      132      COIL 1B.
CC      FT      DOMAIN      133      149      LINKER 12.
CC      FT      DOMAIN      150      171      COIL 2A.
CC      FT      DOMAIN      172      175      LINKER 2.
CC      FT      DOMAIN      176      296      COIL 2B.
CC      FT      DOMAIN      503      582      8 X 13 AA TANDEM REPEATS.
CC      SQ      SEQUENCE      810 AA; 90799 MM; B8477D85560AC3F6 CRC64;

Query Match      68.4%; Score 39; DB 1; Length 810;
Best Local Similarity      58.3%; Pred. No. 37;
Matches      7; Conservative      3; Mismatches      2; Indels      0; Gaps      0;

OY      1 FLESLNKELEAE 12
      :|: |||:|
Db      5 YLEQNKKELEAE 16

RESULT 10
NFM_RAT ID NFM_RAT STANDARD; PRT; 845 AA.
AC P12639; Q63370;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurofilament triplet M protein (160 kDa neurofilament protein)
DE (Neurofilament medium polypeptide) (NF-M).
DE NEF3 OR NEFM OR NFM.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
OX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87282618; PubMed=2441012;
RA Napolitano E.W., Chin S.S.M., Colman D.R., Liem R.K.H.;
RT "Complete amino acid sequence and in vitro expression of rat NF-M,
RL the middle molecular weight neurofilament protein."
RL J. Neurosci. 7:2590-2599(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC SRRAIN-WISTAR;
RX MEDLINE=92332596; PubMed=1321159;
RA Kelly B.M., Gillespie C.S., Sherman D.L., Brophy P.J.;
RT "Schwann cells of the myelin-forming phenotype express neurofilament

```

RT	protein NF-M.";	
RL	J. Cell Biol. 118:397-410(1992).	
RN		
RP	PHOSPHORYLATION SITES, AND REVISION TO 500.	
RX	MEDLINE=92165797; Pubmed=1537832.	
RA	Xu Z.-S., Liu W.-S., Willard M.B.;	
RT	"Identification of six phosphorylation sites in the COOH-terminal	
RL	tall region of the rat neurofilament protein M.";	
RN	J. Biol. Chem. 267:4467-4471(1992).	
RP	[4]	
RX	CARBOHYDRATE-LINKAGE SITES	
RA	MEDLINE=93346421; Pubmed=8344946.	
RT	Dong D.-Y., Xu Z.-S., Chevrier M.R., Cotter R.J., Cleveland D.W.,	
RL	Hart G.W.;	
RN	"Glycosylation of mammalian neurofilaments. Localization of multiple	
RT	O-linked N-acetylglucosamine moieties on neurofilament polypeptides	
RL	L and M.";	
RN	J. Biol. Chem. 268:16679-16687(1993).	
CC	-I- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M,	
CC	AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.	
CC	-I- PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P. NEM IS	
CC	PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS	
CC	THOUGHT THAT PHOSPHORYLATION OF NEM RESULTS IN THE FORMATION OF	
CC	INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE	
CC	OF AXONAL CALIBER.	
CC	-I- PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING	
CC	OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE	
CC	LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND	
CC	COINCIDENT WITH A CHANGE IN THE INTERMEDIATE FILAMENT FAMILY.	
CC	-I- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.	
CC		
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CC	use by non-profit institutions as long as its content is in no way	
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CC	entities requires a license agreement (See http://www.isb-sb.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
DR	EMBL; M18628; AAA11696.1; -	
DR	EMBL; Z12152; CAA78136.1; -	
DR	GlycoSuiteDB; P12839; -	
DR	InterPro; IPR001664; IF.	
DR	Pfam; PF00038; filament; 1.	
DR	PROSITE; PS00226; IF; 1.	
KW	Intermediate filament; Coiled coil; Neuron; Phosphorylation;	
KW	Glycoprotein.	
FT	INIT_MET 0	
FT	DOMAIN 1 103	BY SIMILARITY.
FT	DOMAIN 103 410	HEAD.
FT	DOMAIN 411 844	ROD.
FT	DOMAIN 103 134	TAIL.
FT	DOMAIN 135 147	COIL 1A.
FT	DOMAIN 148 246	LINKER 1.
FT	DOMAIN 247 263	COIL 1B.
FT	DOMAIN 264 285	LINKER 12.
FT	DOMAIN 286 289	COIL 2A.
FT	DOMAIN 290 410	LINKER 2.
FT	CARBOHYD 47 47	COIL 2B.
FT		O-LINKED (GLCNAC).
FT		/FTID-CAR 000130.
FT		O-LINKED (GLCNAC).
FT	CARBOHYD 430 430	/FTID-CAR 000131.
FT		PHOSPHORYLATION.
FT	MOD_RES 502 502	PHOSPHORYLATION.
FT	MOD_RES 506 506	PHOSPHORYLATION.
FT	MOD_RES 536 536	PHOSPHORYLATION.
FT	MOD_RES 603 603	PHOSPHORYLATION.
FT	MOD_RES 608 608	PHOSPHORYLATION.
FT	MOD_RES 666 666	PHOSPHORYLATION.
FT	CONFLICT 17 17	MISSING (IN REF. 2).
FT	CONFLICT 21 21	R -> P (IN REF. 2).
FT	CONFLICT 204 204	V -> L (IN REF. 2).
FT	CONFLICT 500 500	MISSING (IN REF. 1).
FT	SEQUENCE 845 AA; 95660 MW; 316C141655B1197D CRC64;	
SO		

Query Match 68.4%; Score 39; DB 1; Length 845;
Best Local Similarity 58.3%; Pred. No. 39;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLESLNKELEAE 12
: | : | | : | | |
DB 119 YLEQONKEIEAE 130

RESULT 11
NFM_MOUSE

ID NFM_MOUSE STANDARD; PRT; 848 AA.
AC P08553; 061961;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurofilament triplet M protein (160 kDa neurofilament protein)
DE (Neurofilament medium polypeptide) (NF-M).
GN NEF3 OR NEFM OR NFM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8724694; PubMed=3036526;
RA Levy E., Liem R.K.H., D'Eustachio P., Cowan N.J.;
RT "Structure and evolutionary origin of the gene encoding mouse NF-M,
RT the middle-molecular-mass neurofilament protein.";
RL Eur. J. Biochem. 166:71-77(1987).
RN [2]
RX SEQUENCE OF 322-540 FROM N.A.
RX MEDLINE=8715837; PubMed=3103956;
RA Julien J.-P., Meyer D., Flavell D., Hurst J., Grosved J.;
RT "Cloning and developmental expression of the murine neurofilament
RT gene family.";
RL Brain Res. 387:243-250(1986).
RN [3]
RX FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M,
RX AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
RX -1- PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFM IS
RX PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS
RX THOUGHT THAT PHOSPHORYLATION OF NEF RESULTS IN THE FORMATION OF
RX INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
RX OF AXONAL CALIBER.
RX -1- PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING
RX OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE
RX LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND
RX COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
RX -1- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.

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CC
CC EMBL; X05640; CAA29127.1; -;
DR EMBL; M20481; AAA39815.1; -;
DR PIR; S00030; S00030.
DR MGI; 97314; Nfm.
DR InterPro; IPR001664; IF.
DR Pfam; PF00038; filament; 1.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Coiled coil; Neurone; Phosphorylation;
KW Glycoprotein.
FT INIT_MET 0
FT DOMAIN 1 102 HEAD.
FT DOMAIN 103 410 ROD.
FT DOMAIN 411 848 TAIL.

FT DOMAIN 103 134 COIL 1A.
FT DOMAIN 135 147 LINKER 1.
FT DOMAIN 148 246 COIL 1B.
FT DOMAIN 247 263 LINKER 12.
FT DOMAIN 264 285 COIL 2A.
FT DOMAIN 286 289 LINKER 2.
FT DOMAIN 290 410 COIL 2B.
FT CARBOHYD 47 47 O-LINKED (GLCNAC) (BY SIMILARITY).
FT CARBOHYD 430 430 O-LINKED (GLCNAC) (BY SIMILARITY).
FT CONFLICT 432 432 S -> F (IN REF. 2).
FT CONFLICT 539 540 QA -> RR (IN REF. 2).
SQ SEQUENCE 848 AA; 95910 MW; 5F251F274D0F13B6 CRC64;

Query Match 68.4%; Score 39; DB 1; Length 848;
Best Local Similarity 58.3%; Pred. No. 39;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLESLNKELEAE 12
: | : | | : | | |
DB 119 YLEQONKEIEAE 130

RESULT 12
NFM_CHICK

ID NFM_CHICK STANDARD; PRT; 857 AA.
AC P16053;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurofilament triplet M protein (160 kDa neurofilament protein)
DE (Neurofilament medium polypeptide) (NF-M).
GN NEFM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174973; PubMed=2106668;
RA Zopf D., Dineva B., Betz H., Gundelfinger E.D.;
RT "Isolation of the chicken middle-molecular weight neurofilament
RT (NF-M) gene and characterization of its promoter.";
RL Nucleic Acids Res. 18:521-529(1990).
RN [2]
RP SEQUENCE OF 259-857 FROM N.A.
RX MEDLINE=88112814; PubMed=3123320;
RA Zopf D., Hermans-Borgmeyer I., Gundelfinger E.D., Betz H.;
RT "Identification of gene products expressed in the developing chick
RT visual system: characterization of a middle-molecular-weight
RT neurofilament cDNA.";
RL Genes Dev. 1:699-708(1987).
RN [3]
RX FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M,
RX AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
RX -1- PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFM IS
RX PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS
RX THOUGHT THAT PHOSPHORYLATION OF NEF RESULTS IN THE FORMATION OF
RX INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
RX OF AXONAL CALIBER.
RX -1- PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING
RX OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE
RX LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND
RX COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
RX -1- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.

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CC or send an email to license@isb-sib.ch).
CC

CC EMBL: X17102; CAA34958.1; -
 DR EMBL: X05558; CAA29073.1; -
 DR PIR: A27040; A27040.
 DR PIR: S08061; S08061.
 DR PIR: S15762; S15762.
 DR InterPro: IPR001664; IF.
 DR Pfam: PF00038; filament; 1.
 DR PROSITE: PS00226; IF; 1.
 KW Intermediate filament; Coiled coil; Neurone; Phosphorylation;
 Glycoprotein.
 FT INIT_MET 0
 FT DOMAIN 1 98 HEAD.
 FT DOMAIN 99 406 ROD.
 FT DOMAIN 407 857 TAIL.
 FT DOMAIN 99 130 COIL 1A.
 FT DOMAIN 131 143 COIL 1A.
 FT DOMAIN 144 242 COIL 1B.
 FT DOMAIN 243 259 LINKER 12.
 FT DOMAIN 260 281 COIL 2A.
 FT DOMAIN 282 285 LINKER 2.
 FT DOMAIN 286 406 COIL 2B.
 FT CARBOHYD 46 46 O-LINKED (GLCNAC) (BY SIMILARITY).
 FT CARBOHYD 426 426 O-LINKED (GLCNAC) (BY SIMILARITY).
 FT CONFLICT 546 546 G -> R (IN REF. 2).
 SQ SEQUENCE 857 AA; 95704 MW; 4E2E0FC6AC64778B CRC64;

Query Match 68.4%; Score 39; DB 1; Length 857;
 Best Local Similarity 58.3%; Pred. No. 40;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSEINKELEAE 12
 Db 115 YLEQNKKEIEAE 126

RESULT 13
 NFM_HUMAN STANDARD; PRT; 915 AA.
 ID NFM_HUMAN
 AC P01197;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neurofilament triplet M protein (160 kDa neurofilament protein)
 DE (Neurofilament medium polypeptide) (NF-M) (Neurofilament 3).
 GN NEF3 OR NFM OR NFM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=87275853; PubMed=3608989;
 RA Myers M.W., Lazzarini R.A., Lee V.M.-Y., Schlepfer W.W., Nelson D.L.;
 RT "The human mid-size neurofilament subunit: a repeated protein
 RT sequence and the relationship of its gene to the intermediate
 RT filament gene family.";
 RL EMBO J. 6:1617-1626(1987).
 RN [2]
 RP SEQUENCE OF ONE OF THE 13 RESIDUE REPEATS.
 RX MEDLINE=88158120; PubMed=2450354;
 RA Lee V.M.-Y., Olivos L. Jr., Carden M.J., Hollosi M., Dietzschold B.,
 RA Lazzarini R.A.;
 RT "Identification of the major multiphosphorylation site in mammalian
 RT neurofilaments.";
 RL J. Biol. Chem. 267:11111-11115 (1992).
 CC -1- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M,
 CC AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
 CC -1- PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P. NFM IS
 CC PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS
 CC THOUGHT THAT PHOSPHORYLATION OF NFM RESULTS IN THE FORMATION OF
 CC INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE

CC OF AXONAL CALIBER.
 CC -1- PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING
 CC OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE
 CC LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND
 CC COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
 CC -1- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
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 CC
 CC EMBL: Y00067; CAA68276.1; -
 DR PIR: A27864; A27864.
 DR PIR: A30157; A30157.
 DR MIM: 162250; -
 DR InterPro: IPR001664; IF.
 DR Pfam: PF00038; filament; 1.
 DR PROSITE: PS00226; IF; 1.
 KW Intermediate filament; Coiled coil; Neurone; Phosphorylation;
 Glycoprotein.
 FT INIT_MET 0
 FT DOMAIN 1 103 HEAD.
 FT DOMAIN 104 411 ROD.
 FT DOMAIN 412 915 TAIL.
 FT DOMAIN 104 135 COIL 1A.
 FT DOMAIN 136 148 LINKER 1.
 FT DOMAIN 149 247 COIL 1B.
 FT DOMAIN 248 264 LINKER 12.
 FT DOMAIN 265 286 COIL 2A.
 FT DOMAIN 287 290 LINKER 2.
 FT DOMAIN 291 411 COIL 2B.
 FT DOMAIN 613 690 6 X 13 AA TANDEM REPEATS.
 FT CARBOHYD 46 46 O-LINKED (GLCNAC) (BY SIMILARITY).
 FT CARBOHYD 430 430 O-LINKED (GLCNAC) (BY SIMILARITY).
 SQ SEQUENCE 915 AA; 102317 MW; 5F5D3DF34C9D9E50 CRC64;

Query Match 68.4%; Score 39; DB 1; Length 915;
 Best Local Similarity 58.3%; Pred. No. 43;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSEINKELEAE 12
 Db 120 YLEQNKKEIEAE 131

RESULT 14
 LKTA_PASSP STANDARD; PRT; 947 AA.
 ID LKTA_PASSP
 AC P55123;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Leukotoxin.
 GN LKTA.
 OS Pasteurella haemolytica-like sp. (strain 5943B).
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 CC Pasteurella
 OX NCBI_TaxID=28165;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93239320; PubMed=8478098;
 RA Chang Y.-F., Ma D.-P., Shi J., Chengappa M.M.;
 RT "Molecular characterization of a leukotoxin gene from a Pasteurella
 RT haemolytica-like organism, encoding a new member of the RTX toxin
 RT family.";
 RL Infect. Immun. 61:2089-2095(1993).
 CC -1- FUNCTION: VIRULENCE FACTOR WHICH IS CYTOTOXIC FOR LEUKOCYTES BUT
 CC IS NOT HEMOLYTIC.


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CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -1- PFM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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CC -----
CC DR EMBL: L12148; AAA16444.1; -.
CC DR InterPro: IPR001343; Hemlysn_Ca_bind.
CC DR InterPro: IPR003355; RTX_N.
CC DR Pfam: PF00353; hemolysinCbind; 1.
CC DR Pfam: PF02382; RTX; 1.
CC DR PRINTS: PR00313; CABNDNGRPT.
CC DR PRINTS: PR01488; RTXTOXINA.
CC DR PROSITE: PS00330; HEMOLYSIN_CALCIUM; 4. Repeat; Calcium;
CC Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
CC Transmembrane; Lipoprotein; Palmitate.
CC FT TRANSMEM 154 170 POTENTIAL.
CC FT TRANSMEM 312 333 POTENTIAL.
CC FT DOMAIN 625 780 POTENTIAL.
CC FT REPEAT 625 630 1.
CC FT REPEAT 730 735 2.
CC FT REPEAT 739 744 3.
CC FT REPEAT 748 753 4.
CC FT REPEAT 757 762 5.
CC FT REPEAT 766 771 6.
CC FT REPEAT 775 780 7.
CC SQ SEQUENCE 947 AA; 101559 MW; 9744F06395E5BED CRC64;

Query Match 68.4%; Score 39; DB 1; Length 947;
Best Local Similarity 72.7%; Pred. No. 44;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 LSELNKELEAE 12
DB 448 LQNLNKELEAE 458

RESULT 15
YE18.METJA STANDARD; PRT; 181 AA.
AC 058613;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical aldolase class II protein MJ1418.
GN MJ1418.
OS Methanococcus jannaschii.
OC Archaea: Euryarchaeota: Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN 11)
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=868087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

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RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uttenback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Outten M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RA jannaschii.";
RA Science 273:1058-1073(1996).
CC -1- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ALDOLASE CLASS II FAMILY. ARAD/EUCA
CC SUBFAMILY. STRONG, TO E.COLI YGBL AND H.INFLUENZA H1012.
CC -----
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CC -----
CC DR EMBL: U67582; AAB99428.1; -.
CC DR HSSP: P11550; 3FUA.
CC DR TIGR: MJ1418; -.
CC DR InterPro: IPR001303; Aldolase_II.
CC DR Pfam: PF00596; Aldolase_II; 1.
CC DR Hypothetical protein; Zinc; Complete proteome.
CC FT METAL 68 68 ZINC (BY SIMILARITY).
CC FT METAL 87 87 ZINC (BY SIMILARITY).
CC FT METAL 89 89 ZINC (BY SIMILARITY).
CC FT METAL 147 147 ZINC (BY SIMILARITY).
CC SQ SEQUENCE 181 AA; 20470 MW; E5F3BF13722145B0 CRC64;

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```

Query Match 66.7%; Score 38; DB 1; Length 181;
Best Local Similarity 70.08%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 FLSELNKELE 10
DB 95 FLSTLNKEIE 104

```

Search completed: September 11, 2002, 09:01:55
Job time: 278 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 11, 2002, 09:00:12 : Search time 40.83 Seconds
(without alignments)
28.241 Million cell updates/sec

Title: US-09-884-696-6

Perfect score: 57

Sequence: 1 FLSELNKLEAE 12

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-71.*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	75.4	953	1 B30169	leukotoxin A - Pas
2	43	75.4	955	1 A35254	leukotoxin A - Pas
3	43	75.4	956	1 B33389	leukotoxin A - Pas
4	43	75.4	956	1 A43834	tox II - Actinob
5	42	73.7	913	2 T52485	neurofilament prot
6	41	71.9	784	2 PN0009	neurofilament trip
7	39	68.4	338	1 B42365	flagellar motor sw
8	39	68.4	332	1 QFPCM	neurofilament trip
9	39	68.4	798	2 T50479	neurofilament medi
10	39	68.4	845	2 A45669	neurofilament trip
11	39	68.4	849	2 S00030	neurofilament trip
12	39	68.4	858	2 S15762	neurofilament trip
13	39	68.4	916	2 A27864	neurofilament trip
14	38	66.7	181	1 A64477	L-fucose-phospha
15	38	66.7	211	2 T03355	gene e12 protein -
16	38	66.7	382	2 E64686	myosin-like protei
17	38	66.7	508	2 T24622	hypothetical prote
18	38	66.7	993	2 C55226	cylm protein - Ent
19	37	64.9	275	2 S21348	probable pol polyp
20	37	64.9	356	2 C40656	regulatory protein
21	37	64.9	359	2 AC1022	two-component sens
22	37	64.9	363	2 F91265	sensor protein Bas
23	37	64.9	363	2 JX0285	sensor protein Bas
24	37	64.9	363	2 C86106	sensor protein for
25	37	64.9	663	2 S69526	hypothetical prote
26	37	64.9	899	2 D96594	unknown protein, 7
27	37	64.9	1534	2 A56734	ribosome receptor,
28	36.5	64.0	617	2 B70425	hypothetical prote
29	36	63.2	117	2 T14283	embryogenic callus

30	36	63.2	159	2 F96794	probable calmodul1
31	36	63.2	196	2 AH1149	hypothetical prote
32	36	63.2	196	2 A11508	hypothetical prote
33	36	63.2	203	2 H83806	hypothetical prote
34	36	63.2	235	2 AF2157	transcription regu
35	36	63.2	379	1 DMDXBF	2-hydroxyglutaryl-
36	36	63.2	462	2 S52528	UAI protein - yea
37	36	63.2	557	2 T47128	heat shock protein
38	36	63.2	828	2 S56250	probable membrane
39	36	63.2	913	2 T25965	hypothetical prote
40	36	63.2	955	2 T21612	hypothetical prote
41	36	63.2	1792	2 T13939	myosin V - fruit f
42	35	61.4	136	2 F97759	hypothetical prote
43	35	61.4	143	2 H71970	hypothetical prote
44	35	61.4	150	2 S60838	M protein precurs
45	35	61.4	152	2 T02703	hypothetical prote

ALIGNMENTS

RESULT 1
B30169
leukotoxin A - Pasteurella haemolytica (serotype 1)
N:Alternate names: lKTA protein
C:Species: Pasteurella haemolytica
C>Date: 12-Oct-1989 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999
C:Accession: B30169; C32051; S29516
R:Highlander, S.K.; Chidambaram, M.; Engler, M.J.; Weinstein, G.M.
DNA 8, 15-28, 1989
A:Title: DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster.
A:Reference number: A30169; MUID:89210283
A:Accession: B30169
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-953 <HIG>
R:Strathee, C.A.; Lo, R.Y.C.
J. Bacteriol. 171, 916-928, 1989
A:Title: Cloning, nucleotide sequence, and characterization of genes encoding the se
A:Reference number: A32051; MUID:89123172
A:Accession: C32051
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 947-953 <STR>
R:Lo, R.Y.C.; Strathee, C.A.; Shewen, P.E.
Infect. Immun. 55, 1987-1996, 1987
A:Title: Nucleotide sequence of the leukotoxin genes of Pasteurella haemolytica A1.
A:Reference number: S29515; MUID:87306837
A:Accession: S29516
A:Molecule type: DNA
A:Residues: 1-741, 'D', 743-953 <LOR>
A:Cross-references: EMBL:M20730; NID:9150492; PIDN:AAA25529.1; PID:9150494
C:Comment: This organism causes bovine pneumonic pasteurellosis (shipping fever).
C:Genetics:
A:Gene: lKTA
C:Function:
A:Description: lyses leukocytes
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytotoxic; exotoxin; hemolysis; lipoprotein; tandem rep
F:238-784/Domain: hemolysin A homology <HLVA>
F:716-807/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVYF]-X)
F:554/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match 75.4%; Score 43; DB 1; Length 953;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKLEAE 12
DB 451 FLNLNKLKLEAE 462

```

RESULT 2
A35254
leukotoxin A - Pasteurella haemolytica (serotype T10)
N:Alternate names: Ikta protein
C:Species: Pasteurella haemolytica
C:Date: 10-Aug-1990 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999
A:Accession: S37145; A35254; S34237; S34235
R:Lincoln, A.F.; Atchison, K.; Donachie, W.
Submitted to the EMBL Data Library, September 1993
A:Description: DNA sequence of the leukotoxin A gene from P. haemolytica T10 serotype.
A:Reference number: S37145
A:Accession: S37145
A:Molecule type: DNA
A:Residues: 1-955 <LA2>
A:Cross-references: EMBL:Z26247; NID:9400424; PIDN:CAA81206.1; PID:9400425
R:Highlander, S.K.; Engler, M.J.; Weinstock, G.M.
J.Bacteriol. 172, 2343-2350, 1990
A:Title: Secretion and expression of the Pasteurella haemolytica leukotoxin.
A:Reference number: A35254; MUID:90236888
A:Accession: A35254
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 950-955 <HIC>
A:Cross-references: GB:M24197; GB:M34943; GB:M34944
R:Lincoln, A.F.; Atchison, K.D.; Donachie, W.
submitted to the EMBL Data Library, June 1993
A:Description: DNA sequence of the carboxy terminal end of leukotoxin A from the T3 sero
A:Reference number: S34235
A:Accession: S34237
A:Molecule type: DNA
A:Residues: 745-955 <LA2>
A:Cross-references: EMBL:Z22884; NID:9311828; PIDN:CAA80498.1; PID:9311829
A:Experimental source: serotype T3
A:Accession: S34235
A:Molecule type: DNA
A:Residues: 723-955 <LA3>
A:Cross-references: EMBL:Z22887; NID:9311824; PIDN:CAA80501.1; PID:9311825
A:Experimental source: serotype T10
C:Function:
A:Description: attacks cell membranes and causes cell lysis
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat;
F:240-786/Domain: hemolysin A homology <HLA>
F:718-809/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVYF]-X)
F:718-726/Region: repeat
F:717-735/Region: repeat
F:736-744/Region: repeat
F:745-753/Region: repeat
F:754-762/Region: repeat
F:763-771/Region: repeat
F:772-780/Region: repeat
F:781-789/Region: repeat
F:792-800/Region: repeat
F:801-809/Region: repeat
F:556/Binding site: palmitate (lys) (covalent) #status predicted

Query Match 75.4%; Score 43; DB 1; Length 955;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLINLNKELEAE 12
II | | | | | | | |
DB 453 FLINLNKELEAE 464

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R:Chang, Y.F.; Young, R.; Struck, D.K.
DNA 8, 635-647, 1989
A:Title: Cloning and characterization of a hemolysin gene from Actinobacillus (Haemop
A:Reference number: A33389; MUID:90126233
A:Accession: B33389
A:Molecule type: DNA
A:Residues: 1-956 <CHA>
A:Cross-references: GB:M30602; NID:9141823; PIDN:AAA87232.1; PID:9141825
A:Experimental source: serotype 5
R:Smith, M.A.; Braite, J.; Jansen, R.; Smith, H.E.; Kamp, E.M.; Gielkens, A.L.J.
submitted to the EMBL Data Library, July 1991
A:Description: Cytolysins of Actinobacillus pleuropneumoniae serotype 9.
A:Reference number: S18852
A:Accession: S18853
A:Molecule type: DNA
A:Residues: 1-956 <SM2>
A:Cross-references: EMBL:X61111; NID:938939; PIDN:CAA43423.1; PID:938941
R:Smith, M.A.; Braite, J.; Jansen, R.; Smith, H.E.; Kamp, E.M.; Gielkens, A.L.J.
Infect. Immun. 59, 4497-4504, 1991
A:Title: Cytolysins of Actinobacillus pleuropneumoniae serotype 9.
A:Reference number: A43599; MUID:92040145
A:Accession: A43599
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-27; 948-956 <SM2>
A:Cross-references: GB:X61111; NID:938939
C:Comment: This organism causes porcine pleuropneumonia.
C:Genetics:
A:Gene: aprA; clyA
C:Function:
A:Description: attacks blood cell membranes and causes cell lysis
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repe
F:243-787/Domain: hemolysin A homology <HLA>
F:719-801/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVYF]-X)
F:557/Binding site: palmitate (lys) (covalent) #status predicted

Query Match 75.4%; Score 43; DB 1; Length 956;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLINLNKELEAE 12
II | | | | | | | |
DB 455 FLINLNKELEAE 466

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RESULT 3
B33389
toxin II - Actinobacillus pleuropneumoniae
N:Alternate names: cytolysin II; RTX-toxin II (AprXII)
C:Species: Actinobacillus pleuropneumoniae
C:Date: 09-Mar-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999
A:Accession: B33389; S18853; B43599

```

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A

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Query Match 75.4%; Score 43; DB 1; Length 956;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSLNKLEAE 12
|||:|||||:
DB 455 FLINLNKELOAE 466

RESULT 5
T52485
neurofilament protein NF-M(2), middle molecular weight [imported] - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000
C:Accession: T52485
R:Gervasi, C.; Szaro, B.G.
Brain Res. Mol. Brain Res. 48, 229-242, 1997
A:Title: Sequence and expression pattern of two forms of the middle molecular weight neu
A:Reference number: 226090
A:Accession: T52485
A:Status: preliminary; translated from GB/EMBL/DDAJ
A:Molecule type: mRNA
A:Residues: 1-913 <GER>
A:Cross-references: EMBL:U85970; PIDN:AAB53390.1

Query Match 73.7%; Score 42; DB 2; Length 913;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSLNKLEAE 12
|||:|||||:
DB 106 FLEQNKLEAE 117

RESULT 6
PND009
neurofilament triplet M protein - Pacific electric ray (fragment)
C:Species: Torpedo californica (Pacific electric ray)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 27-Oct-1995
C:Accession: PND009
R:Linal, M.; Scheller, R.H.
J. Neurochem. 54, 762-770, 1990
A:Title: A unique neurofilament from Torpedo electric lobe: sequence, expression, and id
A:Reference number: PND009; MUID:90155300
A:Accession: PND009
A:Molecule type: mRNA
A:Residues: 1-784 <LIN>
C:Comment: Neurofilaments are a subgroup of intermediate filaments which are expressed s
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; cytoskeleton; intermediate filament; nerve; phosphoprotein; tan
F:1-52/Region: serine-rich
F:53-84/Region: coil Ia
F:98-194/Region: coil Ib
F:217-367/Region: coil II
F:400-597/Region: glutamic acid-rich
F:598-674/Region: 6-residue repeats
F:773-784/Domain: carboxyl-terminal #status predicted <CTD>
F:616,622,628,634,640,646,652,658,670/Binding site: phosphate (Ser) (covalent) #status p

Query Match 71.9%; Score 41; DB 2; Length 784;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSLNKLEAE 12
|||:|||||:
DB 72 YLDQNKLEAE 83

RESULT 7
B42365
flagellar motor switch protein flig - Bacillus subtilis

C:Species: Bacillus subtilis
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: B42365; C69624; S14495
R:Albertini, A.M.; Caramori, T.; Crabb, W.D.; Scoffone, F.; Gallizzi, A.
J. Bacteriol. 173, 3573-3579, 1991
A:Title: The flia locus of Bacillus subtilis is part of a large operon coding for fl
A:Reference number: A42365; MUID:91258343
A:Accession: B42365

A:Molecule type: DNA
A:Residues: 1-338 <ALB>
A:Cross-references: EMBL:X56049; NID:g39904; PIDN:CA39521.1; PID:g39905
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Be
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ethlich, S.D.; Emerson, P.T.; Eutlian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Ga
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, I
Koelter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardin
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mei
Y., M.; Ogawa, K.; Ogilwa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scan
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; S
akeuchi, M.; Yamakoshi, A.; Tanaka, T.; Tepstra, P.; Tognoni, A.; Tosato, V.; Uchiy
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshid
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtil
A:Reference number: A69580; MUID:98044033
A:Accession: C69624
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-338 <KUN>
A:Cross-references: GB:299112; GB:AL009126; NID:g2633902; PIDN:CA313495.1; PID:g2633
A:Experimental source: strain 168
C:Genetics:
A:Gene: flig
C:Superfamily: flagellar switch protein flig
C:Keywords: flagellar rotation

Query Match 68.4%; Score 39; DB 1; Length 338;
Best Local Similarity 72.7%; Pred. No. 41;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LSLNKELEAE 12
|||||:|:
DB 150 LSLNPEVQAE 160

RESULT 8
QFPCM
neurofilament triplet M protein - pig (fragments)
N:Alternate names: 160K neurofilament protein; NF-M(medium) protein; type IV IF prot
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 31-Mar-1988 #sequence_revision 02-Jul-1998 #text_change 10-Jul-1998
C:Accession: A05075; S02570
R:Geisler, N.; Fischer, S.; Vandekerckhove, J.; Plessmann, U.; Weber, K.
EMBO J. 3, 2701-2706, 1984
A:Title: Hybrid character of a large neurofilament protein (NF-M): intermediate filai
A:Reference number: A05075; MUID:85076594
A:Accession: A05075

A:Molecule type: protein
A:Residues: 1-454 <GEI>
A:Experimental source: spinal cord
R:Geisler, N.; Vandekerckhove, J.; Weber, K.
FEBS Lett. 221, 403-407, 1987
A:Title: Location and sequence characterization of the major phosphorylation sites o
A:Reference number: S02570; MUID:87304852
A:Accession: S02570

A:Molecule type: protein
A:Residues: 438-450; 453-459; 460-475; 476-514; 515-532 <GEI2>
A:Experimental source: spinal cord
C:Superfamily: cytoskeletal keratin
C:Keywords: blocked amino end; coiled coil; intermediate filament; phosphoprotein

F:1-98/Domain: head #status predicted <HBD>
 F:99-412/Domain: alpha-helical rod <RBD>
 F:438-454,455-459,460-475,476-514/Domain: tail (fragments) #status predicted <TRIP>
 F:515-532/Domain: tail (fragment) #status predicted <TRIP2>
 F:1/Modified site: blocked amino end (Ser) (probably acetylated) #status experimental
 F:456,462,465,479/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 68.4%; Score 39; DB 1; Length 532;
 Best Local Similarity 58.3%; Pred. No. 66;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSLNKLEAE 12
 : | : |||: |||
 Db 121 YLEQONKEIEAE 132

RESULT 9

150479
 neurofilament medium protein - goldfish
 C:Species: Carassius auratus (goldfish)
 C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 13-Aug-1999
 C:Accession: 150479
 R:Glasgow, E.; Hall, C.M.; Schechter, N.
 J. Neurochem. 63, 52-61, 1994
 A:Title: Organization, sequence, and expression of a gene encoding goldfish neurofilament
 A:Reference number: 150479; MUID:94267484
 A:Accession: 150479
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-798 <GLA>
 A:Cross-references: GB:L09742; NID:g213019; PIDN:AAA72341.1; PID:g213020
 C:Genetics:
 A:introns: 343/3; 385/2
 C:Superfamily: cytoskeletal keratin

Query Match 68.4%; Score 39; DB 2; Length 798;
 Best Local Similarity 58.3%; Pred. No. 1e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSLNKLEAE 12
 : | : |||: |||
 Db 104 FLEQONKEIEAE 115

RESULT 10

A45669
 neurofilament triplet M protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 13-Aug-1999
 C:Accession: A45669; S25712; A42393
 R:Napolitano, E.W.; Chin, S.S.M.; Colman, D.R.; Liem, R.K.H.
 J. Neurosci. 7, 2590-2599, 1987
 A:Title: Complete amino acid sequence and in vitro expression of rat NF-M, the middle mo
 A:Reference number: A45669; MUID:87282618
 A:Accession: A45669
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-845 <NAP>
 A:Cross-references: EMBL:M18628; NID:g205687; PIDN:AAA41696.1; PID:g205688
 R:Kelly, B.M.; Gillespie, C.S.; Sherman, D.L.; Brophy, P.J.
 J. Cell Biol. 118, 397-410, 1992
 A:Title: Schwann cells of the myelin-forming phenotype express neurofilament protein NF-
 A:Reference number: S25712; MUID:92332596
 A:Accession: S25712
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-17,19-21,'P',23-204,'L',206-500,'E',501-845 <REL>
 A:Cross-references: EMBL:212152; NID:g56751; PIDN:CAA78136.1; PID:g56752
 R:Xu, Z.S.; Liu W.S.; Willard, M.B.
 J. Biol. Chem. 267, 4467-4471, 1992
 A:Title: Identification of six phosphorylation sites in the COOH-terminal tail region of

A:Reference number: A42393; MUID:92165797
 A:Accession: A42393
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 411-500,'E',501-843,'D' <XID>
 A:Note: sequence extracted from NCBI backbone (NCBIP:83673)
 C:Superfamily: cytoskeletal keratin

Query Match 68.4%; Score 39; DB 2; Length 845;
 Best Local Similarity 58.3%; Pred. No. 1e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSLNKLEAE 12
 : | : |||: |||
 Db 120 YLEQONKEIEAE 131

RESULT 11

S00030
 neurofilament triplet M protein - mouse
 N:Alternate names: 160K NF protein; NF-M
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
 C:Accession: S00030
 R:Levy, E.; Liem, R.K.H.; d'Eustachio, P.; Cowan, N.J.
 Eur. J. Biochem. 166, 71-77, 1987
 A:Title: Structure and evolutionary origin of the gene encoding mouse NF-M, the middl
 A:Reference number: S00030; MUID:87246594
 A:Accession: S00030
 A:Molecule type: DNA
 A:Residues: 1-849 <LEV>
 A:Cross-references: GB:X05640; NID:g53357; PIDN:CAA29127.1; PID:g297529
 C:Genetics:
 A:Map position: 14
 A:introns: 359/3; 401/2
 C:Superfamily: cytoskeletal keratin
 C:Keywords: coiled coil; intermediate filament
 F:99-244/Domain: coiled coil <COL>
 F:267-411/Domain: coiled coil <CO2>
 F:412-849/Domain: tail <TAI>

Query Match 68.4%; Score 39; DB 2; Length 849;
 Best Local Similarity 58.3%; Pred. No. 1e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSLNKLEAE 12
 : | : |||: |||
 Db 120 YLEQONKEIEAE 131

RESULT 12

S15762
 neurofilament triplet M protein - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Aug-1999
 C:Accession: S15762; S08061; A27040
 R:Zopf, D.; Dineva, B.; Betz, H.; Gundelfinger, E.D.
 Nucleic Acids Res. 18, 521-529, 1990
 A:Title: Isolation of the chicken middle-molecular weight neurofilament (NF-M) gene a
 A:Reference number: S15762; MUID:90174973
 A:Accession: S15762
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-858 <ZOP>
 A:Cross-references: EMBL:X17102; NID:g63688; PIDN:CAA34958.1; PID:g63689
 R:Zopf, D.; Dineva, B.; Betz, H.; Gundelfinger, E.
 Submitted to the EMBL Data Library, November 1989
 A:Reference number: S08061
 A:Accession: S08061
 A:Molecule type: DNA
 A:Residues: 1-355,368-858 <ZO2>

A:Cross-references: EMBL:X17102
 R;20pfl, D.; Hermans-Borgmeyer, I.; Gundelfinger, E.D.; Betz, H.
 Genes Dev. 1, 699-708, 1987
 A:Title: Identification of gene products expressed in the developing chick visual system
 A:Reference number: A27040; MUID:88112814
 A:Accession: A27040
 A:Molecule type: mRNA
 A:Residues: 350-546; 'R',548-858 <Z03>
 A:Cross-references: GB:X05558; NID:g63685; PIDN:CAA29073.1; PID:g63686
 C:Genetics:
 A:Introns: 355/3; 397/2
 C:Superfamily: cytoskeletal keratin
 C:Keywords: coiled coil

Query Match 68.4%; Score 39; DB 2; Length 858;
 Best Local Similarity 58.3%; Pred. No. 1,1e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
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 Db 116 YLEQNKKEIEAE 127

RESULT 13
 A27864
 neurofilament triplet M protein - human
 N:Alternate names: NF-M (medium) protein
 C:Species: Homo sapiens (hmn)
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
 C:Accession: A27864; A30157
 R:Myers, M.W.; Lazzarini, R.A.; Lee, V.M.Y.; Schlaepfer, W.W.; Nelson, D.L.
 EMBO J. 6, 1617-1626, 1987
 A:Title: The human mid-size neurofilament subunit: a repeated protein sequence and the
 A:Reference number: A27864; MUID:87275833
 A:Accession: A27864
 A:Molecule type: DNA
 A:Residues: 1-916 <MVE>
 A:Cross-references: GB:Y00067; NID:g35045; PIDN:CAA68276.1; PID:g35046
 R:Lee, V.M.Y.; Ouyos Jr., L.; Carden, M.J.; Hollosi, M.; Dietzschold, B.; Lazzarini, R.A.
 Proc. Natl. Acad. Sci. U.S.A. 85, 1998-2002, 1988
 A:Title: Identification of the major multiphosphorylation site in mammalian neurofilament
 A:Reference number: A30157; MUID:88158120
 A:Contents: annotation; phosphorylation sites
 C:Genetics:
 A:Introns: 360/3; 402/2
 C:Superfamily: cytoskeletal keratin
 C:Keywords: coiled coil; phosphoprotein
 F:615,628,641,654,680/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 68.4%; Score 39; DB 2; Length 916;
 Best Local Similarity 58.3%; Pred. No. 1,2e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
 :|:|||||
 Db 121 YLEQNKKEIEAE 132

RESULT 14
 A64477
 L-fucose-phosphate aldolase homolog - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
 C:Accession: A64477
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 ; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weissbrock, K.G.; Merrick, J.M.; Glodek, A.;
 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Frazer, C.M.; Smith, H.O.; Woese, C
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A:Reference number: A64300; MUID:96337999

A:Accession: A64477
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-181 <BU>
 A:Cross-references: GB:067582; GB:L77117; NID:g1592064; PIDN:AA899428.1; PID:g159206
 C:Genetics:
 A:Map position: FOR138152-1381697
 C:Superfamily: L-ribulose-phosphate 4-epimerase

Query Match 66.7%; Score 38; DB 1; Length 181;
 Best Local Similarity 70.0%; Pred. No. 32;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 FLSELNKELE 10
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 Db 95 FLSELNKEIE 104

RESULT 15
 T03355
 gene e12 protein - Lactococcus phage bL170
 C:Species: Lactococcus phage bL170
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 04-Mar-2000
 C:Accession: T03355
 R:Crutz-Le Cog, A.M.; Cesselin, B.; Commissaire, J.; Anba, J.; Kyriakidis, S.; Chopi
 submitted to the EMBL Data Library, June 1997
 A:Description: Sequence and organization of the lactococcal isometric bL170 phage g
 A:Reference number: Z14903
 A:Accession: T03355
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-211 <CRU>
 A:Cross-references: EMBL:AF009630; NID:g3282260; PIDN:AA027226.1; PID:g3282307
 C:Genetics:
 A:Gene: e12
 C:Superfamily: Lactococcus phage bL170 gene e12 protein

Query Match 66.7%; Score 38; DB 2; Length 211;
 Best Local Similarity 81.8%; Pred. No. 37;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 LSELNKELEAE 12
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 Db 151 LSEQKELEAE 161

Search completed: September 11, 2002, 09:00:14
 Job time: 232 sec

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GenCore version 4.5
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OW protein - protein search, using sw model

Run on: September 11, 2002, 08:59:25 : Search time 30.68 Seconds
(without alignments)
9.554 Million cell updates/sec

Title: US-09-884-696-6

Sequence: 1 FLSELNKLEAE 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	75.4	924	3	US-08-619-812-8
2	43	75.4	926	1	US-07-908-253-2
3	43	75.4	926	1	US-08-455-970A-2
4	43	75.4	926	1	US-08-387-156-6
5	43	75.4	926	2	US-08-694-865-6
6	43	75.4	926	2	US-08-878-748-6
7	43	75.4	926	2	US-08-535-837-2
8	43	75.4	926	3	US-09-124-491-6
9	43	75.4	926	6	5476657-3
10	43	75.4	936	1	US-08-455-970A-12
11	43	75.4	943	1	US-08-455-970A-10
12	43	75.4	951	1	US-08-455-970A-14
13	43	75.4	956	3	US-08-772-370A-8
14	43	75.4	977	1	US-08-387-156-8
15	43	75.4	977	2	US-08-694-865-8
16	43	75.4	977	2	US-08-878-748-8
17	43	75.4	977	3	US-09-124-491-8
18	43	75.4	1069	1	US-07-777-715-9
19	43	75.4	1069	1	US-08-170-126-4
20	43	75.4	1069	3	US-08-954-418-4
21	43	75.4	1098	1	US-07-777-715-7
22	43	75.4	1098	1	US-08-170-126-2
23	43	75.4	1098	3	US-08-954-418-2
24	39	68.4	934	1	US-08-215-805A-80
25	37	64.9	30	4	US-09-623-618B-21
26	37	64.9	31	4	US-09-623-618B-20
27	37	64.9	2763	3	US-08-496-944-2

28	35	61.4	229	4	US-09-045-973-7	Sequence 7, Appl
29	35	61.4	1866	4	US-08-938-105-3	Sequence 3, Appl
30	35	61.4	1939	4	US-09-310-187A-1	Sequence 1, Appl
31	34	59.6	20	1	US-08-468-543-10	Sequence 10, Appl
32	34	59.6	20	2	US-08-469-692-10	Sequence 10, Appl
33	34	59.6	20	2	US-08-398-046-10	Sequence 8, Appl
34	34	59.6	22	1	US-07-928-930A-8	Sequence 8, Appl
35	34	59.6	22	1	US-08-288-568-8	Sequence 8, Appl
36	34	59.6	22	1	US-08-487-461-8	Sequence 8, Appl
37	34	59.6	22	1	US-08-432-691-8	Sequence 8, Appl
38	34	59.6	22	1	US-08-487-459-8	Sequence 8, Appl
39	34	59.6	22	3	US-08-940-095-75	Sequence 75, Appl
40	34	59.6	22	3	US-08-940-095-106	Sequence 106, Appl
41	34	59.6	22	3	US-08-940-095-119	Sequence 119, Appl
42	34	59.6	22	3	US-08-940-095-121	Sequence 121, Appl
43	34	59.6	22	3	US-08-940-093-75	Sequence 75, Appl
44	34	59.6	22	3	US-08-940-093-106	Sequence 106, Appl
45	34	59.6	22	3	US-08-940-093-119	Sequence 119, Appl

ALIGNMENTS

RESULT 1
US-08-619-812-8
: Sequence 8, Application US/08619812
: Patent No. 6100066
: GENERAL INFORMATION:
: APPLICANT: POTTER, ANDREW A.
: APPLICANT: THEISEN, MICHAEL
: APPLICANT: HARLAND, RICHARD J.
: APPLICANT: RHOX, CLEMENT R.
: TITLE OF INVENTION: VACCINES FOR HAEMOPHILUS SOMNUS
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: REED & ROBINS
: STREET: 635 BRYANT STREET
: CITY: PALO ALTO
: STATE: CALIFORNIA
: COUNTRY: UNITED STATES OF AMERICA
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/619,812
: FILING DATE: 15-MAR-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/038,719
: FILING DATE: 29-MAR-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: ROBINS, ROBERTA L.
: REGISTRATION NUMBER: 33,208
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 617-8999
: TELEFAX: (415) 327-9231
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 924 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-619-812-8

Query Match. 75.4% Score 43; DB 3; Length 924;
Best Local Similarity 75.0% Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
DB 424 FLNLNKELEAE 435

RESULT 2

US-07-908-253-2
Sequence 2, Application US/07908253
Patent No. 5534256
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: HARLAND, RICHARD J.
TITLE OF INVENTION: HAEMOPHILUS SOMNUS OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L. ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/908,253
FILING DATE: 19920702
CLASSIFICATION: 420
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000-0026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-908-253-2

Query Match 75.4%; Score 43; DB 1; Length 926;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
DB 424 FLNLNKELEAE 435

RESULT 3

US-08-455-970A-2
Sequence 2, Application US/08455970A
Patent No. 5708155
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HOW P.A.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
TITLE OF INVENTION: CHIMERAS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,970A

FILING DATE: 31-MAY-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/960,932

FILING DATE: 14-OCT-1992

ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 9001-0016.10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 327-3400

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 926 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-455-970A-2

Query Match 75.4%; Score 43; DB 1; Length 926;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
DB 424 FLNLNKELEAE 435

RESULT 4

US-08-387-156-6
Sequence 6, Application US/08387156
Patent No. 5723129
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HOW P.A.
TITLE OF INVENTION: GMRH-LEUKOTOXIN CHIMERAS
TITLE OF INVENTION: 28
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,156
FILING DATE: 10-FEB-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 9001-0016.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-387-156-6

Query Match 75.4%; Score 43; DB 1; Length 926;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
|| |||||:
Db 424 FLNLNKELEAE 435

RESULT 5
US-08-694-865-6
Sequence 6, Application US/08694865
Patent No. 5837268
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: MANNIS, JOHN G.
TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,865
FILING DATE: 09-AUG-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-694-865-6

Query Match 75.4%; Score 43; DB 2; Length 926;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
|| |||||:
Db 424 FLNLNKELEAE 435

RESULT 6

US-08-878-748-6
Sequence 6, Application US/08878748
Patent No. 5969126
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUI P. A.
TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,748

FILING DATE: 19-JUN-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171

FILING DATE: 16-OCT-1991

ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 9001-0016.21

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-878-748-6

Query Match 75.4%; Score 43; DB 2; Length 926;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
|| |||||:
Db 424 FLNLNKELEAE 435

RESULT 7
US-08-535-837-2
Sequence 2, Application US/08535837
Patent No. 5985289
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: HARLAND, RICHARD J.
TITLE OF INVENTION: HEMOPHILUS SOMNUS OUTER MEMBRANE
PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L. ROBINS
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CALIFORNIA

Query Match 75.4%; Score 43; DB 2; Length 926;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,837
FILING DATE: 27-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0026.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-535-837-2

Query Match 75.4%; Score 43; DB 2; Length 926;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
|| |||||:
Db 424 FLINLNKELEAE 435

RESULT 8
US-09-124-491-6
Sequence 6, Application US/09124491
Patent No. 6022960
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: MANN, JOHN G.
TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,491
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,865
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:

NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-124-491-6

Query Match 75.4%; Score 43; DB 3; Length 926;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
|| |||||:
Db 424 FLINLNKELEAE 435

RESULT 9
5476657-3
Patent No. 5476657
APPLICANT: POTTER, ANDREW A.
TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA LEUKOTOXIN
COMPOSITIONS AND USES THEREOF
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/15,537
FILING DATE: 09-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 504,850
FILING DATE: 05-APR-1990
APPLICATION NUMBER: 335,018
FILING DATE: 07-APR-1989
SEQ ID NO:3:
LENGTH: 926
5476657-3

Query Match 75.4%; Score 43; DB 6; Length 926;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLSELNKELEAE 12
|| |||||:
Db 424 FLINLNKELEAE 435

RESULT 10
US-08-455-970A-12
Sequence 12, Application US/08455970A
Patent No. 5708155
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,970A
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,932
; FILING DATE: 14-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9001-0016.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-3400
; TELEFAX: (415) 327-3231
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 936 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-455-970A-12

Query Match          75.4%; Score 43; DB 1; Length 936;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      1 FLSELNKELEAE 12
        || |||||:|
Db      424 FLNLNKELEAE 435

RESULT 11
; US-08-455-970A-10
; Sequence 10, Application US/08455970A
; Patent No. 5708155
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: REDMOND, MARK J.
; APPLICANT: HUGHES, HUM P.A.
; TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
; TITLE OF INVENTION: CHIMERAS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 285 HAMILTON AVENUE, SUITE 200
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,970A
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,932
; FILING DATE: 14-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9001-0016.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-3400
; TELEFAX: (415) 327-3231
;
; INFORMATION FOR SEQ ID NO: 10:
; INFORMATION FOR SEQ ID NO: 10:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 943 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; US-08-455-970A-10

Query Match          75.4%; Score 43; DB 1; Length 943;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      1 FLSELNKELEAE 12
        || |||||:|
Db      424 FLNLNKELEAE 435

RESULT 12
; US-08-455-970A-14
; Sequence 14, Application US/08455970A
; Patent No. 5708155
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: REDMOND, MARK J.
; APPLICANT: HUGHES, HUM P.A.
; TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
; TITLE OF INVENTION: CHIMERAS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 285 HAMILTON AVENUE, SUITE 200
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,970A
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,932
; FILING DATE: 14-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9001-0016.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-3400
; TELEFAX: (415) 327-3231
;
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 951 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-455-970A-14

Query Match          75.4%; Score 43; DB 1; Length 951;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      1 FLSELNKELEAE 12
        || |||||:|
Db      424 FLNLNKELEAE 435

RESULT 13
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US-08-772-270A-8
; Sequence 8, Application US/08772270A
; Patent No. 6019984
; GENERAL INFORMATION:
; APPLICANT: MacInnes, Janet
; APPLICANT: Ricciatti, Paul
; APPLICANT: Mallard, Bonnie
; APPLICANT: Rosendal, Soren
; TITLE OF INVENTION: NOVEL BACTERIAL PREPARATIONS, METHOD FOR
; TITLE OF INVENTION: PRODUCING SAME, AND THEIR USE AS VACCINES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bereskin & Parr
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,270A
; FILING DATE: December 23, 1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gravelle, Micheline
; REGISTRATION NUMBER: 40,261
; REFERENCE/DOCKET NUMBER: 6580-81
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 956 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Actinobacillus pleuropneumoniae
; US-08-772-270A-8

Query Match 75.4%; Score 43; DB 3; Length 956;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
|| |||||:||
Db 455 FLINLNKELEAE 466

RESULT 14
US-08-387-156-8
; Sequence 8, Application US/08387156
; Patent No. 5723129
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: REDMOND, MARK J.
; APPLICANT: HUGHES, HOW P.A.
; TITLE OF INVENTION: GnRH-LEUKOTOXIN CHIMERAS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 635 BRYANT STREET
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,156
FILING DATE: 10-FEB-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 977 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-387-156-8

Query Match 75.4%; Score 43; DB 1; Length 977;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
|| |||||:||
Db 424 FLINLNKELEAE 435

RESULT 15
US-08-694-865-8
; Sequence 8, Application US/08694865
; Patent No. 5837268
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: MANN, JOHN G.
; TITLE OF INVENTION: GnRH-LEUKOTOXIN CHIMERAS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS LLP
; STREET: 265 HAMILTON AVENUE, SUITE 200
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/694,865
; FILING DATE: 09-AUG-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 9001-0016.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)327-3231
; TELEFAX: (415)327-3231
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 977 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-694-865-8

Query Match 75.4%; Score 43; DB 2; Length 977;
 Best Local Similarity 75.0%; Pred. NO. 16;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FISELNKELEAE 12
 || |||||:
 DB 424 FLINLNKELEQAE 435

Search completed: September 11, 2002, 08:59:26
 Job time: 209 sec

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DE LEUKOTOXIN.
 GN I.K.T.A.
 OS Actinobacillus actinomycetemcomitans (Haemophilus
 actinomycetemcomitans).
 OC Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Actinobacillus.
 OX NCBI_TaxID=714;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JP2;
 RA Kolodrubetz J., Dailey T., Kraig E.;
 RT "Nucleotide sequence of the leukotoxin gene from actino-bacillus
 actinomycetemcomitans: Homology to the A-hemolysin/leukotoxin gene
 family.";
 RL Infect. Immun. 58:920-929(1991).
 DR EMBL: X16829; CAA34731.1; -;
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003995; RTX_A.
 DR InterPro: IPR003355; RTX_N.
 DR InterPro: IPR001441; OIP_synth.
 DR Pfam: PF00353; hemolysincabind; 3.
 DR Pfam: PF02382; RTX_1.
 DR PRINTS: PRO0313; CABNDNGRPT.
 DR PRINTS: PRO1488; RTXTOXIN.
 DR PROSITE: PS00330; HEMOLYSIN_CALCITUM; 3
 SQ SEQUENCE 1055 AA; 113853 MW; 531C396FA76669E CRC64;

Query Match 76.6%; Score 59; DB 2; Length 1055;
 Best Local Similarity 64.3%; Pred. No. 0.13;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FNDIFHSGEGDDL 14
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 Db 734 FNDVFGHGDGDL 747

RESULT 3
 Q9RCG8 PRELIMINARY; PRT; 1049 AA.
 AC Q9RCG8;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE PAXA.
 GN PAXA.
 OS Pasteurella aerogenes.
 OC Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Pasteurella.
 OX NCBI_TaxID=749;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FIELD STRAIN JF1319;
 RA Heyberger-Meyer B., Frey J., Nicolet J., Kuhnert P.;
 RT "Identification and characterization of a new RTX toxin operon (pax)
 in Pasteurella aerogenes.";
 RL Submitted (JUG-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U66588; AAF15370.1; -;
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003995; RTX_A.
 DR InterPro: IPR003355; RTX_N.
 DR Pfam: PF00353; hemolysincabind; 2.
 DR Pfam: PF02382; RTX_1.
 DR PRINTS: PRO0313; CABNDNGRPT.
 DR PRINTS: PRO1488; RTXTOXIN.
 DR PROSITE: PS00330; HEMOLYSIN_CALCITUM; 2
 SQ SEQUENCE 1049 AA; 112308 MW; 9FA5070EA8CC3127 CRC64;

Query Match 75.3%; Score 58; DB 2; Length 1049;
 Best Local Similarity 71.4%; Pred. No. 0.19;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGEGDDL 14
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 Db 748 FRDIFHGADGDDL 761

RESULT 4
 Q93NPO PRELIMINARY; PRT; 1052 AA.
 AC Q93NPO;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE RTX-TOXIN IIIA.
 OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
 OC Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Actinobacillus.
 OX NCBI_TaxID=715;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shin S.J., Park J.Y., Choi I.S., Shin N.R., Yoo H.S.;
 RT "Cloning and Sequencing of Apx IIIA from Actinobacillus
 pleuropneumoniae.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF363363; AAK50053.1; -;
 SQ SEQUENCE 1052 AA; 112862 MW; CA0E160F02101FA2 CRC64;

Query Match 75.3%; Score 58; DB 2; Length 1052;
 Best Local Similarity 71.4%; Pred. No. 0.19;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGEGDDL 14
 ||||| :||||
 Db 748 FRDIFHGADGDDL 761

RESULT 5
 Q46716 PRELIMINARY; PRT; 998 AA.
 AC Q46716;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE HEMOLYSIN A (HLXA).
 GN HLXA OR EHEC-HLXA.
 OS Escherichia coli O157:H7.
 OG Plasmid pO157.
 OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98290540; PubMed=9628576;
 RA Makino K., Ishii K., Yasunaga T., Hattori M., Yokoyama K.,
 RA Yatsudo H.C., Kubota Y., Yamachi Y., Iida T., Yamamoto K., Honda T.,
 RA Han C., Ohtsubo A., Kasamatsu M., Hayashi T., Kuwara S., Shinagawa H.;
 RT "Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an
 enterohemorrhagic Escherichia coli O157:H7 derived from Sakai
 outbreak.";
 RL DNA Res. 5:1-9(1998).
 RN [2]
 RP SEQUENCE OF 241-998 FROM N.A.
 RC STRAIN=EHEC;
 RA Hall R.H., Xu J., Walderhaug M.O.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EDL933;
 RX MEDLINE=98391744; PubMed=9722640;
 RA Burland V., Shao Y., Perna N.T., Plunkett G., Sofia H.J.,
 RA Blattner F.R.;
 RT "The complete DNA sequence and analysis of the large virulence plasmid
 of Escherichia coli O157:H7.";

RL Nucleic Acids Res. 26:4196-4204(1998).
 DR EMBL: AB011549; BAA31774.1; -
 DR EMBL: U12572; AAA20544.1; -
 DR EMBL: AF074613; AAC70116.1; -
 DR InterPro: IPR001343; HemIysn_Ca_bind.
 DR InterPro: IPR003995; RTX_A.
 DR InterPro: IPR003355; RTX_N.
 DR Pfam: PF00353; hemolysinCbind; 2.
 DR Pfam: PF02382; RTX; 1.
 DR PRINTS: PR00313; CABNDNGRPT.
 DR PRINTS: PR01488; RTXTOXINA.
 DR PROSITE: PS00330; HEMOLYSIN_CALCITUM; 2.
 KW Plasmid.
 SQ SEQUENCE 998 AA; 107047 MW; BB3CD36FCBB9EBD CRC64;

Query Match 67.5%; Score 52; DB 2; Length 998;
 Best Local Similarity 57.1%; Pred. No. 2;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 FNDIFHSGEDDL 14
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 Db 720 FNDIFHGADGNDYI 733

RESULT 6
 ID 09LC58 PRELIMINARY; PRT; 998 AA.
 AC 09LC58;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE HEMOLYSIN A.
 GN EHEC-HLYA.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tanelike I., Wakisaka-Saito N., Harada Y., Zhang H.-M., Yamamoto T.;
 RT "The enterohemorrhagic Escherichia coli (EHEC)-hemolysin genes of a
 RT Shiga toxin 1 (Stx1)- and Stx2-producing, serotype O128 Escherichia
 RT coli strain with a greatest hemolytic activity.";
 RL Acta Med. Biol. (Mligata) 0:0-0(2000).
 DR EMBL: AB032930; BAA93708.1; -
 DR InterPro: IPR001343; HemIysn_Ca_bind.
 DR InterPro: IPR003355; RTX_N.
 DR Pfam: PF00353; hemolysinCbind; 2.
 DR Pfam: PF02382; RTX; 1.
 DR PRINTS: PR00313; CABNDNGRPT.
 DR PROSITE: PS00330; HEMOLYSIN_CALCITUM; 2.
 SQ SEQUENCE 998 AA; 107196 MW; CD7A88E9BD862DB6 CRC64;

Query Match 67.5%; Score 52; DB 2; Length 998;
 Best Local Similarity 57.1%; Pred. No. 2;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 FNDIFHSGEDDL 14
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 Db 720 FNDIFHGADGNDYI 733

RESULT 7
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 AC 085101;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HEMOLYSIN.
 GN EHEC-HLYA.

OS Escherichia coli.
 OG Plasmid EHEC-hemolysin plasmid.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ENTEROHEMORRHAGIC EC920006;
 RX MEDLINE=98261495; PubMed=9596716;
 RA Boerlin P., Chen S., Colbourne J.K., Johnson R., De Grandis S.,
 RA Gyles C.;
 RT "Evolution of enterohemorrhagic escherichia coli hemolysin plasmids
 RT and the locus for enterocyte effacement in Shiga toxin-producing E.
 RT coli.";
 RL Infect. Immun. 66:2553-2561(1998).
 DR EMBL: AF043471; AAC24352.1; -
 DR InterPro: IPR001343; HemIysn_Ca_bind.
 DR InterPro: IPR003995; RTX_A.
 DR InterPro: IPR003355; RTX_N.
 DR Pfam: PF00353; hemolysinCbind; 2.
 DR Pfam: PF02382; RTX; 1.
 DR PRINTS: PR00313; CABNDNGRPT.
 DR PRINTS: PR01488; RTXTOXINA.
 DR PROSITE: PS00330; HEMOLYSIN_CALCITUM; 2.
 KW Plasmid.
 SQ SEQUENCE 998 AA; 107095 MW; E5A56B239DCBE55 CRC64;

Query Match 67.5%; Score 52; DB 2; Length 998;
 Best Local Similarity 57.1%; Pred. No. 2;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 FNDIFHSGEDDL 14
 ||||| :|:| :
 Db 720 FNDIFHGADGNDYI 733

RESULT 8
 ID 047262 PRELIMINARY; PRT; 998 AA.
 AC 047262;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HEMOLYSIN.
 GN EHEC-HLYA.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95172699; PubMed=7868227;
 RA Schmidt H., Beutin L., Karch H.;
 RT "Molecular analysis of the plasmid-encoded hemolysin of Escherichia
 RT coli O157:H7 strain Ed1933.";
 RL Infect. Immun. 63:1055-1061(1995).
 DR EMBL: X79839; CAA56234.1; -
 DR InterPro: IPR001343; HemIysn_Ca_bind.
 DR InterPro: IPR003995; RTX_A.
 DR InterPro: IPR003355; RTX_N.
 DR Pfam: PF00353; hemolysinCbind; 2.
 DR Pfam: PF02382; RTX; 1.
 DR PRINTS: PR00313; CABNDNGRPT.
 DR PRINTS: PR01488; RTXTOXINA.
 DR PROSITE: PS00330; HEMOLYSIN_CALCITUM; 2.
 SQ SEQUENCE 998 AA; 107058 MW; OD3BE108C309B8B3 CRC64;

Query Match 67.5%; Score 52; DB 2; Length 998;
 Best Local Similarity 57.1%; Pred. No. 2;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY      1  FNDIFHSGEGDDL 14
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Db      720 FNDIFHGADGNDYI 733

RESULT  9
ID      047461      PRELIMINARY;      PRT;      998 AA.
AC      047461;
DT      01-NOV-1996 (TREMBlrel. 01, Created)
DT      01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT      01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE      EHEC-HLYA PROTEIN.
GN      EHEC-HLYA.
OS      Escherichia coli.
OG      Plasmid p0157.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX      Escherichia.
NCBI_TaxID=562;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-EDL 933;
RX      MEDLINE=95172699; PubMed=7868227;
RA      Schmidt H., Beutin L., Karch H.;
RT      "Molecular analysis of the plasmid-encoded hemolysin of Escherichia
RT      coli 0157:H7 strain Edl933."
RL      Infect. Immun. 63:1055-1061(1995).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN-EDL 933;
RX      MEDLINE=97090409; PubMed=8936317;
RA      Schmidt H., Kernbach C., Karch H.;
RT      "Analysis of the EHEC hly operon and its location in the physical map
RT      of the large plasmid of enterohemorrhagic Escherichia coli 0157:H7."
RL      Microbiology 142:907-914(1996).
DR      EMBL; X86087; CA60042.1; -
DR      InterPro: IPR001343; Hemlysn_Ca_bind.
DR      InterPro: IPR003995; RTX.N.
DR      InterPro: IPR003355; RTX.N.
DR      Pfam; PF00353; hemolysincbind; 2.
DR      Pfam; PF02382; RTX; 1.
DR      PRINTS; PR00313; CABNDNGRPT.
DR      PRINTS; PR01488; RTXTOXINA.
DR      PROSITE; PS00330; HEMOLYSIN_CALCITUM; 2.
KW      Plasmid
SQ      SEQUENCE 998 AA; 107032 MW; 4D8BE108C309BF7E CRC64;

Query Match      67.5%; Score 52; DB 2; Length 998;
Best Local Similarity 57.1%; Pred. No. 2;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1  FNDIFHSGEGDDL 14
      11111 :1:1 :
Db      720 FNDIFHGADGNDYI 733

RESULT 10
ID      P71223      PRELIMINARY;      PRT;      998 AA.
AC      P71223;
DT      01-FEB-1997 (TREMBlrel. 02, Created)
DT      01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT      01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE      EHEC-HEMOLYSIN.
GN      EHEC-HLYA.
OS      Escherichia coli.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX      Escherichia.
NCBI_TaxID=562;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=78-92;

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RX      MEDLINE=97034824; PubMed=8880480;
RA      Schmidt H., Karch H.;
RT      "Enterohemolytic phenotypes and genotypes of Shiga Toxin-producing
RT      Escherichia coli O111 strain from patients with diarrhea and hemolytic-
RT      uremic syndrome."
RL      J. Clin. Microbiol. 34:2364-2367(1996).
DR      EMBL; X94129; CA63849.1; -
DR      InterPro: IPR001343; Hemlysn_Ca_bind.
DR      InterPro: IPR003995; RTX.N.
DR      InterPro: IPR003355; RTX.N.
DR      Pfam; PF00353; hemolysincbind; 2.
DR      Pfam; PF02382; RTX; 1.
DR      PRINTS; PR00313; CABNDNGRPT.
DR      PRINTS; PR01488; RTXTOXINA.
DR      PROSITE; PS00330; HEMOLYSIN_CALCITUM; 2.
SQ      SEQUENCE 998 AA; 107255 MW; DA3EF078C7E4131E CRC64;

Query Match      67.5%; Score 52; DB 2; Length 998;
Best Local Similarity 57.1%; Pred. No. 2;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1  FNDIFHSGEGDDL 14
      11111 :1:1 :
Db      720 FNDIFHGADGNDYI 733

RESULT 11
ID      092UA7      PRELIMINARY;      PRT;      387 AA.
AC      092UA7;
DT      01-DEC-2001 (TREMBlrel. 19, Created)
DT      01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT      01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE      HYPOTHELICAL CALCIUM BINDING PROTEIN SMB21402.
GN      SMB21402.
OS      Rhizobium meliloti (Sinorhizobium meliloti).
OC      Plasmid pSymb (megaplasmid 2).
OC      Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC      Rhizobiaceae; Sinorhizobium.
OX      NCBI_TaxID=382;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=1021;
RX      MEDLINE=21396508; PubMed=11481431;
RA      Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Gouzy J.,
RA      Vorhölter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
RA      Golding B., Puehler A.;
RT      "The complete sequence of the 1.683-kb PSYMB megaplasmid from the N2-
RT      fixing endosymbiont Sinorhizobium meliloti."
RL      Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
DR      EMBL; AL603646; CAC49629.1; -
KW      Plasmid; Hypothetical protein; Complete proteome.
SQ      SEQUENCE 387 AA; 39149 MW; 759202216369F18E CRC64;

Query Match      64.9%; Score 50; DB 16; Length 387;
Best Local Similarity 69.2%; Pred. No. 1.6;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2  NDFIFHSGEGDDL 14
      1111 11111 :1:1 :
Db      81 NDFIFGEGGNDVL 93

RESULT 12
ID      051868      PRELIMINARY;      PRT;      208 AA.
AC      051868; 051866;
DT      01-NOV-1996 (TREMBlrel. 01, Created)
DT      01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT      01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE      LEUKOTOXIN A (FRAGMENT).

```

OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-T4 SEROTYPE AND T15 SEROTYPE;
RA Lalson A.F., Atchison K.D., Donachie W.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; 222885; CAA80499.1; -.
DR EMBL; 222886; CAA80500.1; -.
DR HSSP; Q03023; 1AKL.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR Pfam: PF00353; hemolysincabind; 1.
DR PRINTS; PR00313; CABNDNGRPT.
DR PROSITE; PS00330; HEMOLYSIN_CALCITUM; 1.
FT NON_TER 1 1
SQ SEQUENCE 208 AA; 22803 MW; 25301410C85AACCS CRC64;

Query Match 63.6%; Score 49; DB 2; Length 208;
Best Local Similarity 58.3%; Pred. No. 1.1;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDIHSGEGDDL 13
DB 29 NDLHGKGGDDI 40

RESULT 13
051865 PRELIMINARY; PRT; 233 AA.
AC 051865; 051867; 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE LEUKOTOXIN A (FRAGMENT).
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-T10 SEROTYPE AND T3 SEROTYPE;
RA Lalson A.F., Atchison K.D., Donachie W.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; 222887; CAA80501.1; -.
DR EMBL; 222884; CAA80498.1; -.
DR HSSP; Q03023; 1KAP.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR Pfam: PF00353; hemolysincabind; 1.
DR PRINTS; PR00313; CABNDNGRPT.
DR PROSITE; PS00330; HEMOLYSIN_CALCITUM; 2.
FT NON_TER 1 1
SQ SEQUENCE 233 AA; 25345 MW; AD6C8408731C3F99 CRC64;

Query Match 63.6%; Score 49; DB 2; Length 233;
Best Local Similarity 58.3%; Pred. No. 1.3;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDIHSGEGDDL 13
DB 54 NDLHGKGGDDI 65

RESULT 14
09EV24

AC 09EV24; PRELIMINARY; PRT; 946 AA.
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)

DE LEUKOTOXIN.
GN LKTA.
OS Mannheimia glucosida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=85401;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PH574;
RA MEDLINE-21101823; PubMed-1157953;
RX Davies R.L., Whittam T.S., Selander R.K.;
RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
RT haemolytica";
RL J. Bacteriol. 183:1394-1404(2001).
DR EMBL; AF314521; AAG40305.1; -.
DR InterPro: IPR001753; Enoyl_COA_hydratse.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PF00353; hemolysincabind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS; PR00313; CABNDNGRPT.
DR PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 946 AA; 101480 MW; 25C07785BBD76C4 CRC64;

Query Match 63.6%; Score 49; DB 2; Length 946;
Best Local Similarity 58.3%; Pred. No. 6.4;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDIHSGEGDDL 13
DB 767 NDLHGKGGDDI 778

RESULT 15
09ETX2 PRELIMINARY; PRT; 953 AA.
AC 09ETX2; 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE LEUKOTOXIN.
GN LKTA.
OS Mannheimia glucosida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=85401;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PH498, AND PH344;
RA Davies R.L., Whittam T.S., Selander R.K.;
RT "Sequence diversity and molecular evolution of the leukotoxin (Lkta)
RT gene in bovine and ovine strains of Mannheimia (Pasteurella)
RT haemolytica";
RL J. Bacteriol. 0:0-0(2001).
DR EMBL; AF314518; AAG40302.1; -.
DR EMBL; AF314517; AAG40301.1; -.
DR InterPro: IPR001753; Enoyl_COA_hydratse.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PF00353; hemolysincabind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS; PR00313; CABNDNGRPT.
DR PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 102135 MW; 70DB354157F5881E CRC64;

Query Match 63.6%; Score 49; DB 2; Length 953;
Best Local Similarity 58.3%; Pred. No. 6.5;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDIHSGEGDDL 13

Mon Sep 16 16:43:31 2002

Db 774 NDLLHGKGDPI 785

Search completed: September 11, 2002, 09:01:27
Job time: 285 sec

DR PRINTS; PR01488; RTXTOXINA.
 DR PROSITE; PS00330; HEMOLYSIN_CALCIUM; 5.
 KW Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
 KW Transmembrane; Lipoprotein; Palmitate.
 FT TRANSMEM 339
 FT TRANSMEM 408
 FT TRANSMEM 477
 FT DOMAIN 722
 FT REPEAT 722
 FT REPEAT 731
 FT REPEAT 740
 FT REPEAT 749
 FT REPEAT 758
 FT REPEAT 767
 FT REPEAT 776
 FT REPEAT 785
 FT REPEAT 794
 FT REPEAT 803
 FT REPEAT 812
 FT REPEAT 821
 FT REPEAT 830
 FT REPEAT 839
 SQ SEQUENCE 1050 AA; 114194 MW; 38DF9AA24649F662 CRC64;

Query Match 76.6%; Score 59; DB 1; Length 1050;
 Best Local Similarity 64.3%; Pred. No. 0.032; Mismatches 2; Indels 0; Gaps 0;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 OY 1 FNDIFHSGEGDDL 14
 Db 734 FNDVPHGHDGDLI 747

RESULT 2
 RT31_ACTPL STANDARD; PRT; 1049 AA.
 AC P55130;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE RTX-III toxin determinant A from serotype 2 (APX-IIIA) (Cytolysin
 DE IIA) (CLY-IIIA).
 GN APXIIIA OR CIIYIIA OR RTXA OR PTXA.
 OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
 CC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 CC Actinobacillus.
 OX NCBI_TaxID=715;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SEROTYPE 2;
 RX MEDLINE=93263992; PubMed=8494611;
 RA Chang Y.-F., Shi J., Ma D.-P., Shin S.J., Lein D.H.;
 RT "Molecular analysis of the Actinobacillus pleuropneumoniae RTX
 RT toxin-III gene cluster.";
 RL DNA Cell Biol. 12:351-362(1993).
 RN [2]
 RP SEQUENCE OF 828-1049 FROM N.A.
 RC STRAIN=1536 / SEROTYPE 2;
 RX MEDLINE=95012630; PubMed=7927703;
 RA Jansen R., Briatne J., van Geel A.B.M., Kamp E.M., Gielkens A.L.J.,
 RA Smits M.A.;
 RT "Genetic map of the Actinobacillus pleuropneumoniae RTX-toxin (ApX)
 RT operons: characterization of the ApXIII operons.";
 RL Infect. Immun. 62:4411-4418(1994).
 CC -1- FUNCTION: DOES NOT HAVE HEMOLYTIC ACTIVITY BUT SHOWS A STRONG
 CC CYTOTOXICITY TOWARDS ALVEOLAR MACROPHAGES AND NEUTROPHILS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
 CC ACTIVITY (BY SIMILARITY).
 CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
 CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).

CC -1- PTM: PALMITOYLATED BY APXIIIC. THE TOXIN ONLY BECOMES ACTIVE WHEN
 CC MODIFIED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: I12145; AAA21924.1; -
 DR EMBL: X80056; CAB37652.1; ALT_SEQ.
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003355; RTX_N.
 DR InterPro: IPR003995; RTX_A.
 DR Pfam: PF00353; hemolysinCbind; 2.
 DR Pfam: PF02382; RTX; 1.
 DR PRINTS: PR00313; CABDNGRPT.
 DR PRINTS: PR01488; RTXTOXINA.
 DR PROSITE: PS00330; HEMOLYSIN_CALCIUM; 3.
 DR TOXIN; Cytolysis; Cytotoxin; Repeat; Calcium; Transmembrane;
 KW Lipoprotein; Palmitate.
 FT TRANSMEM 154
 FT TRANSMEM 170
 FT TRANSMEM 315
 FT TRANSMEM 397
 FT DOMAIN 753
 FT REPEAT 753
 FT REPEAT 762
 FT REPEAT 771
 FT REPEAT 776
 FT REPEAT 780
 FT REPEAT 789
 FT REPEAT 798
 FT REPEAT 807
 FT REPEAT 826
 FT REPEAT 835
 FT REPEAT 844
 FT REPEAT 853
 SQ SEQUENCE 1049 AA; 112491 MW; P99846BFD45CE72 CRC64;

Query Match 75.3%; Score 58; DB 1; Length 1049;
 Best Local Similarity 71.4%; Pred. No. 0.047;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 1 FNDIFHSGEGDDL 14
 Db 747 FNDIFHSGEGDDL 760

RESULT 3
 RT32_ACTPL STANDARD; PRT; 1052 AA.
 AC P55131;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE RTX-III toxin determinant A from serotype 8 (APX-IIIA) (Cytolysin
 DE IIA) (CLY-IIIA).
 GN APXIIIA OR CIIYIIA OR RTXA OR PTXA.
 OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
 CC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 CC Actinobacillus.
 OX NCBI_TaxID=715;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=405 / SEROTYPE 8;
 RX MEDLINE=95012630; PubMed=7927703;
 RA Jansen R., Briatne J., van Geel A.B.M., Kamp E.M., Gielkens A.L.J.,
 RA Smits M.A.;
 RT "Genetic map of the Actinobacillus pleuropneumoniae RTX-toxin (ApX)
 RT operons: characterization of the ApXIII operons.";

RL Infect. Immun. 62:4411-4418(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SEROTYPE 8;
 RX MEDLINE-93162836; PubMed-8432615;
 RA Jansen R., Briatore J., Kamp E.M., Gielkens A.L.J., Smits M.A.;
 RT "Cloning and characterization of the Actinobacillus
 RT pleuropneumoniae-RTX-toxin III (ApxIII) gene.";
 RL Infect Immun. 61:947-954(1993).
 CC -1- FUNCTION: DOES NOT HAVE HEMOLYTIC ACTIVITY BUT SHOWS A STRONG
 CC CYTOTOXICITY TOWARDS ALVEOLAR MACROPHAGES AND NEUTROPHILS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
 CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
 CC ACTIVITY (BY SIMILARITY).
 CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
 CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
 CC -1- PTM: PALMITOYLATED BY APMYC. THE TOXIN ONLY BECOMES ACTIVE WHEN
 CC MODIFIED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X80055; CAA56358.1; -
 CC DR EMBL: X68815; CAA48711.1; -
 CC DR InterPro: IPR001343; Hemlysn_Ca_bind.
 CC DR InterPro: IPR003355; RTX_N.
 CC DR InterPro: IPR003395; RTX_N.
 CC DR Pfam: PF00353; hemolysinCbind; 2.
 CC DR Pfam: PF02382; RTX; 1.
 CC DR PRINTS: PR00313; CABDNCRPT.
 CC DR PRINTS: PR01488; RTXTOXINA.
 CC DR PROSITE: PS00330; HEMOLYSIN_CALCIUM; 3.
 CC KW Toxin; Cytolysis; Cytotoxin; Repeat; Calcium; Transmembrane;
 CC Lipoprotein; Palmitate.
 CC KW Lipoprotein; Palmitate.
 CC FT TRANSMEM 248 265 POTENTIAL.
 CC FT TRANSMEM 275 334 POTENTIAL.
 CC FT TRANSMEM 372 418 POTENTIAL.
 CC FT DOMAIN 754 859 7 X REPEATS, GLY-RICH.
 CC FT REPEAT 754 759 1.
 CC FT REPEAT 763 768 2.
 CC FT REPEAT 772 777 3.
 CC FT REPEAT 781 786 4.
 CC FT REPEAT 790 795 5.
 CC FT REPEAT 799 804 6.
 CC FT REPEAT 808 813 7.
 CC FT REPEAT 827 832 8.
 CC FT REPEAT 841 846 9.
 CC FT REPEAT 845 850 10.
 CC FT REPEAT 854 859 11.
 CC SQ SEQUENCE 1052 AA; 112809 MW; F83AFEE25A6FD8758 CRC64;

Query Match 75.3%; Score 58; DB 1; Length 1052;
 Best Local Similarity 71.4%; Pred. No. 0.047;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

DT 01-JAN-1988 (Rel. 06, last sequence update)
 DT 01-MAR-2002 (Rel. 41, last annotation update)
 DE Hemolysin, plasmid.
 GN HLXA.
 OS Escherichia coli.
 OG Plasmid Inc12 pHLX152.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hess J., Wels W., Vogel M., Goebel W.;
 RT "Nucleotide sequence of a plasmid-encoded hemolysin determinant and
 RT its comparison with a corresponding chromosomal hemolysin sequence.";
 RL FEMS Microbiol. Lett. 34:1-11(1986).
 RN [2]
 RP PALMITOYLATION OF LYS-564 AND LYS-690.
 RX MEDLINE-95099325; PubMed-7801126;
 RA Stanley P., Packman L.C., Koronakis V., Hughes C.;
 RT "Fatty acylation of two internal lysine residues required for the
 RT toxic activity of Escherichia coli hemolysin.";
 RL Science 266:1992-1996(1994).
 RN [3]
 RP PALMITOYLATION OF LYS-564 AND LYS-690.
 RX MEDLINE-96404790; PubMed-8808931;
 RA Ludwig A., Garcia F., Bauer S., Jarchau T., Benz R., Hoppe J.,
 RA Goebel W.;
 RT "Analysis of the in vivo activation of hemolysin (HLXA) from
 RT Escherichia coli.";
 RL J. Bacteriol. 178:5422-5430(1996).
 CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
 CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
 CC DEFINED.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
 CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
 CC ACTIVITY.
 CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
 CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN.
 CC -1- PTM: PALMITOYLATED BY HLC. THE TOXIN ONLY BECOMES ACTIVE WHEN
 CC MODIFIED.
 CC -1- DISEASE: THE HEMOLYSIN OF E. COLI IS PRODUCED PREDOMINANTLY BY
 CC STRAINS CAUSING EXTRAINTestinal INFECTIONS, SUCH AS THOSE OF THE
 CC URINARY TRACT.
 CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
 CC -----
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 CC -----
 CC EMBL: M14107; AAA98233.1; -
 CC DR InterPro: IPR001343; Hemlysn_Ca_bind.
 CC DR InterPro: IPR003355; RTX_N.
 CC DR InterPro: IPR003395; RTX_N.
 CC DR Pfam: PF00353; hemolysinCbind; 2.
 CC DR Pfam: PF02382; RTX; 1.
 CC DR PRINTS: PR00313; CABDNCRPT.
 CC DR PRINTS: PR01488; RTXTOXINA.
 CC DR PROSITE: PS00330; HEMOLYSIN_CALCIUM; 4. Repeat; Calcium;
 CC KW Hemolysis; Toxin; Cytolysis; Cytotoxin; Palmitate; Plasmid;
 CC Transmembrane; Lipoprotein; Palmitate; Plasmid.
 CC KW Transmembrane; Lipoprotein; Palmitate; Plasmid.
 CC FT TRANSMEM 238 260 POTENTIAL.
 CC FT TRANSMEM 268 327 POTENTIAL.
 CC FT TRANSMEM 365 411 POTENTIAL.
 CC FT DOMAIN 724 870 16 X REPEATS, GLY-RICH.
 CC FT REPEAT 724 729 1.
 CC FT REPEAT 733 738 2.
 CC FT REPEAT 742 747 3.
 CC FT REPEAT 751 756 4.

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CC      -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC      -----
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CC      or send an email to license@isb.ch).
CC      -----
CC      EMBL; M20730; AAA25529.1; -.
CC      DR EMBL; M24197; AAA25543.1; -.
CC      DR PIR; S29516; S29516.
CC      DR HSSP; P02392; 1CTF.
CC      DR InterPro; IPR001343; Hemolysn_Ca_bind.
CC      DR InterPro; IPR003355; RTX_N.
CC      DR InterPro; IPR003995; RTX_A.
CC      DR Pfam; PF00353; hemolysincabind. 1.
CC      DR Pfam; PF02382; RTX_1.
CC      DR PRINTS; PR00313; CANNONGRPT.
CC      DR PRINTS; PR01488; RTXTOXINA.
CC      DR PROSITE; PS00330; HEMOLYSIN_CALCIIUM; 4.
CC      KW Hemolysis; Toxin; Cytolysis; Cytooxin; Repeat; Calcium;
CC      Transmembrane; Lipoprotein; Palmitate.
CC      FT TRANSMEM 229 349 POTENTIAL.
CC      FT TRANSMEM 297 318 POTENTIAL.
CC      FT TRANSMEM 366 390 POTENTIAL.
CC      FT DOMAIN 734 784 6 X REPEATS. GLY-RICH (BY SIMILARITY).
CC      FT REPEAT 734 739 1.
CC      FT REPEAT 743 748 2.
CC      FT REPEAT 752 757 3.
CC      FT REPEAT 761 766 4.
CC      FT REPEAT 770 775 5.
CC      FT REPEAT 779 784 6.
CC      FT REPEAT 799 814 FEHVAN -> LSTDOI (IN REF. 2).
CC      FT CONFLICT 409 414 D -> Y (IN REF. 2).
CC      FT CONFLICT 742 742
CC      SQ SEQUENCE 953 AA; 101996 MW; 7F93D113A118C05F CRC64;
CC      -----
CC      Query Match 63.6%; Score 49; DB 1; Length 953;
CC      Best Local Similarity 58.3%; Pred No. 14;
CC      Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0
CC      DB 774 NDHLHGKGDDI 785
CC      QY 2 NDHFSGEGDDL 13
CC      ||:|:|:|:|
CC      LKAB_PASHA STANDARD; PRT; 953 AA.
CC      ID LKAB_PASHA
CC      AC P55118;
CC      DT 01-OCT-1996 (Rel. 34, Created)
CC      DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC      DT 30-MAY-2000 (Rel. 39, Last annotation update)
CC      DE Leukotoxin from serotype A11.
CC      GN LKTA.
CC      OS Pasteurella haemolytica.
CC      OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
CC      OC Mannheimia.
CC      OX NCBI_TaxID=75985;
CC      RN (1)
CC      RP SEQUENCE FROM N.A.
CC      RC STRAIN-SEROTYPE A11;
CC      RX MEDLINE=94041617; PubMed=8225575;
CC      RA Burrows L.L., Olah-Wanfield E., Io R.Y.C.;
CC      RT "Molecular analysis of the leukotoxin determinants from Pasteurella
CC      haemolytica serotypes 1 to 16."
CC      RL Infect. Immun. 61:5001-5007(1993).
CC      -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CC      CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
CC      DEFINED.
CC      -1- SUBCELLULAR LOCATION: secreted.

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CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -1- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U01215; AAB36689.1; -
CC InterPro: IPR001343; HemLysn_Ca_bind.
CC InterPro: IPR003355; RTX_N.
CC InterPro: IPR003995; RtxA.
CC Pfam: PF00353; hemolysinCbind; 1.
CC Pfam: PF02382; RTX; 1.
CC PRINTS: PRO0313; CABNDNGRPT.
CC PRINTS: PRO1488; RTXTOXIN.
CC PROSITE: PS00330; HEMOLYSIN_CALCIUM; 4.
CC Hemolysins; Toxin; Cytolysis; Cytoleisin; Repeat; Calcium;
CC Transmembrane; Lipoprotein; Palmitate.
CC TRANSMEM 230 250
CC TRANSMEM 297 317 POTENTIAL.
CC TRANSMEM 381 401 POTENTIAL.
CC DOMAIN 734 784 6 X REPEATS, GLY-RICH.
CC REPEAT 734 739 1.
CC REPEAT 743 748 2.
CC REPEAT 752 757 3.
CC REPEAT 761 766 4.
CC REPEAT 770 775 5.
CC REPEAT 779 784 6.
CC SEQUENCE 953 AA; 102206 MW; 927FF56CFC84F12 CRC64;

Query Match 63.6%; Score 49; DB 1; Length 953;
Best Local Similarity 58.3%; Pred. No. 1.4;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHFSGEGDDL 13
Db 774 NDLLHGKGDID 785

RESULT 7
LKAA_PASHA STANDARD; PRT; 955 AA.
ID LKAA_PASHA
AC P5117;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Leukotoxin from serotype T10.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OC NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-SEROTYPE T10;
RX MEDLINE=96425875; Pubmed=8828217;
RA Lainsone F.A., Murray J., Davies R.C., Donachie W.;
RT "Characterization of epitopes involved in the neutralization of
RT Pasteurella haemolytica serotype A1 leukotoxin.";
RL Microbiology 142:2499-2507(1996).
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
```

```
CC DEFINED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -1- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Z26247; CAA81206.1; -
CC InterPro: IPR001343; HemLysn_Ca_bind.
CC InterPro: IPR003355; RTX_N.
CC InterPro: IPR003995; RtxA.
CC Pfam: PF00353; hemolysinCbind; 1.
CC Pfam: PF02382; RTX; 1.
CC PRINTS: PRO0313; CABNDNGRPT.
CC PRINTS: PRO1488; RTXTOXIN.
CC PROSITE: PS00330; HEMOLYSIN_CALCIUM; 4.
CC Hemolysins; Toxin; Cytolysis; Cytoleisin; Repeat; Calcium;
CC Transmembrane; Lipoprotein; Palmitate.
CC TRANSMEM 299 319 POTENTIAL.
CC TRANSMEM 361 381 POTENTIAL.
CC TRANSMEM 383 403 POTENTIAL.
CC DOMAIN 736 786 6 X REPEATS, GLY-RICH.
CC REPEAT 736 741 1.
CC REPEAT 745 750 2.
CC REPEAT 754 759 3.
CC REPEAT 763 768 4.
CC REPEAT 772 777 5.
CC REPEAT 781 786 6.
CC SEQUENCE 955 AA; 102187 MW; B60F2DB8168BCAF CRC64;

Query Match 63.6%; Score 49; DB 1; Length 955;
Best Local Similarity 58.3%; Pred. No. 1.4;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHFSGEGDDL 13
Db 776 NDLLHGKGDID 787

RESULT 8
RTLL_ACPPL STANDARD; PRT; 1023 AA.
ID RTLL_ACPPL
AC P5128;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE RTX-I toxin determinant A from serotypes 1/9 (APX-1A) (Hemolysin 1A)
DE (HLX-1A) (Cytolysin 1A) (CLY-1A).
GN APXIA OR CLYIA OR HLXIA.
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Actinobacillus.
OC NCBI_TaxID=715;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-S 4074 / SEROTYPE 1;
RX MEDLINE=91348845; Pubmed=1879928;
RA Frey J., Meier R., Gygi D., Nicolet J.;
RT "Nucleotide sequence of the hemolysin I gene from Actinobacillus
RT pleuropneumoniae.";
```

RL Infect. Immun. 59:3026-3032(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S 4074 / SEROTYPE 1;
 RX MEDLINE=94237497; PubMed=8181764;
 RA Frey J., Haidemann A., Nicolet J., Boffini A., Prentki P.;
 RT "Sequence analysis and transcription of the apxi operon (hemolysin 1)
 RL from *Actinobacillus pleuropneumoniae*.";
 RL Gene 142:97-102(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ISOLATE CVI 13261 / SEROTYPE 9;
 RX MEDLINE=93366425; PubMed=8359891;
 RA Jansen R., Briatore J., Kamp E.M., Gielkens A.L.J., Smits M.A.;
 RT "Structural analysis of the *Actinobacillus pleuropneumoniae*-RTX-toxin
 RL infect. Immun. 61:3688-3695(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S 4074 / SEROTYPE 1;
 RA Chang Y., Wang Y., Chin N.;
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ONE OF THE VIRULENCE FACTORS OF *A. PLEUROPNEUMONIAE*,
 CC WHICH HAS A STRONG HEMOLYTIC ACTIVITY AND IS CYTOTOXIC FOR
 CC ALVEOLAR MACROPHAGES AND NEUTROPHILS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
 CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
 CC ACTIVITY.
 CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
 CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
 CC -1- PTM: PALMITOYLATED BY APXIC. THE TOXIN ONLY BECOMES ACTIVE WHEN
 CC MODIFIED (BY SIMILARITY).
 CC -1- MISCELLANEOUS: APXIA IS PARTIALLY DELETED IN SEROTYPES 2, 4, 6, 7,
 CC 8, 12, AND TOTALLY DELETED IN SEROTYPE 3.
 CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
 CC -----
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 CC -----
 CC EMBL: X52899; CAA37081.1; -
 CC EMBL: X68595; CAA48586.1; -
 CC EMBL: X73117; CAA51348.1; -
 CC EMBL: U05042; AAB05034.1; -
 CC DR InterPro: IPR001343; Hemlysn_Ca_bind.
 CC DR InterPro: IPR003355; RTX_N.
 CC DR InterPro: IPR003995; RtxA.
 CC DR Pfam: PF00353; hemolysincabind; 2.
 CC DR Pfam: PF02382; RTX; 1.
 CC DR PRINTS: PR00313; CABNDNGRPT.
 CC DR PRINTS: PR01488; RTXTOXINA.
 CC DR PROSITE: PS00330; HEMOLYSIN-CALCIUM; 2.
 CC KW Hemolysin; Toxin; Cytolysis; Cytolextin; Repeat; Calcium;
 CC Transmembrane; Lipoprotein; Palmitate.
 CC FT TRANSMEM 226 256
 CC FT TRANSMEM 297 326
 CC FT TRANSMEM 367 406
 CC FT DOMAIN 722 845
 CC FT REPEAT 722 727
 CC FT REPEAT 731 736
 CC FT REPEAT 740 745
 CC FT REPEAT 749 754
 CC FT REPEAT 758 763
 CC FT REPEAT 767 772
 CC FT REPEAT 776 781
 CC FT REPEAT 785 790
 CC FT REPEAT 794 799

FT REPEAT 813 818 10.
 FT REPEAT 822 827 11.
 FT REPEAT 831 836 12.
 FT REPEAT 840 845 13.
 FT CONFLICT 210 217
 FT CONFLICT 374 374 R -> A (IN REF. 3 AND 4).
 FT CONFLICT 562 562 Q -> E (IN REF. 3 AND 4).
 FT CONFLICT 687 687 TC -> R (IN REF. 3 AND 4).
 SQ SEQUENCE 1023 AA; 110193 MW; F99A88CFC9F1A598 CRC64;

 Query Match 63.6%; Score 49; DB 1; Length 1023;
 Best Local Similarity 66.7%; Pred. No. 1.6;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 FNDFHSGGDD 12
 Db 734 FTDFHFGAKGDD 745

 RESULT 9
 RT12 ACNPL STANDARD; PRT; 1023 AA.
 ID RT12 ACNPL
 AC P55129;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE RTX-I toxin determinant A from serotypes 5/10 (APX-1A) (*Hemolysin 1A*)
 DE (HLX-1A) (*Cytolysin 1A*) (CLY-1A).
 GN *Actinobacillus pleuropneumoniae* (Haemophilus pleuropneumoniae).
 OS *Actinobacillus pleuropneumoniae* (Haemophilus pleuropneumoniae).
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;
 CC *Actinobacillus*.
 OX NCBI_Taxid=715;
 RX MEDLINE=94276858; PubMed=8007819;
 RP STRAIN=13039 / SEROTYPE 10;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S 4074 / SEROTYPE 10;
 RX MEDLINE=94276858; PubMed=8007819;
 RA Nagai S., Yagihashi T., Ishihama A.;
 RT "DNA sequence analysis of an allelic variant of the *Actinobacillus*
 RT *pleuropneumoniae*-RTX-toxin I (APXIA) from serotype 10.";
 RL Microb. Pathog. 15:485-495(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K17 / SEROTYPE 5;
 RX MEDLINE=96401417; PubMed=8807793;
 RA Chin N., Frey J., Chang C.F., Chang Y.F.;
 RT "Identification of a locus involved in the utilization of iron by
 RT *Actinobacillus pleuropneumoniae*.";
 RT FEMS Microbiol. Lett. 143:1-6(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K17 / SEROTYPE 5;
 RX MEDLINE=93366425; PubMed=8359891;
 RA Jansen R., Briatore J., Kamp E.M., Gielkens A.L.J., Smits M.A.;
 RT "Structural analysis of the *Actinobacillus pleuropneumoniae*-RTX-toxin
 RT I (Apxi) operon.";
 RL Infect. Immun. 61:3688-3695(1993).
 CC -1- FUNCTION: ONE OF THE VIRULENCE FACTORS OF *A. PLEUROPNEUMONIAE*,
 CC WHICH HAS A STRONG HEMOLYTIC ACTIVITY AND IS CYTOTOXIC FOR
 CC ALVEOLAR MACROPHAGES AND NEUTROPHILS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
 CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
 CC ACTIVITY.
 CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
 CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
 CC -1- PTM: PALMITOYLATED BY APXIC. THE TOXIN ONLY BECOMES ACTIVE WHEN
 CC MODIFIED (BY SIMILARITY).
 CC -1- MISCELLANEOUS: APXIA IS PARTIALLY DELETED IN SEROTYPES 2, 4, 6, 7,
 CC 8, 12, AND TOTALLY DELETED IN SEROTYPE 3.
 CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.

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CC -----
DR EMBL: D16582; BA04014.1; -
DR EMBL: U04954; AAB17220.1; -
DR EMBL: X73116; CAA51546.1; -
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR InterPro: IPR003995; RTX.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABDNGRPT.
DR PRINTS: PR01488; RTXTOXINA.
DR PROSITE: PS00330; HEMOLYSIN_CALCIUM; 2.
KM Hemolysis: Toxin; Cytolysis; Cytoxin; Repeat; Calcium;
FT Transmembrane; Lipoprotein; Palmitate.
FT TRANSMEM 226 256
FT TRANSMEM 297 326
FT TRANSMEM 367 406
FT DOMAIN 722 727 1.
FT REPEAT 722 727 13 X REPEATS, GLY-RICH.
FT REPEAT 731 736 2.
FT REPEAT 740 745 3.
FT REPEAT 749 754 4.
FT REPEAT 758 763 5.
FT REPEAT 767 772 6.
FT REPEAT 776 781 7.
FT REPEAT 785 790 8.
FT REPEAT 794 799 9.
FT REPEAT 813 818 10.
FT REPEAT 822 827 11.
FT REPEAT 831 836 12.
FT REPEAT 840 845 13.
FT CONFLICT 210 217 AMPYLTLA -> GNALSNTR (IN REF. 2).
FT CONFLICT 581 581 E -> Q (IN REF. 2).
FT CONFLICT 687 688 TC -> R (IN REF. 2).
FT CONFLICT 1015 1015 F -> L (IN REF. 2).
SQ SEQUENCE 1023 AA; 110129 MW; 183C7C15E57DB55 CRC64;

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Query Match 63.6%; Score 49; DB 1; Length 1023;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY 1 FNDIFHSGEDD 12
Db 734 FTDIFHGAAGDD 745

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RESULT 10
ID_HLY1_ECOLI STANDARD; PRT: 1023 AA.
AC P09983;
DT 01-MAR-1989 (Rel. 10; Created)
DT 01-MAR-1989 (Rel. 10; Last sequence update)
DT 30-MAY-2000 (Rel. 39; Last annotation update)
DE Hemolysin, chromosomal.
GN HLYA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J96 / SEROTYPE O4;
RX MEDLINE=85234404; PubMed=3891743;
RA Feilmee T., Pellett S., Welch R.A.;

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RT "Nucleotide sequence of an Escherichia coli chromosomal hemolysin.";
RL J. Bacteriol. 163:94-105(1985).
RN [2]
RP SEQUENCE OF 1-44 FROM N.A.
RC STRAIN=2001;
RX MEDLINE=85258115; PubMed=3894051;
RA Nicoud J.-M., Mackman N., Gray L., Holland I.B.;
RT "Characterisation of HlyC and mechanism of activation and secretion
of haemolysin from E. coli 2001.";
RL FEBS Lett. 187:339-344(1985).
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
DEFINED.
CC -1- SUBCELLULAR LOCATION: Secreted
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
ACTIVITY.
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
INVOLVED IN PORE FORMATION BY THE CYTOTOXIN.
CC -1- PTM: PALMITOYLATED BY HLYC. THE TOXIN ONLY BECOMES ACTIVE WHEN
MODIFIED.
CC -1- DISEASE: THE HEMOLYSIN OF E. COLI IS PRODUCED PREDOMINANTLY BY
STRAINS CAUSING EXTRAINTESTINAL INFECTIONS, SUCH AS THOSE OF THE
URINARY TRACT.
CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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CC -----
DR EMBL: M10133; AAA23975.1; -
DR EMBL: X02768; CAA26546.1; -
DR PIR: A24433; LEECA.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR InterPro: IPR003995; RTX.
DR Pfam: PF00353; hemolysin_Ca_bind.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABDNGRPT.
DR PRINTS: PR01488; RTXTOXINA.
DR PROSITE: PS00330; HEMOLYSIN_CALCIUM; 4.
KM Hemolysis: Toxin; Cytolysis; Cytoxin; Repeat; Calcium;
KW Transmembrane; Lipoprotein; Palmitate.
FT TRANSMEM 237 259
FT TRANSMEM 267 326
FT TRANSMEM 364 410
FT TRANSMEM 723 728
FT DOMAIN 723 728 16 X REPEATS, GLY-RICH.
FT REPEAT 723 728 1.
FT REPEAT 732 737 2.
FT REPEAT 741 746 3.
FT REPEAT 750 755 4.
FT REPEAT 759 764 5.
FT REPEAT 768 773 6.
FT REPEAT 777 782 7.
FT REPEAT 786 791 8.
FT REPEAT 795 800 9.
FT REPEAT 806 812 10.
FT REPEAT 816 821 11.
FT REPEAT 825 830 12.
FT REPEAT 834 839 13.
FT REPEAT 843 848 14.
FT REPEAT 853 860 15.
FT REPEAT 864 869 16.
FT LIPID 563 563 PALMITATE (BY SIMILARITY).
FT LIPID 689 689 PALMITATE (BY SIMILARITY).
FT VARIANT 6 6 A -> T (IN STRAIN 2001).
SQ SEQUENCE 1023 AA; 109867 MW; 196D5C0A9A28B54D CRC64;

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Query Match 62.3%; Score 48; DB 1; Length 1023;
 Best Local Similarity 66.7%; Pred. No. 2.3;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FNDIFHSRGEDD 12
 DB 735 FADIFHGAGDGD 746

RESULT 11
 NODO_RHIV
 ID NODO_RHIV STANDARD; PRT; 284 AA.
 AC P15728;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-MAR-1992 (Rel. 21, Last annotation update)
 DE Nodulation protein O.
 GN NODO OR NOLR.
 OS Rhizobium leguminosarum (biovar viciae).
 OC Plasmid sym pRLJ1.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=387;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-8.
 RC STRAIN=8401;
 RX MEDLINE=90151607; PubMed=2303029;
 RA Economou A., Hamilton W.D.O., Johnston A.W.B., Downie J.A.;
 RT "The Rhizobium nodulation gene noda encodes a Ca2(+)-binding protein
 RT that is exported without N-terminal cleavage and is homologous to
 RT hemolysin and related proteins.";
 RL EMO J. 9:349-354(1990).
 RN [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 4-18.
 RX MEDLINE=90078125; PubMed=2687250.
 RA de Maagd R.A., Wijffes A.H.M., Spaik H.P., Ruiz-Salaz J.E.,
 RA Willemsen C.A., Okker R.J.H., Lugtenberg B.J.J.;
 RT "noda, a new nod gene of the Rhizobium leguminosarum biovar viciae
 RT sym plasmid pRLJ1, encodes a secreted protein.";
 RL J. Bacteriol. 171:6764-6770(1989).
 CC -1- FUNCTION: THE NODO PROTEIN MAY PLAY A ROLE IN NODULE DEVELOPMENT
 CC BY DIRECT INTERACTION WITH THE ROOT HAIR CELLS OR SOME OTHER PLANT
 CC SURFACE IN A CA2(+)-DEPENDENT MANNER.
 CC -1- SUBCELLULAR LOCATION: SECRETED. BY A MECHANISM THAT DOES NOT
 CC INVOLVE AN N-TERMINAL SIGNAL PEPTIDE.
 CC -1- INDUCTION: BY NARINGENIN (FLAVONOID).
 CC -1- SIMILARITY: TO HEMOLYSIN AND RELATED PROTEINS.
 CC -----
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 CC -----
 CC EMBL: X17285; CAA35178.1; -;
 CC EMBL: M29532; AAA26341.1; -;
 CC PIR: S08385; S08385.
 CC PIR: A43721; A43721.
 CC InterPro: IPR001343; Hemlysn_Ca_bind.
 CC InterPro: IPR003355; RTX_N.
 CC Pfam: PF00353; hemolysincabind; 2.
 CC PRINTS: PR00313; CABNDNGRPT.
 CC PROSITE: PS00330; HEMOLYSIN_CALCIUM; 1.
 CC Plasmid: Nodulation; Calcium-binding; Repeat.
 CC DOMAIN 2 73 8 X APPROXIMATE TANDEM REPEATS.
 CC DOMAIN 92 127 4 X APPROXIMATE TANDEM REPEATS.
 CC CA_BIND 92 131 POTENTIAL.
 CC DOMAIN 208 222 EXPORT SIGNAL (ASPARTIC ACID BOX)
 CC (POTENTIAL).
 CC SEQUENCE 284 AA; 30002 MW; 9CA4IDCFGBF8E15 CRC64;

Query Match 59.7%; Score 46; DB 1; Length 284;
 Best Local Similarity 88.9%; Pred. No. 1.2;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HSGEGDDL 14
 DB 94 HSGEGDVL 102

RESULT 12
 HLVA_ACTSU
 ID HLVA_ACTSU STANDARD; PRT; 956 AA.
 AC Q00951;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Hemolysin (Cytolysin II) (CLY-IIA) (HLV-IIA) (CYTC) (APPA).
 GN APPA OR CLYIIA OR HLVIIA OR CYTC.
 OS Actinobacillus suis.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Actinobacillus.
 OX NCBI_TaxID=716;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3714;
 RX MEDLINE=92267623; PubMed=1587585;
 RA Burrows L.L., Lo R.Y.;
 RT "Molecular characterization of an RTX toxin determinant from
 RT Actinobacillus suis.";
 RL Infect. Immun. 60:2166-2173(1992).
 CC -1- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A. SUIS. MIGHT BE A
 CC SECRETED CYTOTOXIN, POSSIBLY THE EXTRACELLULAR HEMOLYSIN.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
 CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
 CC ACTIVITY.
 CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
 CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
 CC -1- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
 CC MODIFIED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M90440; AAA21918.1; -;
 CC InterPro: IPR001343; Hemlysn_Ca_bind.
 CC InterPro: IPR003355; RTX_N.
 CC InterPro: IPR003995; RLXA.
 CC Pfam: PF00353; hemolysincabind; 1.
 CC Pfam: PF02382; RTX; 1.
 CC PRINTS: PR00313; CABNDNGRPT.
 CC PRINTS: PR01488; RTXTOXINA.
 CC PROSITE: PS00330; HEMOLYSIN_CALCIUM; 1.
 CC Hemolysis; Toxin; Cytolysin; Cytotoxin; Repeat; Calcium;
 CC Transmembrane; Lipoprotein; Palmitate.
 CC TRANSMEM 238 254 POTENTIAL.
 CC TRANSMEM 302 320 POTENTIAL.
 CC TRANSMEM 383 406 POTENTIAL.
 CC DOMAIN 719 799 9 X REPEATS, GLY-RICH.
 CC REPEAT 719 724 1.
 CC REPEAT 728 733 2.
 CC REPEAT 737 742 3.
 CC REPEAT 746 751 4.
 CC REPEAT 755 760 5.
 CC REPEAT 764 769 6.
 CC REPEAT 773 778 7.

DR InterPro: IPR003355; RTX_N.
 DR InterPro: IPR003995; RtxA.
 DR Pfam: PF00353; hemolysincabind; 1.
 DR Pfam: PF02382; RTX_1.
 DR PRINTS: PR00313; CABNDNGRPT.
 DR PRINTS: PR01488; RTXTOXINA.
 DR PROSITE: PS00330; HEMOLYSIN_CALCIUM; 4.
 DR PROSITE: Toxin; Cytolysin; Repeat; Calcium;
 KM Transmembrane; Lipoprotein; Palmitate.
 FT TRANSMEM 154 170 POTENTIAL.
 FT TRANSMEM 312 333 POTENTIAL.
 FT TRANSMEM 393 414 POTENTIAL.
 FT DOMAIN 625 780 7 X REPEATS, GLY-RICH.
 FT REPEAT 625 630 1.
 FT REPEAT 730 735 2.
 FT REPEAT 739 744 3.
 FT REPEAT 748 753 4.
 FT REPEAT 757 762 5.
 FT REPEAT 766 771 6.
 FT REPEAT 775 780 7.
 SQ SEQUENCE 947 AA; 101559 MW; 9744F06395EF5BED CRC64;

Query Match 58.4%; Score 45; DB 1; Length 947;
 Best Local Similarity 53.8%; Pred. No. 6.9;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 2 NDIHSGEGDDL 14
 Db 770 DDILHGKGNL 782

RESULT 15
 ZAPA_PROMI STANDARD; PRT; 491 AA.
 AC 011137;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Extracellular metalloprotease precursor (EC 3.4.24.-).
 GN ZAPA.
 OS Proteus mirabilis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Proteus.
 OX NCBI_TaxID=584;
 RN 111
 RP SEQUENCE FROM N.A.
 RC STRAIN=BB2000;
 RX MEDLINE=96011363; PubMed=7592325;
 RA Wassif C., Cheek D., Belas R.;
 RT "Molecular analysis of a metalloprotease from Proteus mirabilis."
 RL J. Bacteriol. 177:5790-5798(1995).
 CC -1- FUNCTION: ONE OF THE VIRULENCE FACTORS PRODUCED DURING SWARMER
 CELL DIFFERENTIATION OF THE BACTERIA. WHICH SEEMS TO BE ASSOCIATED
 WITH PATHOGENESIS. THE PROTEASE ACTIVITY IS LIMITED TO IG A1,
 IG A2, AS WELL AS IG G DEGRADATION.
 CC -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
 CC -1- ENZYME REGULATION: CA2+ INCREASES PROTEASE ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MISCELLANEOUS: THE GLY-RICH REPEATS MAY BE IMPORTANT IN THE
 EXTRACELLULAR SECRETION OF THIS METALLOPROTEASE.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10B (ZINC
 METALLOPROTEASE); ALSO KNOWN AS THE SERRALYSIN SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: U25950; AAA86729.1; ALT_INIT.

DR HSSP: P23694; 1SAT.
 DR MEROPS: M10.057; -;
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR00130; Zn_Mtpeptidse.
 DR Pfam: PF00353; hemolysincabind; 1.
 DR PRINTS: PR00313; CABNDNGRPT.
 DR SMART: SM00235; zmc; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 DR PROSITE: PS00330; HEMOLYSIN_CALCIUM; FALSE NEG.
 DR PROSITE: Metalloprotease; zinc; zymogen; Repeat; Virulence; Calcium.
 KM Hydrolyase; Metalloprotease; zinc; zymogen; Repeat; Virulence; Calcium.
 FT PROPEP 1 16 POTENTIAL.
 FT CHAIN 17 491 EXTRACELLULAR METALLOPROTEASE.
 FT METAL 186 186 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 187 187 BY SIMILARITY.
 FT METAL 190 190 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 196 196 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 226 226 ZINC (CATALYTIC) (BY SIMILARITY).
 FT DOMAIN 343 393 4 X REPEATS, GLY-RICH.
 FT REPEAT 343 348 1.
 FT REPEAT 361 366 2.
 FT REPEAT 379 384 3.
 FT REPEAT 388 393 4.
 SQ SEQUENCE 491 AA; 54000 MW; 1E6DEE3F6243A97 CRC64;

Query Match 55.2%; Score 42.5; DB 1; Length 491;
 Best Local Similarity 40.9%; Pred. No. 8.9;
 Matches 9; Conservative 2; Mismatches 2; Indels 9; Gaps 1;
 QY 2 NDIH-----SGEGDDL 14
 Db 347 NDIHGNADNDTLGGEGDDIT 368

Search completed: September 11, 2002, 09:01:55
 Job time: 278 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 11, 2002, 09:00:14 ; Search time 40.83 Seconds
(without alignments)
32.948 Million cell updates/sec

Title: US-09-884-696-13
Perfect score: 77
Sequence: 1 FNDIFHSGECDLL 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	76.6	1055	1 A37205	Leukotoxin A - Act
2	58	75.3	1049	1 S51784	Leukotoxin III - Actino
3	58	75.3	1052	1 B49219	Leukotoxin III - Actino
4	56	72.7	1024	2 S10056	hemolysin A - Esch
5	52	67.5	998	2 I41078	hemolysin - Escher
6	52	67.5	998	2 T00227	hemolysin A toxin
7	52	67.5	998	2 AH2137	hypothetical prote
8	50	64.9	387	2 E95995	hypothetical calci
9	49	63.6	208	2 S34238	leukotoxin A - Pas
10	49	63.6	953	1 B30169	leukotoxin A - Pas
11	49	63.6	955	1 A35254	leukotoxin A - Pas
12	49	63.6	1022	1 I39643	RTX-toxin I - Acti
13	48	62.3	334	2 E69361	signal transducing
14	48	62.3	1023	1 LEECA	hemolysin A - Esch
15	47	61.0	302	2 AD2546	hypothetical prote
16	47	61.0	1417	2 AG2137	hypothetical prote
17	46	59.7	284	2 S08385	nodo protein - Rhl
18	46	59.7	284	2 A43721	nodo protein - Rhl
19	46	59.7	644	2 C95991	conserved hypotet
20	46	59.7	956	1 B33389	toxins II - Actinob
21	46	59.7	956	1 A43834	toxins II - Actinob
22	45	58.4	1771	2 S76851	hypothetical prote
23	43	55.8	219	2 B95953	probable secreted
24	43	55.8	1112	2 H95964	probable outer mem
25	42	54.5	282	2 F90077	conserved hypotet
26	42	54.5	395	2 T00574	probable protein K
27	42	54.5	539	2 G95405	hypothetical prote
28	42	54.5	591	2 S74999	iron-regulated pro
29	42	54.5	650	2 G87572	calcium-binding pr

30	42	54.5	1208	2 C82779	hemolysin-type cal
31	42	54.5	1254	2 G66379	protein F5A9.24 [1
32	42	54.5	1706	1 OYBRC	cycloleucin - Borde
33	42	54.5	1741	2 S74910	hemolysin - Synec
34	42	54.5	2064	2 G82562	Dactylocin XE2407
35	41	53.2	143	2 T13214	minor capsid prote
36	41	53.2	218	2 H84328	3-phosphoglycerate
37	41	53.2	319	2 F82348	hypothetical prote
38	41	53.2	387	2 E95933	probable calcium-b
39	41	53.2	681	2 AB2155	hypothetical prote
40	41	53.2	826	2 AB1841	hypothetical prote
41	41	53.2	993	2 AE1905	outer membrane sec
42	41	53.2	1072	2 G95851	probable hemolysin
43	41	53.2	1290	2 S76853	hypothetical prote
44	41	53.2	1403	2 S77624	mannuronan C-5-epi
45	41	53.2	1705	2 S51672	adenylate cyclase

ALIGNMENTS

RESULT 1
A37205
Leukotoxin A - Actinobacillus actinomycetemcomitans
C:Species: Actinobacillus actinomycetemcomitans
C:Date: 16-Sep-1992 #sequence-revision 01-Nov-1996 #text-change 31-Mar-2000
C:Accession: A37205; A60768; B34345; A32276; PH0267; PH0266; S17284
R:Kraly, E.; Dailey, T.; Kolodrubetz, D.
Infect. Immun. 58, 920-929, 1990
A:Title: Nucleotide sequence of the leukotoxin gene from Actinobacillus actinomycetemcomitans
A:Reference number: A37205; M01D:90202154
A:Accession: A37205
A:Molecule type: DNA
A:Residues: 1-1055 <KRA>
A:Cross-references: GB:X16829; M1D:938643; P1D:CAA34731.1; P1D:938645
A:Note: the authors present evidence that the nucleotide sequence is correct in the v
sing nucleotide
R:Kolodrubetz, D.; Dailey, T.; Ebersole, J.; Kraly, E.
Infect. Immun. 57, 1465-1469, 1989
A:Title: Cloning and expression of the leukotoxin gene from Actinobacillus actinomycetemcomitans
A:Reference number: A60768; M01D:89212893
A:Accession: A60768
A:Molecule type: DNA
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Residues: 297-309, 'Y', 311-364, 434-440, 'KC', 443-474, 'H', 476-489, 'S', 491-493, 'VLK', 49
R:Kraly, E.T.; Golub, E.E.; Kieba, I.R.; Talchman, N.S.; Rosenbloom, J.; Rosenbloom, J.
J. Biol. Chem. 264, 15451-15456, 1989
A:Title: Analysis of the Actinobacillus actinomycetemcomitans leukotoxin gene. Delin
A:Reference number: A34345; M01D:89359382
A:Accession: B34345
A:Molecule type: DNA
A:Residues: 1-239, 'Y', 241-259, 'H', 261-335, 'A', 337-415, 'S', 417-438, 'S', 440-723, 'N', 725
PVRKRYPRHCRPIITLTIQIR' <LAL>
A:Cross-references: GB:M27933
R:Kraly, E.T.; Kieba, I.R.; Demuth, D.R.; Rosenbloom, J.; Golub, E.E.; Talchman, N.S
Biochem. Biophys. Res. Commun. 159, 256-262, 1989
A:Title: Identification and expression of the Actinobacillus actinomycetemcomitans le
A:Reference number: A32276; M01D:89165863
A:Accession: A32276
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 430-438, 'S', 440-476, 'R', 478-506, 'KRS', 511, 'QSAINSLNTD', 523-541, 'I', 543,
A:Note: this sequence is revised in reference A34345
R:Ohta, H.; Miyagi, A.; Kato, K.; Fukui, K.
Submitted to JIPID, July 1995
A:Description: Modulation of leukotoxin production by growth rate and bicarbonate in
A:Reference number: PH0267
A:Accession: PH0267
A:Molecule type: protein
A:Residues: 17-42 <OHT>
A:Experimental source: strain 301-b
A:Accession: PH0266

A:Molecule type: protein
 A:Residues: 2-6, 'L', 8-26 <OH2>
 C:Genetics:
 A:Gene: ltxA
 C:Function:
 A:Description: lyses human polymorphonuclear lymphocytes and monocytes
 C:Superfamily: hemolysin A; hemolysin A homology
 C:Keywords: cytolysis; hemolysis; lipoprotein; periplasmic space; tandem repeat; thioles
 F:245-790/Domain: hemolysin A homology <HLVA>
 F:731-847/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIRYF]-X)
 F:562,687/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match 76.6%; Score 59; DB 1; Length 1055;
 Best Local Similarity 64.3%; Pred. No. 0.088;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FNDIFHSGGDDL 14
 DB 734 FNDIFHGHGDDL 747

RESULT 2
 S51784
 toxin III - Actinobacillus pleuropneumoniae (serotype 2)
 N:Alternate names: RTX-toxin IIIA (ApXIIIA)
 C:Species: Actinobacillus pleuropneumoniae
 C>Date: 14-Jul-1995 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999
 C:Accession: S51784
 R:Chang, Y.F.; Shu, J.; Ma, D.P.; Shin, S.J.; Lein, D.H.
 DNA Cell Biol. 12, 351-362, 1993
 A:Title: Molecular analysis of the Actinobacillus pleuropneumoniae RTX toxin-III gene cl
 A:Reference number: S51783; MUID:93263992
 A:Accession: S51784
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1049 <CH>
 A:Cross-references: EMBL:L12145; NID:9349605; PIDN:AAA21924.1; PID:9470685
 C:Comment: This organism causes porcine pleuropneumonia.
 C:Genetics:
 A:Gene: apXIIIA
 C:Function:
 A:Description: lyses lung macrophages
 C:Superfamily: hemolysin A; hemolysin A homology
 C:Keywords: calcium binding; cytolysis; exotoxin; lipoprotein; tandem repeat; thiolester
 F:254-803/Domain: hemolysin A homology <HLVA>
 F:735-861/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIRYF]-X)
 F:571,702/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match 75.3%; Score 58; DB 1; Length 1049;
 Best Local Similarity 71.4%; Pred. No. 0.13;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGGDDL 14
 DB 747 FRDIFHGADDDL 760

RESULT 3
 B49219
 toxin III - Actinobacillus pleuropneumoniae (serotype 8)
 N:Alternate names: RTX-toxin III (ApXIIIA)
 C:Species: Actinobacillus pleuropneumoniae
 C>Date: 19-Dec-1993 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999
 C:Accession: B49219; S48043; S29958
 R:Jansen, R.; Briatore, J.; Kamp, E.M.; Gielkens, A.L.; Smits, M.A.
 Infect. Immun. 61, 947-954, 1993
 A:Title: Cloning and characterization of the Actinobacillus pleuropneumoniae-RTX-toxin I
 A:Reference number: A49219; MUID:93162836
 A:Accession: B49219
 A:Molecule type: DNA
 A:Residues: 1-1052 <JANI>

A:Cross-references: EMBL:X68815; NID:938956; PIDN:CAA48711.1; PID:938958
 A:Experimental source: strain 405, serotype 8
 A>Note: sequence extracted from NCBI backbone (NCBIN:125168, NCBI:P.125170)
 R:Jansen, R.; Briatore, J.; van Geel, A.B.M.; Kamp, E.M.; Gielkens, A.L.J.; Smits, M.A.
 Infect. Immun. 62, 4411-4418, 1994
 A:Title: Genetic map of the Actinobacillus pleuropneumoniae RTX-toxin (ApX) operons:
 A:Accession: S48043
 A:Reference number: S48042; MUID:95012630
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1052 <JANI>
 A:Cross-references: EMBL:X60055; NID:9558150; PIDN:CAA56358.1; PID:9558152
 A:Experimental source: strain 405, serotype 8
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
 C:Comment: This organism causes porcine pleuropneumonia.
 C:Genetics:
 A:Gene: apXIIIA
 C:Function:
 A:Description: lyses lung macrophages
 C:Superfamily: hemolysin A; hemolysin A homology
 C:Keywords: calcium binding; cytolysis; exotoxin; lipoprotein; tandem repeat; thioles
 F:254-804/Domain: hemolysin A homology <HLVA>
 F:736-862/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIRYF]-X)
 F:571,702/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match 75.3%; Score 58; DB 1; Length 1052;
 Best Local Similarity 71.4%; Pred. No. 0.13;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGGDDL 14
 DB 748 FRDIFHGADDDL 761

RESULT 4
 S10056
 hemolysin A - Escherichia coli plasmid pHLy152
 C:Species: Escherichia coli
 C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 04-Mar-2000
 C:Accession: S10056
 R:Hess, J.; Wels, W.; Vogel, M.; Goebel, W.
 FEMS Microbiol. Lett. 34, 111, 1986
 A:Title: Nucleotide sequence of a plasmid-encoded hemolysin determinant and its compa
 A:Reference number: S07209
 A:Accession: S10056
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1024 <HES>
 A:Cross-references: EMBL:M14107
 C:Genetics:
 A:Genome: plasmid pHLy152
 C:Superfamily: hemolysin A; hemolysin A homology
 C:Keywords: lipoprotein
 F:247-792/Domain: hemolysin A homology <HLVA>
 F:564,690/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match 72.7%; Score 56; DB 2; Length 1024;
 Best Local Similarity 64.3%; Pred. No. 0.28;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGGDDL 14
 DB 736 FTDIFHGADDDL 749

RESULT 5
 I41078
 hemolysin - Escherichia coli
 C:Species: Escherichia coli
 C>Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jul-2000
 C:Accession: I41078

R:Schmidt, H.; Beutin, L.; Karch, H.
Infect. Immun. 63, 1055-1061, 1995
A:Title: Molecular analysis of the plasmid-encoded hemolysin of *Escherichia coli* O157:H7
A:Reference number: I41077; PMID:95172659
A:Accession: I41078
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-998 <RES>
A:Cross-references: EMBL:X79839; NID:g860924; PID:CAAS6234.1; PID:g4388764
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: lipoprotein
F:233-776/Domain: hemolysin A homology <HLXA>
F:550,675/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match 67.5%; Score 52; DB 2; Length 998;
Best Local Similarity 57.1%; Pred. No. 1.3;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
OY 1 FNDIFHSGGDDL 14
DB 720 FNDIFHSGGNDYI 733

RESULT 6
T00227
hemolysin A toxin protein - *Escherichia coli* plasmid pO157

C:Species: *Escherichia coli*
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C:Accession: T00227; T42148
R:Makino, K.; Ishii, K.; Yasunaga, T.; Hattori, M.; Yokoyama, K.; Yatsudo, H.C.; Kubota, S.; Shingawa, H.
DNA Res. 5, 1-9, 1998
A:Title: Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an enterohemorrhagic *E. coli* O157:H7
A:Reference number: Z14127; PMID:98290540
A:Accession: T00227
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-998 <MAX>
A:Cross-references: EMBL:AB011549; NID:g4589740; PID:BAAS1774.1; PID:g3337015
A:Experimental source: strain EHEC O157:H7, substrain RIMD 0509952
R:Burland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
Nucleic Acids Res. 26, 4196-4204, 1998
A:Title: The complete DNA sequence and analysis of the large virulence plasmid of *Escherichia coli* O157:H7
A:Reference number: Z22066; PMID:98391744
A:Accession: T42148
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-998 <BUR>
A:Cross-references: EMBL:AF074613; PID:NAAC70116.1
A:Experimental source: strain EDL933; serotype O157:H7
C:Genetics:
A:Gene: hlyA
A:Genome: plasmid pO157
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: cytotoxic; hemolysin; lipoprotein; toxin
F:233-776/Domain: hemolysin A homology <HLXA>
F:550,675/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match 67.5%; Score 52; DB 2; Length 998;
Best Local Similarity 57.1%; Pred. No. 1.3;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
OY 1 FNDIFHSGGDDL 14
DB 720 FNDIFHSGGNDYI 733

RESULT 7
AH2137
hypothetical protein all2655 [imported] - *Anabaena* sp. (strain PCC 7120)
C:Species: *Anabaena* sp.

A:Note: *Anabaena* sp. (strain PCC 7120) is a synonym of *Nostoc* sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C:Accession: AH2137
R:Kaneke, T.; Nakamura, Y.; Molk, C.P.; Kultz, T.; Sasamoto, S.; Watanabe, A.; Iriyama, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. PCC 7120
A:Reference number: AB1807; PMID:21595285; PMID:11759840
A:Accession: AH2137
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-3262 <KUR>
A:Cross-references: GB:BA000019; PID:BAW74354.1; PID:g17131748; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all2655

Query Match 67.5%; Score 52; DB 2; Length 3262;
Best Local Similarity 69.2%; Pred. No. 4.7;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 2 NDIIFHSGGDDL 14
DB 3162 NDIIFHSGGDDL 3174

RESULT 8
E95995

hypothetical calcium binding protein [imported] - *Sinorhizobium meliloti* (strain 1021)
C:Species: *Sinorhizobium meliloti*
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: E95995
R:Finan, T.M.; Weidner, S.; Wong, K.; Bhurmesler, J.; Chain, P.; Vorholter, F.J.; Herr
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb *psymb* megaplasmid from the N2-fixing *Sinorhizobium meliloti*
A:Reference number: A95842; PMID:21396508; PMID:11481431
A:Accession: E95995
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-387 <KUR>
A:Cross-references: GB:AL591985; PID:CAAC49629.1; PID:g15141116; GSPDB:GN00167
A:Experimental source: strain 1021, megaplasmid *psymb*
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barlow-Hubel, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
Science 293, 668-672, 2001
L.: Hyman, R.W.; Jones, T.
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, A.
A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*
A:Reference number: A96039; PMID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Smb21402
A:Genome: plasmid

Query Match 64.9%; Score 50; DB 2; Length 387;
Best Local Similarity 69.2%; Pred. No. 0.99;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 2 NDIIFHSGGDDL 14
DB 81 NDIIFHSGGNDVL 93

RESULT 9
S34238
Leukotoxin A - *Pasteurella haemolytica* (fragment)
N:Alternate names: Ikta protein
C:Species: *Pasteurella haemolytica*
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001
C:Accession: S34238; S34236

R:lainson, A.F.; Aitchison, K.D.; Donachie, W.
submitted to the EMBL Data Library, June 1993
A:Description: DNA sequence of the carboxy terminal end of leukotoxin A from the T4 sero
of *Pasteurella haemolytica*.
A:Reference number: S34236
A:Accession: S34238
A:Molecule type: DNA
A:Residues: 1-208 <LA1>
A:Cross-references: EMBL:Z22885; NID:9311830; PIDN:CAA80499.1; PID:9311831
A:Experimental source: serotype T4
A:Accession: S34236
A:Molecule type: DNA
A:Residues: 9-208 <LA2>
A:Cross-references: EMBL:Z22886; NID:9311826; PIDN:CAA80500.1; PID:9311827
A:Experimental source: serotype T15
A:Genetics:
A:Gene: lktA
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat

Query Match 63.6%; Score 49; DB 2; Length 208;
Best Local Similarity 58.3%; Pred. No. 0.74;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDIRHSGEGDDL 13
Db 29 NDHLHGKGGDDI 40

RESULT 10
B30169
leukotoxin A - *Pasteurella haemolytica* (serotype 1)
N:Alternate names: lktA protein
C:Species: *Pasteurella haemolytica*
C>Date: 12-Oct-1989 #sequence revision 15-Nov-1996 #text_change 18-Jun-1999
C:Accession: B30169; C32051; S29516
R:Highlander, S.K.; Chidambaram, M.; Engler, M.J.; Weinstein, G.M.
DNA 8, 15-28, 1989
A:Title: DNA sequence of the *Pasteurella haemolytica* leukotoxin gene cluster.
A:Reference number: A30169; MUID:89210283
A:Accession: B30169
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-953 <HIG>
R:Strathdee, C.A.; Lo, R.Y.C.
J. Bacteriol. 171, 916-928, 1989
A:Title: Cloning, nucleotide sequence, and characterization of genes encoding the secret
A:Reference number: A32051; MUID:89123172
A:Accession: C32051
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 947-953 <STR>
R:Lo, R.Y.C.; Strathdee, C.A.; Shewen, P.E.
Infect. Immun. 55, 1987-1996, 1987
A:Title: Nucleotide sequence of the leukotoxin genes of *Pasteurella haemolytica* A1.
A:Reference number: S29515; MUID:87306837
A:Accession: S29516
A:Molecule type: DNA
A:Residues: 1-741, 'D', 743-953 <LOR>
A:Cross-references: EMBL:M20730; NID:9150492; PIDN:AAA25529.1; PID:9150494
C:Comment: This organism causes bovine pneumonic pasteurellosis (shipping fever).
C:Genetics:
A:Gene: lktA
C:Function:
A:Description: lyses leukocytes
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat;
F:238-784/Domain: hemolysin A homology <HLVA>
F:716-807/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVLYF]-X)
F:554/Binding site: palmitate (lys) (covalent) #status predicted

Query Match 63.6%; Score 49; DB 1; Length 953;
Best Local Similarity 58.3%; Pred. No. 4;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDIRHSGEGDDL 13
Db 774 NDHLHGKGGDDI 785

RESULT 11
A35254
leukotoxin A - *Pasteurella haemolytica* (serotype T10)
N:Alternate names: lktA protein
C:Species: *Pasteurella haemolytica*
C>Date: 10-Aug-1990 #sequence revision 15-Nov-1996 #text_change 18-Jun-1999
C:Accession: S37145; A35254; S34237; S34235
R:lainson, A.F.; Aitchison, K.; Donachie, W.
submitted to the EMBL Data Library, September 1993
A:Description: DNA sequence of the leukotoxin A gene from *P. haemolytica* T10 serotype
A:Reference number: S37145
A:Accession: S37145
A:Molecule type: DNA
A:Residues: 1-955 <LA1>
A:Cross-references: EMBL:Z26247; NID:9400424; PIDN:CAA81206.1; PID:9400425
R:Highlander, S.K.; Engler, M.J.; Weinstein, G.M.
J. Bacteriol. 172, 2343-2350, 1990
A:Title: Secretion and expression of the *Pasteurella haemolytica* leukotoxin.
A:Reference number: A35254; MUID:90236888
A:Accession: A35254
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 950-955 <HIG>
A:Cross-references: GB:M24197; GB:M34943; GB:M34944
R:lainson, A.F.; Aitchison, K.D.; Donachie, W.
submitted to the EMBL Data Library, June 1993
A:Description: DNA sequence of the carboxy terminal end of leukotoxin A from the T3 s
A:Reference number: S34235
A:Accession: S34237
A:Molecule type: DNA
A:Residues: 745-955 <LA2>
A:Cross-references: EMBL:Z22884; NID:9311828; PIDN:CAA80498.1; PID:9311829
A:Experimental source: serotype T3
A:Accession: S34235
A:Molecule type: DNA
A:Residues: 723-955 <LA3>
A:Cross-references: EMBL:Z22887; NID:9311824; PIDN:CAA80501.1; PID:9311825
A:Experimental source: serotype T10
C:Function:
A:Description: attacks cell membranes and causes cell lysis
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repe
F:240-786/Domain: hemolysin A homology <HLVA>
F:718-809/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVLYF]-X)
F:718-809/Region: repeat
F:727-726/Region: repeat
F:727-735/Region: repeat
F:736-744/Region: repeat
F:745-753/Region: repeat
F:754-762/Region: repeat
F:763-771/Region: repeat
F:772-780/Region: repeat
F:781-789/Region: repeat
F:792-800/Region: repeat
F:801-809/Region: repeat
F:556/Binding site: palmitate (lys) (covalent) #status predicted

Query Match 63.6%; Score 49; DB 1; Length 955;
Best Local Similarity 58.3%; Pred. No. 4;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDIRHSGEGDDL 13
Db 776 NDHLHGKGGDDI 787

RESULT 12

RTX-toxin I - Actinobacillus pleuropneumoniae

N:Alternate names: hemolysin Apxi

C:Species: Actinobacillus pleuropneumoniae

C.Date: 19-Jul-1996 #sequence-revision 08-Nov-1996 #text-change 18-Jun-1999

C:Accession: I39643; S18769; I39645; S60733; S35781

R:Jansen, R.; Bialtre, J.; Kamp, E.M.; Gielkens, A.L.; Smits, M.A.

Infect. Immun. 61, 3688-3695, 1993

A:Title: Structural analysis of the Actinobacillus pleuropneumoniae-RTX-toxin I (Apxi) C

A:Reference number: I39641; MUID:93366425

A:Accession: I39643

A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL

A:Molecule type: DNA

A:Residues: 1-1022 <RES>

A:Cross-references: EMBL:X73117; NID:g312897; PIDD:CAA51548.1; PID:g312899

R:Freij, J.; Meier, R.; Gygi, D.; Nicolet, J.

Infect. Immun. 59, 3026-3032, 1991

A:Title: Nucleotide sequence of the hemolysin I gene from Actinobacillus pleuropneumoniae

A:Reference number: S18769; MUID:91348845

A:Accession: S18769

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-209, 'AMPYLTAA', 218-373, 'R', 375-561, 'Q', 563-686, 'TC', 688-1022 <PRE>

A:Cross-references: EMBL:X52899; NID:g38948; PIDD:CAA37081.1; PID:g38950

R:Freij, J.; Halldmann, A.; Nicolet, J.; Boffin, A.; Prenzki, P.

Gene 142, 97-102, 1994

A:Title: Sequence analysis and transcription of the apxi operon (hemolysin I) from Actin

A:Reference number: I39644; MUID:94237497

A:Accession: I39645

A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL

A:Molecule type: DNA

A:Residues: 1-209, 'AMPYLTAA', 218-373, 'R', 375-561, 'Q', 563-686, 'TC', 688-1022 <RES>

A:Cross-references: EMBL:X68595; NID:g505568; PIDD:CAA48586.1; PID:g505570

R:Rascon, R.I.; Vazquez-Boland, J.A.; Gutierrez-Martin, C.B.; Rodriguez-Barbosa, I.; Rod

Mol. Microbiol. 14, 207-216, 1994

A:Title: The RTX hemolysins Apxi and ApxiI are major virulence factors of the swine pat

A:Reference number: S60731; MUID:95331743

A:Accession: S60732

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 604-685 <TRAS>

C:Comment: This organism causes porcine pleuropneumonia.

C:Genetics:

A:Gene: apxiA

C:Function: attacks blood cell membranes and causes cell lysis

C:Superfamily: hemolysin A; hemolysin A homology

C:Keywords: calcium binding; cytotoxins; exotoxin; hemolysis; lipoprotein; tandem repeat;

F:243-789/Domain: hemolysin A homology <HLVA>

F:721-847/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVYF]-X)

F:560,686/Binding site: palmitate (lys) (covalent) #status predicted

Query Match

Best Local Similarity 63.6%; Score 49; DB 1; Length 1022;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 FNDIFSGEGDD 12

Db 733 FTDIFHGAKGDD 744

RESULT 13

E69361

signal-transducing histidine kinase homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C.Date: 05-Dec-1997 #sequence-revision 05-Dec-1997 #text-change 02-Sep-2000

C:Accession: E69361

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

., Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Glodok, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kane, B.P.; Sykes,

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arc

A:Reference number: A69250; MUID:98049343

A:Accession: E69361

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-334 <RES>

A:Cross-references: GB:AE001042; GB:AE000782; NID:g2689365; PIDD:AAB90347.1; PID:g264

C:Superfamily: sensor histidine kinase homology

F:120-330/Domain: sensor histidine kinase homology <SKH>

Query Match

Best Local Similarity 62.3%; Score 48; DB 2; Length 334;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 FNDIFSGEGDD 13

Db 285 FNEGFSGEGGL 297

RESULT 14

LEBGA

hemolysin A - Escherichia coli

C:Species: Escherichia coli

C.Date: 30-Sep-1988 #sequence-revision 30-Sep-1988 #text-change 18-Jun-1999

C:Accession: A24433; I41280

R:Felmler, T.; Pellett, S.; Welch, R.A.

J. Bacteriol. 163, 94-105, 1985

A:Title: Nucleotide sequence of an Escherichia coli chromosomal hemolysin.

A:Reference number: A24433; MUID:85234404

A:Accession: A24433

A:Molecule type: DNA

A:Residues: 1-1023 <PRE>

A:Cross-references: GB:M10133; GB:M12863; NID:g146377; PIDD:AAA23975.1; PID:g146379

A:Experimental source: strain J96, O4 serotype

R:Stanley, P.; Packman, L.C.; Koronakis, V.; Hughes, C.

Science 266, 1992-1996, 1994

A:Title: Fatty acylation of two internal lysine residues required for the toxic acti

A:Reference number: A55387; MUID:95099325

A:Contents: annotation: lysine palmitoylation

A:Note: lysine modification is performed by the hlyC gene product

R:Haertlein, M.; Schlessl, S.; Wagner, W.; Rdest, U.; Krefel, J.; Goebel, W.

J. Cell Biol. 22, 87-97, 1983

A:Title: Transport of hemolysin by Escherichia coli.

A:Reference number: I41280

A:Accession: I41280

A:Status: translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1, 'T', 3, 'V', 5, 'T', 7-44 <RES>

A:Cross-references: GB:M29173; NID:g146337; PIDD:AAA23957.1; PID:g146338

C:Genetics:

A:Gene: hlyA

C:Function: attacks blood cell membranes and causes cell lysis

C:Superfamily: hemolysin A; hemolysin A homology

C:Keywords: calcium binding; cytotoxins; exotoxin; hemolysis; lipoprotein; tandem rep

F:246-791/Domain: hemolysin A homology <HLVA>

F:723-851/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVYF]-X)

F:563,689/Binding site: palmitate (lys) (covalent) #status experimental

Query Match

Best Local Similarity 62.3%; Score 48; DB 1; Length 1023;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 FNDIFSGEGDD 12

Db 735 FADIFGADGDD 746

RESULT 15

AD2546
 hypothetical protein all17655 [imported] - Anabaena sp. (strain PCC 7120) plasmid pcc7120
 C:Species: Anabaena sp.
 C:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
 C:Accession: AD2546
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, S.
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AD2546
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-302 <KUR>
 A:Cross-references: GB:AF003602; PIDN:BAH7298.1; PID:917134740; GSPDB:GN00181
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: all17655
 A:Genome: plasmid

Query Match 61.0%; Score 47; DB 2; Length 302;
 Best Local Similarity 75.0%; Pred. No. 2.4;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 DIFHSGEGDDL 14
 |||||
 Db 85 DIFHRGAGDDL 96

Search completed: September 11, 2002, 09:00:14
 Job time: 232 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 11, 2002, 08:59:26 : Search time 30.68 Seconds
(without alignments)
11.146 Million cell updates/sec

Title: US-09-884-696-13
Perfect score: 77
Sequence: 1 FNDIFHSGEDDL 14

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued_Patents_AA:*
2: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5C_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/5D_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/5E_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	75.3	1049	3	US-08-772-270A-11
2	58	75.3	1244	5	PCT-US93-10500-2
3	52	67.5	758	1	US-08-258-188-2
4	52	67.5	758	1	US-08-526-813-2
5	52	67.5	758	5	PCT-US95-08554-2
6	49	63.6	924	3	US-08-619-812-8
7	49	63.6	926	1	US-07-908-253-2
8	49	63.6	926	1	US-08-455-970A-2
9	49	63.6	926	1	US-08-387-156-6
10	49	63.6	926	2	US-08-694-865-6
11	49	63.6	926	2	US-08-878-148-6
12	49	63.6	926	2	US-08-535-837-2
13	49	63.6	926	3	US-09-124-491-6
14	49	63.6	926	6	5476657-3
15	49	63.6	936	1	US-08-455-970A-12
16	49	63.6	943	1	US-08-455-970A-10
17	49	63.6	951	1	US-08-455-970A-14
18	49	63.6	977	1	US-08-387-156-8
19	49	63.6	977	2	US-08-694-865-8
20	49	63.6	977	2	US-08-878-148-8
21	49	63.6	977	3	US-09-124-491-8
22	49	63.6	1022	3	US-08-772-270A-2
23	49	63.6	1069	1	US-07-777-715-9
24	49	63.6	1069	1	US-08-170-126-4
25	49	63.6	1069	3	US-08-954-418-4
26	49	63.6	1098	1	US-07-777-715-7
27	49	63.6	1098	1	US-08-170-126-2

28	49	63.6	1098	3	US-08-954-418-2	Sequence 2, Appl
29	46	59.7	956	3	US-08-772-270A-8	Sequence 8, Appl
30	45	58.4	934	1	US-08-215-805A-80.	Sequence 80, Appl
31	42	54.5	1706	4	US-08-609-785-2	Sequence 2, Appl
32	42	54.5	1794	6	5183745-6	Sequence 43, Appl
33	41	53.2	153	2	US-08-387-942C-43	Sequence 3, Appl
34	41	53.2	1403	2	US-08-387-942C-3	Sequence 4, Appl
35	41	53.2	1705	4	US-08-669-785-4	Sequence 10, Appl
36	40	51.9	213	1	US-09-609-224A-10	Sequence 10, Appl
37	40	51.9	213	2	US-08-920-440B-10	Sequence 10, Appl
38	40	51.9	213	4	US-09-173-492-10	Sequence 10, Appl
39	40	51.9	213	4	US-09-173-133-10	Sequence 10, Appl
40	40	51.9	823	1	US-07-745-206A-15	Sequence 15, Appl
41	40	51.9	823	2	US-08-311-363-15	Sequence 15, Appl
42	40	51.9	1754	1	US-07-745-206A-13	Sequence 13, Appl
43	40	51.9	1754	2	US-08-311-363-13	Sequence 13, Appl
44	40	51.9	2237	1	US-08-455-943A-48	Sequence 48, Appl
45	40	51.9	2237	2	US-08-223-305C-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-08-772-270A-11
; Sequence 11, Application US/08772270A
; Patent No. 6019984
; GENERAL INFORMATION:
; APPLICANT: MacInnes, Janet
; APPLICANT: Ricciardi, Paul
; APPLICANT: Mallard, Bonnie
; APPLICANT: Rosendal, Soren
; TITLE OF INVENTION: NOVEL BACTERIAL PREPARATIONS METHOD FOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,270A
; FILING DATE: December 23, 1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gravelle, Michelle
; REGISTRATION NUMBER: 40,261
; REFERENCE/DOCKET NUMBER: 6580-81
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1049 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Actinobacillus pleuropneumoniae
; US-08-772-270A-11

Query Match 75.3%, Score 58; DB 3; Length 1049;
Best local Similarity 71.4%; Pred. No. 0.11;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGDDLL 14
| | | | : | | | |
Db 747 FNDIFHSGDDLL 760

RESULT 2
PCT-US93-10500-2
; Sequence 2, Application PC/TUS9310500
; GENERAL INFORMATION:
; APPLICANT: Chang, Yung-Fu
; TITLE OF INVENTION: Recombinant Vaccine For Procine
; PLEUROPNEUMONIAE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Alan S. Korman
; STREET: 1600 Empire Tower
; CITY: Buffalo
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10500
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/972,229
; FILING DATE: 05-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Korman, Alan S.
; REGISTRATION NUMBER: 33,932
; REFERENCE/DOCKET NUMBER: 19603/00001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-853-8104
; TELEFAX: 716-853-8109
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1244 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Actinobacillus pleuropneumoniae
; STRAIN: Serotypes 2, 3, 4, 6 and 8
; INDIVIDUAL ISOLATE: Swine
; CELL TYPE: Gram negative bacterium
; PCT-US93-10500-2

Query Match 75.3%; Score 58; DB 5; Length 1244;
Best Local Similarity 71.4%; Pred. No. 0.13;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGDDLL 14
| | | | : | | | |
Db 920 FNDIFHSGDDLL 933

RESULT 3
US-08-258-188-2
; Sequence 2, Application US/08258188
; Patent No. 5475098
; GENERAL INFORMATION:
; APPLICANT: Hall, Robert H.

APPLICANT: Xu, Jian Guo
; TITLE OF INVENTION: A NEW AND DISTINCTIVE DNA SEQUENCE OF E.
; COLI O157:H7 AND ITS USE FOR THE RAPID, SENSITIVE AND
; SPECIFIC DETECTION OF O157:H7 AND OTHER ENTEROHEMORRHAGIC
; E. COLI
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/258,188
; FILING DATE: 14-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Mackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 15280206, DHHS135940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 758 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-258-188-2

Query-Match 67.5%; Score 52; DB 1; Length 758;
Best Local Similarity 57.1%; Pred. No. 0.75;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 FNDIFHSGDDLL 14
| | | | : | | | |
Db 480 FNDIFHSGDDLL 493

RESULT 4
US-08-526-813-2
; Sequence 2, Application US/08526813
; Patent No. 5756293
; GENERAL INFORMATION:
; APPLICANT: Hall, Robert H.
; APPLICANT: Xu, Jian Guo
; TITLE OF INVENTION: A New and Distinctive DNA Sequence of E.
; COLI O157:H7 and Its Use for the Rapid, Sensitive and
; SPECIFIC DETECTION OF O157:H7 and Other Enterohemorrhagic
; E. COLI
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/526,813
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,188
FILING DATE: 14-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280-206-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-526-813-2

Query Match 67.5%; Score 52; DB 1; Length 758;
Best Local Similarity 57.1%; Pred. No. 0.75;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 FNDIFHSGEDDL 14
Db 480 FNDIFHSGDNDYI 493

RESULT 5
PCT-US95-08554-2
Sequence 2, Application PC/TUS9508554
GENERAL INFORMATION:
APPLICANT: HALL, Robert H.
APPLICANT: XU, Jian Guo
TITLE OF INVENTION: A NEW AND DISTINCTIVE DNA SEQUENCE OF E.
TITLE OF INVENTION: COIL 0157:H7 AND ITS USE FOR THE RAPID, SENSITIVE AND
TITLE OF INVENTION: SPECIFIC DETECTION OF 0157:H7 AND OTHER ENTEROHEMORRHAGIC
TITLE OF INVENTION: E. coli
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourile and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08554
FILING DATE: 14-JUN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280206, DHHS135940
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08554-2

Query Match 67.5%; Score 52; DB 5; Length 758;
Best Local Similarity 57.1%; Pred. No. 0.75;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 FNDIFHSGEDDL 14
Db 480 FNDIFHSGDNDYI 493

RESULT 6
US-08-619-812-8
Sequence 8, Application US/08619812
Patent No. 6100066
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: THEISEN, MICHAEL
APPLICANT: HARLAND, RICHARD J.
APPLICANT: RIOUX, CLEMENT R.
TITLE OF INVENTION: VACCINES FOR HAEMOPHILUS SOMNUS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,812
FILING DATE: 15-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/038,719
FILING DATE: 29-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000-0019.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 924 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-619-812-8

Query Match 63.6%; Score 49; DB 3; Length 924;
Best Local Similarity 58.3%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHSGEDDL 13
Db 747 NDLHSGKDDI 758

RESULT 7
US-07-908-253-2
Sequence 2, Application US/07908253
Patent No. 5534256
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: HARLAND, RICHARD J.
TITLE OF INVENTION: HAEMOPHILUS SOMNUS OUTER MEMBRANE

TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L. ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/908,253
FILING DATE: 19920702
CLASSIFICATION: 420
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000-0026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-908-253-2

Query Match 63.6%; Score 49; DB 1; Length 926;
Best Local Similarity 58.3%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHSGEGDDL 13
||:|:|:|:
Db 747 NDHLHGKGDDI 758

RESULT 8
US-08-455-970A-2
Sequence 2, Application US/08455970A
Patent No. 578155
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HOW P.A.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
TITLE OF INVENTION: CHIMERAS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,970A
FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992

ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-455-970A-2

Query Match 63.6%; Score 49; DB 1; Length 926;
Best Local Similarity 58.3%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHSGEGDDL 13
||:|:|:|:
Db 747 NDHLHGKGDDI 758

RESULT 9
US-08-387-156-6
Sequence 6, Application US/08387156
Patent No. 5723129
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HOW P.A.
TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,156
FILING DATE: 10-FEB-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-387-156-6

Query Match 63.6%; Score 49; DB 1; Length 926;
Best Local Similarity 58.3%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHSGEGDDL 13

Db 747 NDLLHGKGD1 758

RESULT 10

US-08-694-865-6
; Sequence 6, Application US/08694865
; Patent No. 5837268
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: MANN, JOHN G.
; TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS LLP
; STREET: 285 HAMILTON AVENUE, SUITE 200
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/694,865
; FILING DATE: 09-AUG-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 9001-0016.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)327-3400
; TELEFAX: (415)327-3231
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-694-865-6

Query Match 63.6%; Score 49; DB 2; Length 926;
Best Local Similarity 58.3%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHSGEGDDL 13

Db 747 NDLLHGKGD1 758

RESULT 11

US-08-878-748-6
; Sequence 6, Application US/08878748
; Patent No. 5969126
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: REDMOND, MARK J.
; APPLICANT: HUGHES, HOW P. A.
; TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 635 BRYANT STREET
; CITY: PALO ALTO

STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/878,748

FILING DATE: 19-JUN-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/387,156

FILING DATE: 10-FEB-1995

APPLICATION NUMBER: US 07/960,932

FILING DATE: 14-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/779,171

FILING DATE: 16-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 9001-0016.21

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 617-8999

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 926 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-878-748-6

Query Match 63.6%; Score 49; DB 2; Length 926;
Best Local Similarity 58.3%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHSGEGDDL 13

Db 747 NDLLHGKGD1 758

RESULT 12

US-08-535-837-2
; Sequence 2, Application US/08535837
; Patent No. 5985289
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: HARLAND, RICHARD J.
; TITLE OF INVENTION: HAEMOPHILUS SOMNUS OUTER MEMBRANE
; PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBERTA L. ROBINS
; STREET: 285 HAMILTON AVENUE, SUITE 200
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,837
; FILING DATE: 27-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.

REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0026.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-535-837-2

Query Match 63.6%; Score 49; DB 2; Length 926;
Best Local Similarity 58.3%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHSGEGDDL 13
||: ||: ||:
Db 747 NDHLHGKGDDI 758

RESULT 13
US-09-124-491-6
Sequence 6, Application US/09124491
Patent No. 6022960
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,491
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,865
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-124-491-6

Query Match 63.6%; Score 49; DB 3; Length 926;
Best Local Similarity 58.3%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHSGEGDDL 13
||: ||: ||:
Db 747 NDHLHGKGDDI 758

RESULT 14
5476657-3
Patent No. 5476657
APPLICANT: POTTER, ANDREW A.
TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA LEUKOTOXIN
COMPOSITIONS AND USES THEREOF
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/15,537
FILING DATE: 09-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 504,850
FILING DATE: 05-APR-1990
APPLICATION NUMBER: 335,018
FILING DATE: 07-APR-1989
SEQ ID NO: 3:
LENGTH: 926
5476657-3

Query Match 63.6%; Score 49; DB 6; Length 926;
Best Local Similarity 58.3%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIHSGEGDDL 13
||: ||: ||:
Db 747 NDHLHGKGDDI 758

RESULT 15
US-08-455-970A-12
Sequence 12, Application US/08455970A
Patent No. 5708155
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,970A
FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208

; REFERENCE/DOCKET NUMBER: 9001-0016.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-3400
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 936 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-455-970A-12

Query Match 63.6%; Score 49; DB 1; Length 936;
Best Local Similarity 58.3%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 NDIFHSGGDDL 13
||:|:|:|:
Db 747 NDLHGGKGDDI 758

Search completed: September 11, 2002, 08:59:26
Job time: 209 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 11, 2002, 08:57:17 ; Search time 22.74 Seconds

(without alignments)
1578.409 Million cell updates/sec

Title: US-09-884-696-2

Perfect score: 4646

Sequence: 1 MSNINVIKSNINQAGLNSTKS.....SSNALPITPTQPGIPLAPSV 927

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2334	50.2	953	LKAL_PASHA	P16535 Pasteurella
2	2332	50.2	953	LKAB_PASHA	P55123 Pasteurella
3	2310	49.7	947	LKTA_PASSP	P55123 Pasteurella
4	2256	48.6	953	LKTA_PASHA	P55116 Pasteurella
5	2240.5	48.2	956	RTA2_ACTPL	P15377 actinobacil
6	2236	48.1	955	LKAA_PASHA	P55117 Pasteurella
7	2218.5	47.8	956	HLVA_ACTSU	Q00951 actinobacil
8	1959.5	42.2	1052	RT32_ACTPL	P55130 actinobacil
9	1928	41.5	1049	RT31_ACTPL	P55130 actinobacil
10	1852.5	39.9	1024	HLVA_ECOLI	P08715 Escherichia
11	1849	39.8	1023	HLV1_ECOLI	P09883 Escherichia
12	1733.5	37.3	1023	RT12_ACTPL	P55129 actinobacil
13	1727	37.2	1023	RT11_ACTPL	P55128 actinobacil
14	1716.5	36.9	1050	LKTA_ACTAC	P16462 actinobacil
15	806	17.3	1706	CYAA_BORPE	P15318 bordetella
16	805.5	17.3	1705	CYAA_BORBR	P57506 bordetella
17	434	9.3	1829	FRPC_MEIMC	P55127 neisseria
18	432.5	9.3	1829	FRPC_MEIMB	Q9JYV5 neisseria m
19	416	9.0	1302	FRPA_NEIMB	Q9K0K9 neisseria m
20	403.5	8.7	1115	FRPA_NEIMC	P55126 neisseria m
21	190.5	4.1	1608	HLVA_SERMA	P15320 serratia ma
22	188.5	4.1	2869	RBP1_PLAVB	Q00798 plasmodium
23	183.5	3.9	1577	HLVA_PROMI	P16466 proteus mir
24	178.5	3.8	284	NODO_RHIV	P15728 rhizobium l
25	175.5	3.8	1228	SLAP_BACST	P35828 bacillus st
26	173.5	3.7	1520	SLAP_CAUCR	Q9P180 caulobacter
27	173	3.7	1520	RBP2_CHIMU	Q9P199 chlamydia m
28	171	3.7	1251	RBP2_PLAVB	Q00653 r outer mem
29	171	3.7	1656	OMPB_RICUA	Q00653 r outer mem
30	171	3.7	2249	OMPA_RICRI	P15137 rickettsia
31	170	3.6	491	ZAPA_PROMI	Q11137 proteus mir
32	165.5	3.6	1592	GTF2_STRDO	P27470 streptococ
33	165	3.6	479	PRTC_ERWCH	P16317 erwania chr

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	953 AA.
AC	LKAL_PASHA			
AC	P16535;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Leukotoxin from serotype A1.			
GN	LKTA.			
OS	Pasteurella haemolytica.			
OC	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;			
OC	Mannheimia.			
OX	NCBI_TaxID=75985;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-SEROTYPE A1:			
RX	MEDLINE=87306837; PubMed=3040588;			
RA	Lo R.Y.C., Strathdee C.A., Shewen P.E.;			
RT	"Nucleotide sequence of the leukotoxin genes of Pasteurella			
RT	haemolytica A1."			
RL	Infect. Immun. 55:1987-1996(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-SEROTYPE A1 / PHU101;			
RX	MEDLINE=89210283; PubMed=2707120;			
RA	Highlander S.K., Chidambaram M., Engler M.J., Weinstein G.M.;			
RT	"DNA sequence of the Pasteurella haemolytica leukotoxin gene			
RT	cluster."			
RL	DNA 8:15-28(1989).			
RN	[3]			
RP	SEQUENCE OF 884-953 FROM N.A.			
RC	STRAIN-SEROTYPE A1 / PHU101;			
RX	MEDLINE=90236888; PubMed=2185213;			
RA	Highlander S.K., Engler M.J., Weinstein G.M.;			
RT	"Secretion and expression of the Pasteurella haemolytica leukotoxin."			
RT	J. Bacteriol. 172:2343-2350(1990).			
CC	- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD			
CC	CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY			
CC	DEFINED.			
CC	- SUBCELLULAR LOCATION: Secreted.			
CC	- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING			
CC	CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC			
CC	ACTIVITY.			
CC	- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE			
CC	INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).			
CC	- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN			
CC	MODIFIED (BY SIMILARITY).			
CC	- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.			
CC	- This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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007162 erwania chr
09265 chlamydia p
P45508 escherichia
P34487 caenorhabd
Q16787 homo sapien
P33666 escherichia
P18177 clostrid
P23694 serratia ma
P52143 escherichia
Q9KRa3 r outer mem
P35827 campylobact
000174 drosophila

FT REPEAT 739 744 3.
 FT REPEAT 748 753 4.
 FT REPEAT 757 762 5.
 FT REPEAT 766 771 6.
 FT REPEAT 775 780 7.
 SQ SEQUENCE 947 AA; 101559 MW; 9744F06395FE5BED CRC64;

Query Match 49.7%; Score 2310; DB 1; Length 947;
 Best Local Similarity 50.1%; Pred. No. 1.8e-11;
 Matches 467; Conservative 173; Mismatches 252; Indels 40; Gaps 16;

QY 1 MSNIN- IKSNIQAGINST-----KSGIKNLVLAIPKD--YDPOKGTLLNDEIK 46
 DB 4 LANISTNKNLSQSLHTGSLNAGSLKAGAKKLLIYIPKDYSGRNGLODLVK 63
 QY 47 AADELGIARLAEPPNHTAKKSVTVNOFLSLTGTGAIASATKLEKLOKHSHTKLAKG 106
 DB 64 AAEDGIEVQREERNIGITAOISLSTIONILGFSRGVLSAPOLDKLOK--KISKA 120
 QY 107 LDVENIDRKLGKASNVSTLSSFLGTALAGIELDSLKKGDAPDALAKASIDLINELI 166
 DB 121 PDSSENVAKNLGNMOTLLSGISITIGSYMAGMDDEILKNGSELD-LAKAGLELTNLI 179
 QY 167 GNLSTOTTEAFSSOLAKLGSTISQARKFSNIGKLOLN-FSKTNLGLLEITGLSGI 225
 DB 180 ENIANSVOTLDFSEQISOLGFKLQNVKGLGTGLKKNFSGSKAGLGLLEVIGLSGA 239
 QY 226 SAGFALADKNATGKKVAAGFELSNOVIGNVKAISVYLORVAAGISTGCAVALITS 285
 DB 240 TAAVLADKNASTDRKVGAFELANOVGNITKAVSYLORVAAGISTGCAVALITS 299
 QY 286 SIMLAISPLAFNANADKFNHANALDEFAKQFRKFGYDGHLLAEYORGVTEASTLTS 345
 DB 300 TVALAISPLAFAGIADKFNNAKALSYAEKFKLGEBSGLAEYORGVTEASTLTS 359
 QY 346 TALGAVSAGVAAVAGSAGAPIALIVAGVTGLISGLEASQAMFESVANKLOKILEM 405
 DB 360 TALAISGVSAAGSAGLGAIALIVSGITGIIITLQYSQAMFEHVAANKHOKIDW 419
 QY 406 EKONGONFEDGYDSRYAAYLANNLKFLSELKLEAEARVAITQOARDNNGELAGIT 465
 DB 420 EKHNGKNTFENGYSRYADIQDNMRQLOANKELQARVIRITQOQDNNGINLAGIS 479
 QY 466 KLGERIKSKAYADAFFEDGKVVAGSNTLLDAKGTIIDISNGKTLQALHFTSPLLTAG 525
 DB 480 RIGEKVMSGKAYADAFFEEKLIKADTFVQLDASGVIINTSKSDNYKTOHILERTPLPBG 539
 QY 526 TESRELTNGKTSYINKLKFGRVKKMVOYDGEASSKLDPISKYIQRA-----ETEGTD 578
 DB 540 VERRERIQGTKEYITKILINRVDSWKITDGNSTFEDLTNNVORIGELDHADVTKY 599
 QY 579 EELGIYNAKAGNDPIVVGSGKNNDGGDHDHRYFYSKDGSGFNTVDTGSAEAGSYTN 638
 DB 600 ERTLIANLGDNDVFTIGGTEVEVDGKNLDKRYHSR-GDYCALITDANESVQSGYTK 658
 QY 639 RKVARGDIYHEVVKROETVYKRTETIQYRDYELRKVGYGYOSTDNLKSVEEYISQFND 698
 DB 659 RFVETKALHEVYATQSVLVGSSEKEIEYR-HSNNTQHGAYTTDPLKSVEEILGHSRD 717
 QY 699 VRKGSFNDIFHSGEDDLIDGAGDRLFGKGNRLSGDEBDDLIDGSGDDVYNGA 758
 DB 718 IFKGSKFDDAFHGGDGVNDIDGAGNDRLFGKGNRLSGDEBDDLIDGSGDDVYNGA 777
 QY 759 GNVYVIFRKGDDGNDLYDGNKDLAFADANISDIEMIERKEGIIYKRDHSGSINIPW 818
 DB 778 GNDILCTVKG-GNDSISDSGNDRLSFADSNLKDLFEKYNHMLM-TVWKEKVIQW 835
 QY 819 Y---TTSNLQNYQSNKTDHKTIPOLIGKDGSYTSDQIDKILQDKGVTGVSQELKLA 874
 DB 836 FREADYAKTVHNYQAT-ADERKIEIIGROGERITSKQIDELIEKRGK--KIDSELERIA 892
 QY 875 DENKSOKLSASDIAS-SLNKLVSMLFGRAN 905

DB 893 E--SSALLKESKFSASNSLNKLVSAGAFASSN 922

RESULT 4
 ID LKA3_PASHA STANDARD; PRT; 953 AA.
 AC P5116;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Leukotoxin from serotype T3.
 GN LKTA.
 OS Pasteurella haemolytica.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Mannheimia.
 OX NCBI_TaxID=75985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SEROTYPE T3;
 RX MEDLINE=94041617; PubMed=8225575;
 RA Burrows L.L., Lo R.Y.C., Olah-Winfield E.;
 RT "Molecular analysis of the leukotoxin determinants from Pasteurella
 haemolytica serotypes 1 to 16".
 RL Infect. Immun. 61:5001-5007(1993).
 CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
 CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
 CC DEFINED.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
 CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
 CC ACTIVITY.
 CC -1- INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
 CC -1- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
 CC MODIFIED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: U01216; AAB36691.1; -.
 CC HSSP: P02392; ICTP.
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003355; RTX_N.
 DR InterPro: IPR003995; Rkx.
 DR Pfam: PF00353; hemolysinCbind; 1.
 DR Pfam: PF02382; RTX; 1.
 DR PRINTS: PR00313; CABNDXGRP.
 DR PRINTS: PR01488; RTXTOXINA.
 DR PROSITE: PS00330; HEMOLYSIN_CALCIUM; 2.
 KW Hemolysis; toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
 KW Transmembrane; Lipoprotein; Palmitate.
 FT TRANSMEM 229 249
 FT TRANSMEM 297 318 POTENTIAL.
 FT TRANSMEM 381 401 POTENTIAL.
 FT DOMAIN 734 784 6 x REPEATS, GLY-RICH.
 FT REPEAT 734 739 1.
 FT REPEAT 743 748 2.
 FT REPEAT 752 757 3.
 FT REPEAT 761 766 4.
 FT REPEAT 770 775 5.
 FT REPEAT 779 784 6.
 SQ SEQUENCE 953 AA; 101948 MW; FDBDCE2FDC85FDF2 CRC64;

Query Match 48.6%; Score 2256; DB 1; Length 953;
 Best Local Similarity 48.7%; Pred. No. 1.1e-108;

Matches 463; Conservative 174; Mismatches 270; Indels 44; Gaps 17;

```

QY 5 NVKSNQA---GLN-----STKSGKMLYLAIRKD--YDQOKGTLNDFIKAA 48
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 10 NGRSTLTARGGGLNRAGOSLTAGOTLKNGVKKILYIRKDYDSGSGGLDILKAA 69
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 49 DELGIARLAEPPNTEFAKSVDFVNOFLSTOTGIAISATKLEKFLQKSTNKLAGLD 108
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 70 EELGIEYQKEGNDIAAQSISLTIONVLTGTERGYLSAPOLDKLQK---MKVGALG 126
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 109 SVENIDRKLKASNVLTSLSSFLGTALAGIELDSLKKGAAPDALAKASIDLINETGN 168
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 127 SSESIAQNFQAKTVLSGVOSILGSVLAGMDLDEAL-QNSDDQTLAKAGELTNLSIEN 185
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 169 LSGSTQTEAFSSQLAKGTSIOAKGFSNIGKNLQNL-NFSKTNLLEIITGLSGISA 227
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 186 IANSVOTLDAFSEQISQFSGKLNQVKGILGDKLNIGDKYKGLDHLVHISGLSGATA 245
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 228 GFALADNASTGKKVAAGFELSNQVGNVTKAISVYLAORVAAGLSTGTGAVALLTSSI 287
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 246 ALVYADADASTAKKVGAGFELANOVGNITKAVSYTLAORVAAKLSTGFPVALLASTV 305
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 288 MLALISPLAFMAADKFHMANALDEFAKQFRKFGYDGDHLAEYQGVGTIEASLTISTA 347
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 306 ALATISPLSFGIADKFPRAKSLFNRYABRFKKLGEYEGDLSLAEYQHTGTIDASVTAINTA 365
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 348 LGAVSAQVSAAGSANGAPALLVAGVTLGSLISLAKQAMPEASVANKQKILEMEK 407
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 366 LAAIAGGVSAAGSAAVSPALLVSGITGVITLQYSKQAMPEHVAANKHNKIVEMK 425
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 408 ONGONFEDGYDSRYAVALANLKLFLSELNKELEAEVRVIAITIOQRDNINIGELAGITKL 467
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 426 NNGSKATFENGQYDARYLANIADNKKFLNLNKEIARVIAITIOQDNDISNIGLAGISRL 485
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 468 GERIKSKAYADAPEDEKRYEAGSNITLDAKTGIIIDISNNGKATQALHFTSPLLAGTE 527
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 486 GEKVLGSKAYVDAPEEGOHKADKLVDLSAKGIIDVSNMGCAKTQIHLFPTPLPTEGE 545
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 528 SRELTGKGYSTINKLKGFKYKKNQVTDGEASSKLDKFSKYIQRVA-----ETEGDEI 580
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 546 KREHVQTKGYEYTKRLHINRVDSWQIKDGAASFTEDLTNVVQRIGVELDAENVIKTKET 605
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 581 GLIYNAKAGNDIDFVGOGKMNIDGSGDGHDRVYFSGKDGFGIYVDTGSATEAGSYTVNRK 640
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 606 KIYATLDDGDNDNVFVSGSTIEIDGEGEYDKVNHYSR-GNYGALITDAIKREPOGSYTVNRF 664
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 641 VARGDIYHEVVKROETKVKRTETIQYRDYELRKVGXYGOSTNMLKSVEEVYIGSQFNDVF 700
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 665 VESGKALHEVTSTHTALVGNREKEIEYR-HSNQNHAGYUUTKDTLKAVEELIGTSHNDIF 723
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 701 KGSFKNDFIHSBEGDDLDDGAGGDRFLFGGKGNDRLSGDEGDDLDDGSGDDVINGAGCN 760
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 724 KGSFKNDFAFGGGDDVDITDNGDNDRLFLFGGDDIIDDGNGDDPIDDGKGNHLLHGSGKV 783
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 761 DVYFFRGKDNLDLYDGTGDKLAFADANISDIIMIERTKEGIIKYRNDHSGSINIPRWY- 819
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 784 DIFVNRGDDGNDSTIESEGDKLSFSDSNLKDOLFKEKVNHNHIV-TYTKQEKVITIQWFR 842
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 820 ---ITSNLYQNSKNTDKHLEQILGDKSGYTSDDQDKLIDKKKDGTVITSQELKLADE 876
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 843 EAEFAKTIQNVATR-DKIEIEIIGNGERTISKYVDLLI--AKNGNKIAQSELTKVYVDN 899
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 877 NKSQKLSASDIASSLNTKLGSMALFGTANSVSSNALOPTIOPGIIAPSV 927
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 900 YQLLKYS-RDASNSLDKLISASAFISSND-SRNVL--ASPT-SMLDPSL 944
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

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DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE RTX-II toxin determinant A (APX-IIA) (Hemolysin IIA) (HLV-IIA)
GN APXIIA OR CLYIIA OR HLYIIA OR APPA OR CYTC.
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
   Actinobacillus.
OX NCBI_TaxID=715;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SEROTYPE 5;
RX MEDLINE=90126233; Pubmed=2693022;
RA Chang Y.-F., Young R., Struck D.K.;
RT "Cloning and characterization of a hemolysin gene from Actinobacillus
   (Haemophilus) pleuropneumoniae."
RL DNA 8:635-647(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ISOLATE CVI 13261 / SEROTYPE 9;
RX MEDLINE=92040145; Pubmed=1937809;
RA Smits M.A., Britaire J., Jansen R., Smith H.E., Kamp E.M.,
   Gielkens A.L.;
RT "Cytolysins of Actinobacillus pleuropneumoniae serotype 9."
RL Infect. Immun. 59:4497-4504(1991).
CC -I- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A.PLEUROPNEUMONIAE,
   WHICH SHOWS A WEAK HEMOLYTIC ACTIVITY AND IS MODERATELY CYTOTOXIC
   FOR ALVEOLAR MACROPHAGES AND NEUTROPHILS.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
   CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
   ACTIVITY (BY SIMILARITY).
CC -I- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
   INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -I- PTM: PALMITOYLATED BY APXIIIC. THE TOXIN ONLY BECOMES ACTIVE WHEN
   MODIFIED (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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   between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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   modified and this statement is not removed. Usage by and for commercial
   entities requires a license agreement (See http://www.isb.ch/announce/
   or send an email to license@isb.ch).
CC -----
DR EMBL; M30602; AAA87232.1; -.
DR EMBL; X61111; CAA43423.1; -.
DR PIR; B33389; B33389.
DR PIR; S18853; S18853.
DR InterPro; IPR001343; Hemlysn_Ca_bind.
DR InterPro; IPR003355; RTX_M.
DR InterPro; IPR003955; RTX_A.
DR Pfam; PF00353; hemolysinCaBind; 1.
DR Pfam; PF02382; RTX_1.
DR PRINTS; PR00313; CABNDNGRPT.
DR PRINTS; PR01488; RTXTOXINA.
DR PROSITE; PS00330; HEMOLYSIN_CALCIIUM; 1.
KW Hemolysins; Toxin; Cytolysins; Cytotoxins; Repeat; Calcium;
   Transmembrane; Lipoprotein; Palmitate.
FT TRANSMEM 233 256 POTENTIAL.
FT TRANSMEM 266 323 POTENTIAL.
FT TRANSMEM 361 406 POTENTIAL.
FT DOMAIN 719 787 8 X REPEATS, GLY-RICH.
FT REPEAT 719 724 1.
FT REPEAT 728 733 2.
FT REPEAT 737 742 3.
FT REPEAT 746 751 4.
FT REPEAT 755 760 5.
FT REPEAT 764 769 6.
FT REPEAT 773 778 7.
FT REPEAT 782 787 8.
SQ SEQUENCE 956 AA; 102531 MW; BDBCABBADEFLA641 CRC64;

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Query Match 48.2%; Score 2240.5; DB 1; Length 956;
 Best Local Similarity 47.8%; Pred. No. 7e-108;
 Matches 454; Conservative 188; Mismatches 254; Indels 53; Caps 15;

QY 1 MSNTNV--IKSNIAQGL-----NSTKSGKRLNYLAIRKDPDQ 36
 DB 1 MSKTTLSLKSLSLOOGLKNGKRLNQAQATTLKNGLTGTGSHLQNAKLLIYIPQGYDSG 60
 QY KGGTLNDFIKADELIGLARLAEPNHTETAKSVDTVNOPLSTOTGTIAISATKLEKPLQ 96
 DB 61 QGNVQDLYKRAANDLGIEVWEERSNDIAKTSPTDTCKILGFDRLGVLEAPOLDNLK 120
 QY KHSNNKLAKGIDSVENIDRKLGKASNVLTSSFLGTALACIELDLSLKDDADALAK 156
 DB 121 KNP--KIGNTLGSASSISQNIQKANTVYLGIOISILGVSGLVNNELLQNDPDLQLEAK 178
 QY 157 ASIDLINIIINLQSOTITAFSSQLAKGSTISOAKGFNIGNIKLQNL--NEKSTNIGL 215
 DB 179 AGLEITINELVGNLSSVQTVDAFAQISKLQSHLQNVGGLGSLSKLQNLDPDLGKASLGL 238
 QY 216 EITGLISGAGFALADKNASTGKKNVAGFELSNOVIGNYTKAISTVYLAQVAAIGLST 275
 DB 239 DIISGLISGASGLILAKKEASTEKKAAGVEFANOIIGNTKAVSSYIIAQVASSGLSS 298
 QY 276 TGAVALITSSIMLAISPLAFMAADKNNANALDEPAKQFRKGYDGDHLLAEYQGVG 335
 DB 299 TGPVALIATSTVALAVSPLESLFNAVDFEKQADLKISYERQKGLGYDGDRLADAFHRETG 358
 QY 336 TIEASITITSTALGAVSGVSAANVAGAPALVAVGVLISGLIEASKOAFEEVA 395
 DB 359 TIDSVITITINLALAISSGVAGASGLVAPALVAVGVLITLITLIEYSKOAFEEVA 418
 QY 396 NRLQGLILEWKEKONGQNYFPKGYDSRYAAYLANNLKFLSELNKELEAERYAIATQQRWD 455
 DB 419 NKVHDRIYEWEMEKH--NKNYFEGGYDSRHLADLDQNMKFLINLKEQLQERVALITQQRWD 477
 QY 456 NNIGGLAITLIGERIKSGKAYADAFAEDGKVEAGSNITTLDAKGIIDISNSNGKKTAL 515
 DB 478 NOIGGLAISRTDKISSGKAYADAFEEGQHQSYSSVQDLNKNKIIINISMTN--RKTQSY 536
 QY 516 HPTSLAGTESRRLNNGKYSYINKLFGKWKWOYTDGASSKLPLFSVYIOHVA--- 572
 DB 537 LFRPTLLPGEENRRRIQEGKNSYITTKLHQVRVSWYTTDGDASSVPTNVQRIAYKF 596
 QY 573 -----ETEGDELGLIVNAKAGNDIIFVQGGKMNIDGGDGHDRVYFSKDGEGNITVD 625
 DB 597 DDAGNIIESKDKR--IIANLGAGNDVNFVGSSTVIDGGDGHDRVHSR--GEYCALVID 652
 QY 626 GTSATFASSTYVNRKVAAGDIYHEVVKROETKVKRTETIQRYELKKGVGYSTQNL 685
 DB 653 ATALETGKSYKRVYVGSKALHETIATHQTNVGNREKIEKR--REDRPFHTGYVTQSL 711
 QY 686 KSVFVVISQFNDVFKSGKFNDFHSGEGDDLDDGAGDDRLFGGKNDRLSGEGDDL 745
 DB 712 KSVFVVISQFNDVFKSGKFNDFHSGEGDDLDDGAGDDRLFGGKNDRLSGEGDDL 771
 QY 746 DGGSGDVLNGAGADNYIIFRKGDNNTLYDGTGNDKLAFAFADANTSIDMIERTKEGIIYK 805
 DB 772 VGGTNDIISGKNDIYVHKTGCDNSITDSGQODKLAFSQVNLKDLFFKQVDSLEI- 830
 QY 806 RNDHSGSINIPRWY-----ITSMLQNYQSNKTDHKEIQLGKDGSTTSQDIDKLIQDKKD 861
 DB 831 INOKGEKVRIGNMWFLIEDLIASVANYKAT--NDRKIEEITIGKGERITSEYVDKLT--KEG 887
 QY 862 GTVITSQELKLADEKNSQKLSASDIASLKNLKVSGSMALFGANVSSN 910
 DB 888 NNQISAEALSKVYNDYNTSK--DROVNSNSLAKLISVGSFTSSSPFRNN 935

RESULT 6
 LKAA_PASHA STANDARD; PRT: 955 AA.
 ID LKAA_PASHA

AC P55117;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Leukotoxin from serotype T10.
 GN LKTA.
 OS Pasteurella haemolytica.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Mannheimia.
 OX NCBI_TaxID=75985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SEROTYPE T10;
 RX MEDLINE=96425875; PubMed=8828217;
 RA Madison F.A., Murray J., Davies R.C., Donachie W.;
 RT "Characterization of epitopes involved in the neutralization of
 RT Pasteurella haemolytica serotype A1 leukotoxin.";
 RL Microbiology 142:2499-2507(1996).
 CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
 CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
 CC DEFINED.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
 CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
 CC ACTIVITY.
 CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
 CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
 CC -1- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
 CC MODIFIED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
 CC -----
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 CC -----
 DR EMBL; Z26247; CAAB1206.1; -
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003355; RTX_N.
 DR InterPro: IPR003995; RTX_A.
 DR Pfam; PF00353; hemolysincbind; 1.
 DR Pfam; PF02382; RTX; 1.
 DR PRINTS; PR00313; CABNDNGRPT.
 DR PRINTS; PR01488; RTXTOXINA.
 DR PROSITE; PS00330; HEMOLYSIN_CALCIUM; 4.
 KW Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
 KW Transmembrane; Lipoprotein; Palmitate.
 FT TRANSMEM 299..319 POTENTIAL.
 FT TRANSMEM 361..381 POTENTIAL.
 FT TRANSMEM 383..403 POTENTIAL.
 FT DOMAIN 736..786 6 X REPEATS, GLY-RICH.
 FT REPEAT 736..741 1.
 FT REPEAT 745..750 2.
 FT REPEAT 754..759 3.
 FT REPEAT 763..768 4.
 FT REPEAT 772..777 5.
 FT REPEAT 781..786 6.
 SQ SEQUENCE 955 AA; 102187 MW; B60F2DB8168EBCAF CRC64;

Query Match 48.1%; Score 2236; DB 1; Length 955;
 Best Local Similarity 48.2%; Pred. No. 1.2e-107;
 Matches 458; Conservative 178; Mismatches 271; Indels 44; Caps 17;
 QY 5 NVKSNIAQGL-----STKSGKRLNYLAIRPD--YDQKGTINDFIKAA 48
 DB 12 NGIRSTLTATRGGLNRAQSLQAGQYTLKNGAKKIIYIPDYVYDGGSGGLDILVAAA 71
 QY 49 DELGIARLAEPNHTETAKSVDTVNOPLSTOTGTIAISATKLEKLOKHSNNKLAKGLD 108

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Db 72 EELGVEQKEEGNDIAKQAGTSLGTLQNVLTGERGIVLSAPOLDKLLQK---NKVGQALG 128
Qy 109 SVENDIRKLGKASNVLTSSSELTGALAEIQLDLSIKKDAAPDALAKSIDLINITGN 168
Db 129 SSESTAQNESQAKTYLISVQSGNSRVLVLAQMDLEAL-QNESQDLTLAKAGLELTNSLIN 187
Qy 169 LQSOTITAEFSSQLAKLTISQAKFGSNIGKQNLQNL-NFSKTNLGLTIGLISGISA 227
Db 188 IANSVOTLDAFSEQJISQFSKIQNLQNGKLGALGDLKLNIGGLDKAGLGLVKKSLSGARA 247
Qy 228 GFALADKNASTGKVAAGFELSNOVIGNVTKAISSVYLAQRYAAGLSTTGAAVALITSSI 287
Db 248 ALVLADKADSTAKKYQAGELANQVYGNITTKAVSSYILAQRYAAGLSTTGPAALASTIV 307
Qy 288 MLASPLAMNAADKFNHNAALDEPAKQKFGYDGDHLLAEQRCVGTLEASTITISA 347
Db 308 AVAISPLSLAGIADKFRKAKSLKLENAERPKKLGEGSDSLAEQHTGTIDLSVAIINFA 367
Qy 348 LGAVSAGVAAVAGSVAVAPIALVAGVTGLISGLEAKSQAMFESVANRLQKLEWEMK 407
Db 368 LLAINGVSAAAAGSVVAPIALVSGITGVISTIQYKQAMFEHVAKINKKIYEMEK 427
Qy 408 QNGGQNYFDKYDSRYAAVLANLKFLELSENLKLEAERYIAITQQRDNNGELAGITKL 467
Db 428 NNGGKRYFENGYDARYLANLQDNMKFLNLNKEQAEVYIAITQOQWDSNIGLAGISRL 487
Qy 468 GERIKSGKRYADAFEDGKRYEAGSNITLDAKGTIDISNSNGKKYQALFTSLTACTE 527
Db 488 GKRVYLSGKRYAVAFEGQHLKADKLQVLDASGIIIDVTMTGKQHLIFRPLPLPGTE 547
Qy 528 SRERLNGKSYIYNKLFGRVKNQVYTDGEASSKIDFESKYIORVA-----ETEGTDEL 580
Db 548 KREPVOTGKRYEYITKLHINRVDSWQIKDAASPTDLTVNQYRIGVELDHAENVITKET 607
Qy 581 GLIVNAKAGNDIDFVGQGMNIDGGDHRVYFKDGFENITVDGTSATFAGSYTVNRK 640
Db 608 KIVATLGDSDDDVFWVSGSTTEIDGEGGYDRVHYSR-GNYGALLTIDATKEEQSYTVNRF 666
Qy 641 VARGDIEHVYVKRQETKVKRFTETIOYRDYELRKVGYGOSTDNKLSVEEVGSGQNDVF 700
Db 667 VESGKALHGTSTHTALVNNREKIEYR-HSNNOHHAGYTTKDTLAAVEIIGTSHNDIF 725
Qy 701 KGSFENDIFHSEGDLDLDGAGDDRLFGGKNDRLSGDEGDDLDLGGSGDDVNLNGAGN 760
Db 726 KGSFENDAFNGGQVDTIDGNGDNDRLFGGKDDIIDGNGDGFIDGGKNDLHGGKGD 785
Qy 761 DVIYIFKGGGNDTLIDGTGNDKLAFFADANISDMIRTEGIIYKRNDSGSINIPRWY- 819
Db 786 DIFVHROGGGNDISITESEGNDKLSFSDSNLKDLPFEKVHMHVLI-TNTRQEKVTTIONWFR 844
Qy 820 ---ITSNLQNYOSNKTDHIEQIDGKDSYITSDDQIDKILQDKKQDVTYTSQELKLADE 876
Db 845 EAEFAKTIONVAYTR-DDKIEIIGONGERITTSKQVDEILE--KGNGKLAQSELIVVDN 901
Qy 877 NKSQKLSASDIASLNKLGVSMALFETANSVSSNALQPIPTQOGLIAPSV 927
Db 902 YQLLAKTS-RDASNSLDKLLSSASAFITSSND-SRNVL---ASPT-SMLDPSL 946
```

```
RESULT 7
HLVA_ACTSU
ID HLVA_ACTSU STANDARD: PR7: 956 AA.
AC 000951:
DT 01-APR-1993 (rel. 25, Created)
DT 01-APR-1993 (rel. 25, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE Hemolysin (Cytolysin II) (Cly-IIA) (Hly-IIA) (CYTC) (APPA) .
GN APPA OR CLYIIA OR HLYIIA OR CYTC.
OS Actinobacillus suis.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Actinobacillus.
OX NCBI_TaxID=716;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN=3714:
RX MEDLINE=92267623; PubMed=1587585;
RA Burrows L., Lo R.Y.;
RT "Molecular characterization of an RTX toxin determinant from
RT Actinobacillus suis.";
RL Infect. Immun. 60:2166-2173(1992).
CC -!- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A.SUIS. MIGHT BE A
CC SECRETED CYTOTOXIN, POSSIBLY THE EXTRACELLULAR HEMOLYSIN.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCULIN, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.
CC -!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE TOXIN (BY SIMILARITY).
CC -!- PFM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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CC -----
DR EMBL: M90440; AAA21918.1; -.
DR InterPro: IPR001343; Hemolysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR InterPro: IPR003995; RtxA.
DR Pfam: PF00353; hemolysinCbind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CAEDNCRPT.
DR PRINTS: PR01488; RTXTOXINA.
DR PROSITE: PS00330; HEMOLYSIN-CALCIUM; 1.
KW Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
KW Transmembrane; Lipoprotein; Palmitate.
FT TRANSMEM 238 254 POTENTIAL.
FT TRANSMEM 302 320 POTENTIAL.
FT TRANSMEM 383 406 POTENTIAL.
FT DOMAIN 719 799 9 X REPEATS, GLY-RICH.
FT REPEAT 719 724 1.
FT REPEAT 728 733 2.
FT REPEAT 737 742 3.
FT REPEAT 746 751 4.
FT REPEAT 755 760 5.
FT REPEAT 764 769 6.
FT REPEAT 773 778 7.
FT REPEAT 782 787 8.
FT REPEAT 794 799 9.
SQ SEQUENCE 956 AA; 102453 MW; 3415FPI7ADDD4365 CAC64;

Query Match 47.8%; Score 2218.5; DB 1; Length 956;
Best Local Similarity 47.5%; Pred. No. 9.4e-107;
Matches 451; Conservative 188; Mismatches 257; Indels 53; Gaps 15;
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QY 166 IGNLSOSTOTIEAFSSOLAKLSTISOAKGFSNIGKNLONL---FSKTNLGLTITGL 222
Db 197 VSNIAKGTITDAFTTQIOENFKLVENAGLGCGVGRQLOLNGSALSGLGLDITISLL 256
QY 223 SGISAGFALADRNASTGGKVAAGFELSNOVIGNVTKAISVYLAORVAAGLSTTGAVAL 282
Db 257 SGVTASFAFLANKNASTSTKVAAGFELSNOVIGITKVAVSYLLAQRLAAGLSTTGAVAL 316
QY 283 ITSSITLAIPLAFNMAADPFHNAALDEFKAKOFRFGYDGHLLAEYRGVCTEASLT 342
Db 317 IASSISLAISPLAFNADNFNRKSEIGFAERFKLGGDKLSEFYHAGTIDASTIT 376
QY 343 TSTSLAGVAGVAAVSAVGAFTALVAGVTGLISITLSEASQAMESVAVNRLOGKI 402
Db 377 TISTALSAIAGTAASAGALVGAFTLLVGTITGLISITLSEKOPMLDHYASKGNKI 436
QY 403 LEMEKONGQNYFDKGYDSRYAAYLANNLKFLSELNKELEARVJAITQORMDNIGELA 462
Db 437 DEMEKKY-GKNYFENGYDARHKAFLFEDSFLLSFNKQYETBRAVLITQORMDYIGELA 495
QY 463 GITKGERKSKATADAEDGKVEAG---SNTTLAKTGIIDISNNGKKTQALHT 518
Db 496 GITGAGDKLSSGKAYVYDEQKLEKPPDSKVVFDETKGEIDISNS--QTSTLKFV 553
QY 519 SPLNAGTESRRLNFKKSYINKLFGKRNMOVTDG--EASSKLDKFKVIOI----- 570
Db 554 TPLLPPTESRERTQGTGKYEITKLKLVKCKDKM-VYNGVKDGAVYDYNLQHAHISS 612
QY 571 VAETEGTDEIGLIVAKAGNDIDFVGQKMNIDGGDGHDRVEYSKDGFGNITVDGTSAT 630
Db 613 VARGEERYREVRILVSHLGNNGNDKVFPLAAGSAEIHAGEGHVVYYDKT-DTGLLVIDGTAKT 671
QY 631 EAGSTTVANKVARG-DIYIEVYKROETKVKRTETIQYDYELKRYG-YGYOSTDNLKRY 688
Db 672 EGRGRSVTRELGAATKILAEVIRKOKSAVGKREETLEYDYELTOSGNSNLKAHDLHSV 731
QY 689 EEVIGSOFNDVFKSGFNDFHSGEGDDLDDGAGDRLFGGKGNRLSGDEG----- 742
Db 732 EETIGSNQDERFKSGFRIFIGAGDGDLLNGNDGDLITGDKGNDELGDNGNDLYCG 791
QY 743 -----DLDDGSGSDV 753
Db 792 EGNDKLLGNGNNYLSGGDGNDELQVLGNGFVNLRGKGDKDLKYGSSGDDLDDGCGNXY 851
QY 754 LMGAGNDVYITRKGDGNDLTLD---GTGNDKLAIFADANISIMERTKEGIIIVKRNDS 810
Db 852 LEGCGGSDFYVYRSTSGNHTIYDQKSSDLKLYLSDFSFDRLLVEKVDNVLRSNESS 911
QY 811 ---GSINIPRWYITSNLQVYOSNKTDKTEOLLKDGSYITSQDIKIIDKKDGVITS 867
Db 912 HNNGVLTITKDF-----KEGNKYNHKTETQIVDKNGKRLTAMENLGTYFRKNAPKADNLIN 964
QY 868 QELKLADENKSOQLASDIASLNLKLVGSMALFGTA 904
Db 965 YATKE--DQNES---NLSSIKTELSKIITNAGNFGVA 996

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RESULT 9
RT31_ACTPL STANDARD: PRT: 1049 AA.
AC P55130:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE RTX-III toxin determinant A from serotype 2 (APX-IIIA) (Cytolysin
  IIA) (CLV-IIIA).
DE APXIIIA OR CLVIIIA OR RTX OR PTXA.
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Actinobacillus.
OX NCBI_TaxID=715;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN-SEROTYPE 2;
RX MEDLINE-93263992; PubMed-8494611;
RA Chang Y.-F., Shi J., Ma D.-P., Shu S.J., Lein D.H.;
RT "Molecular analysis of the Actinobacillus pleuropneumoniae RTX
  toxin-III gene cluster.";
RL DNA Cell Biol. 12:351-362(1993).
RN [2]
RP SEQUENCE OF 828-1049 FROM N.A.
RC STRAIN-1536 / SEROTYPE 2;
RX MEDLINE-95012630; PubMed-7927703;
RA Jansen R., Briatte J., van Geel A.B.M., Kamp E.M., Gielkens A.L.J.,
  Smits M.A.;
RT "Genetic map of the Actinobacillus pleuropneumoniae RTX-toxin (apx)
  operon: characterization of the AprXII operons.";
RL Infect. Immun. 62:4411-4418(1994).
CC -I- FUNCTION: DOES NOT HAVE HEMOLYTIC ACTIVITY BUT SHOWS A STRONG
  CYTOTOXICITY TOWARDS ALVEOLAR MACROPHAGES AND NEUTROPHILS.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
  CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
  ACTIVITY (BY SIMILARITY).
CC -I- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
  INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -I- PTM: PALMITOYLATED BY APXIII. THE TOXIN ONLY BECOMES ACTIVE WHEN
  MODIFIED (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
CC -----
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CC -----
DR EMBL, L12145; AAA1924.1;
DR EMBL, X80056; CAB37652.1; ALT_SEQ.
DR InterPro: IPR001343; Hemlyan_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR InterPro: IPR003995; RTX_A.
DR Pfam: PF00353; hemolysinCbind; 2.
DR PRINTS: PR00313; CABDNGRPT.
DR PRINTS: PR01488; RTXTOXINA.
DR PROSITE: PS00330; HEMOLYSIN_CALCIUM; 3.
KW Toxin; Cytolysin; Cytotoxin; Repeat; Calcium; Transmembrane;
KW Lipoprotein; Palmitate.
FT TRANSMEM 154 170 POTENTIAL.
FT TRANSMEM 315 331 POTENTIAL.
FT TRANSMEM 397 413 POTENTIAL.
FT DOMAIN 753 858 11 X REPEATS, GLY-RICH.
FT REPEAT 753 758 1.
FT REPEAT 762 767 2.
FT REPEAT 771 776 3.
FT REPEAT 780 785 4.
FT REPEAT 789 794 5.
FT REPEAT 798 803 6.
FT REPEAT 807 812 7.
FT REPEAT 826 831 8.
FT REPEAT 835 840 9.
FT REPEAT 844 849 10.
FT REPEAT 853 858 11.
SQ SEQUENCE 1049 AA; 112491 MW; F99846BFD45CE72 CRC64;

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Query Match

Best Local Similarity 43.1%; Score 1928; DB 1; Length 1049;

Matches 429; Conservative 152; Mismatches 295; Indels 120; Gaps 21;

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QY 8 KSNIAQNLNSTRSGK-----NLVLAIPKDYDPOKGGTLNDFI 45
Db 19 KRQVKKGYDVTNKGIDVGSQAKLQALAGKAVQKGNKLVIVIPREYDGSVGNCFDLV 78

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QY 46 KADELGIARLAEPNHTETAKSVDTVNOFLSTOTGIATSATKLEFLQKHSNTKLAK 105
DB 79 KAAEELGIQVYVNNENLEVAHKSLSGTADQFLTLEAPOLDLQKHSXSNV 138
QY 106 GLDSVENIDRLKASNAVSTLSSFLGTALGIELDSIKKGDAPADAKASIDLINEL 165
DB 139 GSSSTGDANS-KLASQTIISGIQVLTGVLGINENELISGSGLE-LAERGVSLSLE 196
QY 166 IGNSOSTOTTEAPSSQIAKLGSTISQAKGFSNIGKLNQIN--FSKTNLGLIITGL 222
DB 197 VSNIAKGTITIDAFETQIQNGKLAENAKGLGVCORQONISGSLXSTKGLDIISLL 256
QY 223 SGISAGFLAKNASTGCKKVAAGFELSNOVIGNTKAISSVLAORVAAGSTTGAVAA 282
DB 257 SGVTRSEFLRNKNASTSKVAAGFELSNOVIGITKVAASYILQRLVAGLSTGPAAL 316
QY 283 ITSSIMLAISPLAFMNADEFNHNALDEFKOFKFGYDDDLAEQORVGTIEAST 342
DB 317 IASSISLAISPLAFLRVADNENRSKEIGEFARFKLGYDDDKLSEYHEAGTIDAST 376
QY 343 TISALGAVSAGVAAVAVAPIALVAGVTGLISGLLEASKQAFESVANRLQKI 402
DB 377 TISTALSAIAGTAASAGALVAPITLVTGILGILGILEFSKQPLDHAASKIKKI 436
QY 403 LEWEKONGGONYFPKGYDSRYAALIANLKLSELNKELEARIATIQORWNNIGELA 462
DB 437 DEMEKTY GKNYFENGIDARKAFLEDSFLLSSBNKQYETERAVLTIQORWDEVIGELA 495
QY 463 GITRLGERIKSGAVADAFEDGKKEVAG---SNITLDKAGIDISNSNKKTOALHFT 518
DB 496 GITKKGKLSGKAVVDYFQSGKLEKKPDPFSKVPPTGGEIDISNS--QTSILKLFV 553
QY 519 SPLLTAGTESERLTNGKYSTINKIKFGRVKNMOVTDG--EASSKLFESKVIQR----- 570
DB 554 TPLLTPTGESREPTQTKYEVYITKLIVYKGDKM--VNVGNKDKGAVYDTNLQHAHSS 612
QY 571 VAHEGTDELGLYNANAGNDIFVGGCKMIDGGDGHDRFYSGKDGFGNITVDGTSAT 630
DB 613 VARBEYREVVLVSHLNGNDKVLGASAEIHAGEGDVYVYKPT-DTGLLVTDGTVAT 671
QY 631 EAGSYTVNRKVAARG-DIYHEVYKROETPVRKRTETIQYRDYELRKVG-YGYOSTDNLKSY 688
DB 672 EQRGYSYTRBELSGATKILREVINKQKAVAGREFTLEVRDELQVSGSNLKADELHAY 731
QY 689 FEVIGSOPNDYFKSGSKENDIFHSEGGDDLDCGAGDDRLFCGKGNDRISGD----- 739
DB 732 EE-IGSNQORDEFKSGFRDIFHGADGDDLNGNDGDILYDKGNDELRCGNDQLYGG 790
QY 740 EGD-----DILLDGGSGDDV 753
DB 791 EGDKLLGNGNNTLSGGDGNDELQVLANGFNVLRGKGDDKLYGSSGSDLLDGGEGNDY 850
QY 754 LMGAGNDVYIFRKGDGNDTLTD--GTGNDKLAFAADANISDIMIERTKEGIYK--RND 808
DB 851 LEGDGDSEFYVYRSTGSHHTIYDQKASDSKLYLSDLSFNILVKNRNDLFEERSNNS 910
QY 809 HSGSINIPRWYITSNLQYNSKTDHKIEQIGKDGSTISDQIDKILQDKKDGTVITSQ 868
DB 911 NSGVLTJTKDWEKGNSTY-----HKIEQIVDKNGRKLITNGLNNEHHD---TQOASS 959
QY 869 ELKKLADENSKOKLASDIASSLKLKLGSMALFETA 904
DB 960 LKNVTOEONESNLS--LKTELCKITTMGNFGVA 993

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DE Hemolysin, plasmid.
GN HTYA.
OS Escherichia coli.
OC Plasmid Incir2 PHUY152.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Hess J., Wels W., Vogel M., Goebel W.;
RT "Nucleotide sequence of a plasmid-encoded hemolysin determinant and
its comparison with a corresponding chromosomal hemolysin sequence.";
RL FEMS Microbiol. Lett. 34:1-11(1986).
RN [2]
RP PALMITOYLATION OF LYS-564 AND LYS-690.
RX MEDLINE=9509325; PubMed=7801126;
RA Stanley P., Packman L.C., Koronakis V., Hughes C.;
RT "Fatty acylation of two internal lysine residues required for the
toxic activity of Escherichia coli hemolysin.";
RL Science 266:1992-1996(1994).
RN [3]
RP PALMITOYLATION OF LYS-564 AND LYS-690.
RX MEDLINE=96404790; PubMed=8808931;
RA Ludwig A., Garcia F., Bauer S., Jarchau T., Benz R., Hoppe J.,
RA Goebel W.;
RT "Analysis of the in vivo activation of hemolysin (HTYA) from
Escherichia coli.";
RL J. Bacteriol. 178:5422-5430(1996).
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
DEFINED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
ACTIVITY.
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
INVOLVED IN PORE FORMATION BY THE CYTOTOXIN.
CC -1- PTM: PALMITOYLATED BY HTYC. THE TOXIN ONLY BECOMES ACTIVE WHEN
MODIFIED.
CC -1- DISEASE: THE HEMOLYSIN OF E. COLI IS PRODUCED PREDOMINANTLY BY
STRAINS CAUSING EXTRAINTestinal INFECTIONS, SUCH AS THOSE OF THE
URINARY TRACT.
CC -1- SIMILARITY: BELONGS TO THE RTX PROCAROTIC TOXIN FAMILY.
CC
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or send an email to license@isb-sib.ch).
CC
DR EMBL: M14107; AAA98233.1; -.
DR InterPro: IPR001343; HemLysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR InterPro: IPR003995; RtxA.
DR Pfam: PF00353; hemolysincbind; 2.
DR Pfam: PF02362; RTX_1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PRINTS: PR01488; RTXTOXINA.
DR PROSITE: PS00330; HEMOLYSIN_CALCIIUM; 4.
KW Hemolysin; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
KW Transmembrane; Lipoprotein; Palmitate; Plasmid.
FT TRANSMEM 238 260
FT TRANSMEM 268 327
FT TRANSMEM 365 411
FT TRANSMEM 470 511
FT DOMAIN 724 870
FT REPEAT 724 729
FT REPEAT 724 729
FT REPEAT 733 738
FT REPEAT 742 747
FT REPEAT 751 756
FT REPEAT 760 765
FT REPEAT 769 774

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FT REPEAT 778 783 7.
 FT REPEAT 787 792 8.
 FT REPEAT 796 801 9.
 FT REPEAT 807 812 10.
 FT REPEAT 817 822 11.
 FT REPEAT 826 831 12.
 FT REPEAT 835 840 13.
 FT REPEAT 844 849 14.
 FT REPEAT 856 861 15.
 FT REPEAT 865 870 16.
 FT LIPID 564 564 PALMITATE.
 FT LIPID 690 690 PALMITATE.
 SQ SEQUENCE 1024 AA; 110201 MW; 83944917F76C945B CRC64;

Query Match 39.9%; Score 1852.5; DB 1; Length 1024;
 Best Local Similarity 41.5%; Pred. No. 6,6e-88;
 Matches 426; Conservative 154; Mismatches 307; Indels 139; Gaps 24;

QY 7 IKSNIQAGL-----NSTKSGLK-----NLVLAIPRDYDPOKGGTLNDF 44
 DB 9 IKSTLOSASOAAANKLHSGQSTKDALKKAEDTRNAGNRLILIRPDYKGO-GSSLNDL 67
 QY 45 IKADELGIARLAEPNHTETAKSVYVNOFLSTOTGIAISATKLEKFLQKH--STNK 102
 DB 68 VRTADELGEIVQYDEKNGTAITQVGFATAKLGITERGVITAPOLDKLQYKQAGNI 127
 QY 103 LAKGLDSVENIDRLKAKASNVISTLSSFLGTALAGIELDSLK---GDAFDALAKAS 158
 DB 128 LGGG---AENIGDNLCKAGIISTPQNFILGTALSSMKIDELIKKQKSGVSSSELAKAS 184
 QY 159 IDLINEILGNLSQTOTIEAFSSQLAKIGSTISQAKGFSNGKLNUL-NFSKTNIGLEI 217
 DB 185 IELINQVDTVASLNNVNSFSQQLNTLGSVSLNTHLNGVGNKLDLPLNDIGAGLDT 244
 QY 218 ITGLISGISAGFALADKNASTGKVAAGELNOVIGNYKAISVLAQRYAGLSTTG 277
 DB 245 VSGIISAISAFILSNADOTRTKAAAGVELTKVLGNNGKIGSQYIIQRAAGLSTSA 304
 QY 278 AVALITSSIMLAISPLAFMAADKFNHANALEDFAKORFKFGYDGDHLIAEYQRYGVTI 337
 DB 305 AAAGLASAVTLAISPLSFLSIADKFRANKIEYQRFKILGYDDSLAFAFKETGAI 364
 QY 338 EASLTITISALGAVSAGVSAAGAVGAPIALLVAGVYGLISGILEASQAMFESVANR 397
 DB 365 DASLTITISVLAIVSSGISAATTSVAGAVSALVGAIVGIIISGILEASQAMFESVANR 424
 QY 398 LQKILEMEKONGQVYFDKGYDRYAAYLANMLKELSELKLEAEARYAIVTQQRDNN 457
 DB 425 MADVIAMWEKKH-GKNYFENGIDARHAAPLEDNFKILSOYKESYVERSVLITQOHMDTL 483
 QY 458 IGLAICITKGERIKSGKAYADAEPDGKAYEAGSN---ITLDAKGIIDISNSNGKKTQ 513
 DB 484 IGLAVTNGDKTSLGKSYIDYEKGKRLKXDEFQKQVDFPLKGNIDLSDS--KSSP 541
 QY 514 ALHFTSPLLTAGTRESREBLNKGYSYINKLKFGRYVKNMOTYD-GEASSKIDPEKVIQRYA 572
 DB 542 LKFEVPLPLTPEEIRERQSGEYETITELVKGVDKMTYKGVODGAVYDYSNLIQHAS 601
 QY 573 ETEGT-DEIGLIYNAKAGNDLIFVGGQKNIDGGDGHDRFYFSK-GGFGFNIVDSTAS 630
 DB 602 VGNNOYREIRIESHLDGDDKQVFLSAGSANIYAGKHDVYVYKDTGTG--LTIIDETKAT 659
 QY 631 EAGSYVNRKVARGD--IYHEVVKROETVYKRTETIYQRYDELKRY-GYGYOSTDNLKS 667
 DB 660 EAGNYVTR-VLEGDVYKVLQEVVKEQEVSGKTEKTOYRSYEFTHINGKNLLETNLYS 718
 QY 688 VEEVISQFNDVFKSGFNDIHFSGEGDDLLOCGAGDDR-----726
 DB 719 VEEIIGTTRADKFFGSKFTDIFHGADGDLISGNDGNDRLYGDGKMDTSLSGGDDQLYG 778
 QY 727 -----LFGGKGNDRLSGEGDDLLOCGAGS 750
 |||||

DB 779 GDCNDKLIAGVAGNNYILNGDGDDEFOYQGNLSLAKNVLFSGKGNDKLYGSEGADLLDGE 838
 QY 751 DDVLNGAGNDVYIFRKQDNDPLDYDTG-NDKLAFPADAMISIMIERTEGIIYKRD- 808
 DB 839 DDLKGGYGDYIRYLSGYHHIIDDGKEDKLSLADIDFROVAFREKNDLIMTKGEG 898
 QY 809 -----HSGSINIPRWITNSLQYOSKNTDHHKIEQLIGDGYTSQDQIDKILQDK-- 860
 DB 899 NVLSIGHKNQITFRNMF-----EKESGDINHEEQIFDKSGRITTPDSLKLALFYQQRN 953
 QY 861 -----DGVYITSQ-----ELKKLADENKSOKLSASDIASSLNKLVSMALEFGT 903
 DB 954 NKASYVGNADALAVSGQDNLPLNIEISKIISAAGSPDYKKEERTAAISLQSGNASDFSY 1013
 QY 904 A-NSVS 908
 DB 1014 GRNSIT 1019
 RESULT 11
 HLX1_ECOLI STANDARD; PRT; 1023 AA.
 ID HLX1_ECOLI
 AC P09983;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Hemolysin, chromosomal.
 GN HLX1.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=J96 / SEROTYPE O4;
 RA MEDLINE=85234404; PubMed=3891743;
 RX Felmele T., Pellett S., Welch R.A.;
 RT "Nucleotide sequence of an Escherichia coli chromosomal hemolysin.";
 RL J. Bacteriol. 163:94-105(1985).
 RN (2)
 RP SEQUENCE OF 1-44 FROM N.A.
 RC STRAIN=2001;
 RX MEDLINE=85258115; PubMed=3894051;
 RA Nicoud J.-M., Mackman N., Gray L., Holland I.B.;
 RT "Characterisation of HlyC and mechanism of activation and secretion
 of hemolysin from E. coli 2001.";
 RL FEBS Lett. 187:339-344(1985).
 CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
 CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
 DEFINED.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
 CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
 ACTIVITY.
 CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
 INVOLVED IN PORE FORMATION BY THE CYTOTOXIN.
 CC -1- PTM: PALMITOYLATED BY HLYC. THE TOXIN ONLY BECOMES ACTIVE WHEN
 MODIFIED.
 CC -1- DISEASE: THE HEMOLYSIN OF E.COLI IS PRODUCED PREDOMINANTLY BY
 STRAINS CAUSING EXTRAINTestinal INFECTIONS, SUCH AS THOSE OF THE
 URINARY TRACT.
 CC -1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC EMBL: M10133; AAA23975.1; -
 CC EMBL: X02768; CAA26546.1; -

DR PIR; A24433; LEECA.
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003355; RTX_N.
 DR InterPro: IPR003995; RTX_A.
 DR Pfam: PF00353; hemolysincabind; 2.
 DR Pfam: PF02382; RTX_1.
 DR PRINTS; PRO0313; CABNDNGRPT.
 DR PRINTS; PRO1488; RTXTOXIN.
 DR PROSITE; PS00330; HEMOLYSIN_CALCITON; 4.
 DR Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
 KW Transmembrane; Lipoprotein; Palmitate.
 FT TRANSMEM 237 259 POTENTIAL.
 FT TRANSMEM 267 326 POTENTIAL.
 FT TRANSMEM 364 410 POTENTIAL.
 FT DOMAIN 723 869 16 X REPEATS, GLY-RICH.
 FT REPEAT 723 728 1.
 FT REPEAT 732 737 2.
 FT REPEAT 741 746 3.
 FT REPEAT 750 755 4.
 FT REPEAT 759 764 5.
 FT REPEAT 768 773 6.
 FT REPEAT 777 782 7.
 FT REPEAT 786 791 8.
 FT REPEAT 795 800 9.
 FT REPEAT 806 812 10.
 FT REPEAT 816 821 11.
 FT REPEAT 825 830 12.
 FT REPEAT 834 839 13.
 FT REPEAT 843 848 14.
 FT REPEAT 855 860 15.
 FT REPEAT 864 869 16.
 FT LIPID 563 563 PALMITATE (BY SIMILARITY).
 FT LIPID 689 689 PALMITATE (BY SIMILARITY).
 FT VARIANT 6 A->T (IN STRAIN 2001).
 SO SEQUENCE 1023 AA; 109867 MW; 196D5C0A9A28B54D CRC64;

Query Match 39.8%; Score 1849; DB 1; Length 1023;
 Best Local Similarity 41.7%; Pred. No. 9.9e-88;
 Matches 429; Conservative 154; Mismatches 306; Indels 140; Gaps 25;

QY 7 IKSNTIAGL-----NSTKSGLK-----NLYLAPKRYDPQKGTINDF 44
 DB 9 IKSSTOSAKOSANKLHSGSTKDALKKAAQOTRNAGNRLLLLPKRYKGO-GSLNDL 67
 QY 45 IKADELGTARLAEPENHETAKSVDTVNOPLSTQTGTIAISATKLEKFLQKH--STNK 102
 DB 68 VRADELGLIEVOYDEKNGTAITKQVGTAKFKLIGTERGVITFAPODLKLOKQKAGK 127
 QY 103 LAKGLDSVENIDRKLGKASNVLSSTFLGTALAGIELDSLKK---GDAAPDALAKS 158
 DB 128 LG---GSANIGDNLGKASVLTQNFGLTALSSMKIDELKQKSGGNVSSSELAKS 184
 QY 159 IDLINEITGNLSQSTOTIAFSSQLAKISTISQAKGFSINIKLONL-NFSKTNLGL 217
 DB 185 IELINOLV-DTAAASLNNVVSFOQLNKLSVLSNTHLGVGNKLNLPNDINICAGLDT 243
 QY 218 ITGLISGASGAFALADKNASTGKVAAGFELSNVIGNTYKAISVYLAQRYAAGISTTG 277
 DB 244 VSGILSAISASFLTSNADDTGKKAAGVLTITKVLGVNGKISQYIIAORAAQGLSTSA 303
 QY 278 AVALATSSIMLAISPLAFMANADKFNHANALDEFKAKQRRKRGYDGDHLAEYQKRGVTI 337
 DB 304 AAGGLIASVYTLAISPLSFLSLADKFKFRANKIEEYSQRFKKGIDSDSLAFAHKETGA 363
 QY 338 EASLTITSRALGAVSAGVSAANGAVCAPIALLVAGVGLISGLEAKQAFESVANR 397
 DB 364 DASLTIRISTYLAIVSSGISAAATISLVGAVSALVAGVGLISGLEASQAFEFVASK 423
 QY 398 LOCKIEMEKONGCONVFDKGYDSRYAAYLANMKFLSELNELAEERYAITQORWNN 457
 DB 424 MALVIAEMEKH-GKNYFENGYDARIHAFLIEDNFKTILSYCNKESYVERSVLLITQHWDTL 482

QY 458 IGLAGITKIGERIKSGKAYADAFEDGKKVEAG----SNITLDAKTIIDISNSNGKTQ 513
 DB 483 IGLAGVITNGDKTSLSKYIDYIEGGRKLEKKPEFGQVDPDLKGNIDLSDS--KST 540
 QY 514 ALHFTSPLTLTAGTESKRLTNGKYSTINKLKGRKAKNNQVTD-GEASSLDPSKYIQRYA 572
 DB 541 LKFTVPLPLTPGEIEREROSGKEYETELVLKGVDKWTVKGVODGSYVDSNLIQHS 600
 QY 573 ETMGST-DEGLLYNANAKANDDIFVGGKMNIDGGDGHDFVYSK-DGCGFNITVDGTSAT 630
 DB 601 VGNNOYREIRIESHLDDGDKVFLSAGSANITAGKCHDVYVDKDTGY--LTIGTKAT 658
 QY 631 EAGSYTVNRKVRGD--IYHEVVKROETVGRKTFETIYRDYELRKV-GYQYSTDNKS 687
 DB 659 EAGNYTVTR-VLGDGVKVLQEVVKEOEVSYGKRTKTEYRSEYFTHINGNLTETDNYS 717
 QY 688 VEIVISQFNDVFKGKFNDFPHSGGDDLDLGGAGDRLF----- 728
 DB 718 VEELIGTRADKFFGSKFADIFHGADGDHIEGNDGNLHKGKNDTLSGGDDQLYG 777
 QY 729 -----GKGNDRLSGBDLDDGSG 750
 DB 778 GDGNDKLIGAGNNYLVGGDDDELQVQNSLAKNVLSGGKNDKLYSGGADLDDGGG 837
 QY 751 DDVINGAGNDVYIFRKGDDNDLIDGTG-NDKLAFAADANISIMIERTEGIVVRND- 808
 DB 838 NDLLKGGVNDIYRYSLGHHIIDDGKDDKLSLADIDFPAARRENDLIMYKAB 897
 QY 809 -----HSGSINIPRWYITSNLQNYOSNKTDRHIEQLGKDSYITSDQIDKLLQDK-- 860
 DB 898 NVLSIGKNGITTFKNMF-----EKESGDISNHQIEQIFDGDGVITPDSLKALEVOQSN 952
 QY 861 -----DGVITTSQ-----ELKTLADENKSKLSASDIASSLNVLSMFLGT 903
 DB 953 NKASYVGNALAYASOGNINPLINEISKIISAAGNDVKEERAASALLQLSNADSFY 1012
 QY 904 A-NSVSSNA 911
 DB 1013 GRNSTITLTA 1021

RESULT 12
 RT12.ACPL STANDARD; PRT; 1023 AA.
 AC P55129;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE RTX-I toxin determinant A from serotypes 5/10 (APX-IA) (Hemolysin IA)
 DE (HLY-IA) (Cytolysin IA) (CLY-IA).
 GN APXIA OR CLYIA OR HLYIA.
 OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Actinobacillus.
 OX NCBI_TaxID=715;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=13039 / SEROTYPE 10;
 RC MEDLINE=94276858; PubMed=8007819;
 RA Nagai S., Yagihashi T., Ishihama A.;
 RT "DNA sequence analysis of an allelic variant of the Actinobacillus
 RT pleuropneumoniae-RTX-toxin I (ApXIA) from serotype 10.";
 RL Microb. Pathog. 15:485-495(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K17 / SEROTYPE 5;
 RC MEDLINE=96401417; PubMed=8807793;
 RA Chiu N., Frey J., Chang C.F., Chang Y.F.;
 RT "Identification of a locus involved in the utilization of iron by
 RT Actinobacillus pleuropneumoniae.";
 RL FEMS Microbiol. Lett. 143:1-6(1996).
 RN [3]
 RP SEQUENCE OF 886-1023 FROM N.A.

DT 30-MAY-2000 (Rel. 39, last annotation update)
 DE RTX-I toxin determinant A from serotypes 1/9 (APX-IA) (Hemolysin IA)
 DE (HLX-IA) (Cytolysin IA) (CLY-IA).
 GN APXIA OR CLYIA OR HLXIA.
 OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Actinobacillus.
 ON NCBI_TaxID=715;
 RX STRAIN=4074 / SEROTYPE 1;
 RX MEDLINE=91348845; PubMed=1879928;
 RA Frey J., Meier R., Gysi D., Nicolet J.;
 RT "Nucleotide sequence of the hemolysin I gene from Actinobacillus
 RT pleuropneumoniae.";
 RL Infect. Immun. 59:3026-3032(1991).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=4074 / SEROTYPE 1;
 RC MEDLINE=94237497; PubMed=8181764;
 RA Frey J., Haldimann A., Nicolet J., Boffini A., Prentki P.;
 RT "Sequence analysis and transcription of the apxi operon (hemolysin I)
 RT from Actinobacillus pleuropneumoniae.";
 RL Gene 142:97-102(1994).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=ISOLATE CYT 13261 / SEROTYPE 9;
 RC MEDLINE=93366425; PubMed=8359691;
 RA Jansen R., Brelaire J., Kamp E.M., Gielkens A.L.J., Smits M.A.;
 RT "Structural analysis of the Actinobacillus pleuropneumoniae-RTX-toxin
 RT I (Apxi) operon.";
 RL Infect. Immun. 61:3688-3695(1993).
 RN [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=S 4074 / SEROTYPE 1;
 RC Chang Y., Wang Y., Chin N.;
 RT Submitted (JUN-1994) to the EMBL/Genbank/DBJ databases.
 RT "-1 FUNCTION: ONE OF THE VIRULENCE FACTORS OF A. PLEUROPNEUMONIAE,
 RT WHICH HAS A STRONG HEMOLYTIC ACTIVITY AND IS CYTOTOXIC FOR
 RT ALVEOLAR MACROPHAGES AND NEUTROPHILS.
 CC "-1 DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
 CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
 CC ACTIVITY.
 CC "-1 DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
 CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
 CC "-1 PTM: PALMITOYLATED BY APXIC. THE TOXIN ONLY BECOMES ACTIVE WHEN
 CC MODIFIED (BY SIMILARITY).
 CC "-1 MISCELLANEOUS: APXIA IS PARTIALLY DELETED IN SEROTYPES 2, 4, 6, 7,
 CC 8, 12, AND TOTALLY DELETED IN SEROTYPE 3.
 CC "-1 MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF SEROTYPE 1.
 CC "-1 SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
 CC
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 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; X52899; CAA37081.1; -
 DR EMBL; X68595; CAA48586.1; -
 DR EMBL; X73117; CAA51548.1; -
 DR EMBL; U05042; AAB05034.1; -
 DR InterPro: IPR001343; Hemlysn_Ca_bld.
 DR InterPro: IPR003355; RTX_N.
 DR InterPro: IPR003959; RTX_A.
 DR Pfam: PF003353; hemolysinCbind; 2.
 DR Pfam: PF02382; RTX_1.
 DR PRINTS: PRO0313; CABDNCRPT.
 DR PRINTS: PRO1488; RTXTOXIN.
 DR PROSITE: PS00330; HEMOLYSIN_CALCIIUM; 2.

KM Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat; Calcium;
 KM Transmembrane; Lipoprotein; Palmitate.
 FT TRANSMEM 226 256 POTENTIAL.
 FT TRANSMEM 257 326 POTENTIAL.
 FT TRANSMEM 367 406 POTENTIAL.
 FT DOMAIN 722 845 13 X REPEATS, GLY-RICH.
 FT REPEAT 722 727 1.
 FT REPEAT 731 736 2.
 FT REPEAT 740 745 3.
 FT REPEAT 749 754 4.
 FT REPEAT 758 763 5.
 FT REPEAT 767 772 6.
 FT REPEAT 776 781 7.
 FT REPEAT 785 790 8.
 FT REPEAT 794 799 9.
 FT REPEAT 813 818 10.
 FT REPEAT 822 827 11.
 FT REPEAT 831 836 12.
 FT REPEAT 840 845 13.
 FT CONFLICT 210 217 AMPYLTLA -> GMLSNTR (IN REF. 3 AND 4).
 FT CONFLICT 374 374 R -> A (IN REF. 3 AND 4).
 FT CONFLICT 562 562 Q -> E (IN REF. 3 AND 4).
 FT CONFLICT 687 688 TC -> R (IN REF. 3 AND 4).
 SQ SEQUENCE 1023 AA; 110193 MW; F99A88CFC9F1A598 CRC64;

 Query Match 37.2%; Score 1727; DB 1; Length 1023;
 Best Local Similarity 39.8%; Pred. No. 1,8e-81;
 Matches 399; Conservative 180; Mismatches 308; Indels 116; Gaps 28;

 QY 8 KSNIOAGLNTKSGSL-----KNVIAIPKVDPPQGGTINFIKADELGIARLAEPP 60
 DB 21 KSAKSGAGALKNGLGVOYKQAGOKLITLYPKDQASTGSSLNLYAAEALGEVIRSEK 80

 QY 61 NHTFAKSVDTYNOFLSTOTGTATSAATLEKFLQSTNKLAKGL-DSVENIDKRLK 119
 DB 81 NGTALAEELGTTPKLLGFSERGALFAPQFDKLNN--OKLSKSGSSSEALGQRLNK 138

 QY 120 ASNVLSLSSFLGTALAGIELDSLTKR---GDAAPALAKASIDLINETIGMLSGSTOR 175
 DB 139 TPTLSALQSPGTALGMDLSLRRRNGEDVSGSELKADLAQVLDNINASTGT 198

 QY 176 TEAFSSOLAKGS--TTSQAKGFSNIGNKLNLFNSKTNLGLEITTLGSLISAGFAL 231
 DB 199 VDAFBEQIGKLAMPYLTLA-----LSGLASKLNLPDLISLGGPDVAVSGILSVASFIL 254

 QY 232 ADKNASTGKVAAGFELSNOYIGNVTAISYVLAQRYAAGLSTGVAALLTSSIMLAI 291
 DB 255 SNKDADAGTKAAAGIEISTKILGNIKNAGVSOYIIAORVAAGLSTTAATGGILSVALLAI 314

 QY 292 SPLAFMNAADPEFNANALDEFKAPRKFGYGDHLLAEYRGVGTITBASLTITSTALGAV 351
 DB 315 SPLSLNVAADFERAKOLEYSEKPKFGYGDLSLAFYEIGALTEALTLTISVLSAR 374

 QY 352 SAGVSAAVGSAVGAIPALLVAVGTGLISGLEASKQAMPESVANKROGLKLEBKONG 411
 DB 375 SAGVGAATAAGSLVGAIPVAAVLSATIGITSLDASKQAFIRVATKLNKIDEEKH-G 433

 QY 412 QNYFPGKDSRAATLANNLKFLSELNKELEAERVATITQORWNNICELAGITKLERI 471
 DB 434 KNYFENGVDARSALFELTFFELLSQYNEYSERYVATITQORWNNICELAGITRKSGDT 493

 QY 472 KSGKAVADAEPDGKRVENG---SNITLDAKTGIDISNSNGKRTQALHTSPILTACTE 527
 DB 494 KSGKAVYDFEFGSKLLEKPEDFDKVDPLEGRKIDLSIN--KTLTLKFTYTPVFTAGEE 551

 QY 528 SREPLTNKSYINKLKFGKRYAKNMQVYTGEBASSKL-DESKYIQRAEFGDEIGLYNA 586
 DB 552 IREKQOTGYQYVTELFYVKGKKEKVVTVGVSHNATYDTNLIQLAIDKRG--EKROYTES 610

 QY 587 KAG--NDLIFVQCGKMNIDGGDGHVRVFSK--DGGFGNLTVDGTSATAGSYTVNRKV-A 642
 DB 611 HUGEKNDRIYLVSSGSIYVAGNGHDVAYIKDTDTG--LTFGGSAQKAGEYIVKELKA 668


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QY 529 RERLTNGKSYINKLKFGRVKNMOTVTDGEASSKL-DESKYIOR-VAETEGTDEIGLIVNA 586
RT 555 RKTQSGKGYEFTEITLAKKGRDVKVCVPNSNGYDESNLIQHVFTDNKVLKARLLANL 614
Db 587 KAGNDIFVCGGKNNINGGCHGDRFVYSKDGFGNITVDGTSATEAGSYVKNRVANGDI 646
QY 615 KAMDYVFGVSGSTIVAGGQYDVADYSK-GRGALITIDGNNAKQYKVERDLSTQV 673
Db 647 YHEVVKQETKRGKRTETIYRDVEL--RKVGYGOSTDNLSVEEYIGSOFNFVFGSK 704
QY 674 LQETVSKQETKRGKRTETIYRDVEL--RKVGYGOSTDNLSVEEYIGSOFNFVFGSK 733
QY 705 FNDIFHSGEGDDL-----LDGAGADDRLF----- 728
Db 734 FNDVFEHGHGDGDLTYGDGDDRLYGDNNGDEIHGGGQGNDKLYGAGANDRLFEGYGNVYLD 793
QY 729 -----GKGNDRLSGDEGDDLDDGSGDDVYNGAGNDVYIFRKGDG 770
Db 794 GGECDHLEGGNGSDILRGSGGNDKLEGNQDDLLDGEEDDQLAGEGNDIYVYRREYG 853
QY 771 NDITLYDGTGN-DKLAFADANSDIMERTKGLIVKRNDHSGSINIFRWYTSN---LQ 825
Db 854 HHTTEHSGDKDLSTANINKDVSEFRNGNDLKTNNRT-AVTFKGFVSKPMSAGLD 912
QY 826 NYQSNKTDHKLIEQLIGKDGSYTSDQIDKILQDKRKGVTYSOELKRLA 874
Db 913 EYQKRLLEYAPE---KD---VHDLRDNLSYSEVKSTNHSLIKLKLS 953

RESULT 15
CYAA_BORPE STANDARD; PRT; 1706 AA.
ID CYAA_BORPE STANDARD; PRT; 1706 AA.
AC P15318;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Bifunctional hemolysin-adenylate cyclase precursor (Cyclolysin) (ACT)
DE (Ac-Hly) [Contains: Calmodulin-sensitive adenylyl cyclase
DE (RC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenylyl cyclase); Hemolysin].
GN CYA OR CYAA.
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
OC Bordetella.
OX NCBI_TaxID=520;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=18323;
RX MEDLINE=88216178; PubMed=2897067;
RA Glaser P., Ladant D., Sezer O., Pichot F., Ullmann A., Danchin A.;
RT "The calmodulin-sensitive adenylyl cyclase of Bordetella pertussis:
RT cloning and expression in Escherichia coli.";
RT Mol. Microbiol. 2:19-30(1988).
RN [2]
RP SEQUENCE OF 1489-1706 FROM N.A., AND BIFUNCTIONAL PROTEIN DESCRIPTION.
RC STRAIN=18323;
RX MEDLINE=89091151; PubMed=2905265;
RA Glaser P., Sakamoto H., Bellalou J., Ullmann A., Danchin A.;
RT "Secretion of cyclolysin, the calmodulin-sensitive adenylyl cyclase-
RT haemolysin bifunctional protein of Bordetella pertussis.";
RT EMO J. 7:3997-4004(1988).
RN [3]
RP DOMAINS.
RX MEDLINE=91177021; PubMed=2007407;
RA Munier H., Gilles A.-M., Glaser P., Danchin A., Sarfati R., Barzu O.;
RT "Isolation and characterization of catalytic and calmodulin-binding
RT domains of Bordetella pertussis adenylyl cyclase.";
RT Eur. J. Biochem. 196:469-474(1991).
RN [4]
RP MOTAGENESIS.
RX MEDLINE=89251630; PubMed=2542030;
RA Glaser P., Elmaoglou-Lazaridou A., Krin E., Ladant D., Barzu O.,
RA Danchin A.;

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RT "Identification of residues essential for catalysis and binding of
RT calmodulin in Bordetella pertussis adenylyl cyclase by site-directed
RT mutagenesis.";
RT EMO J. 8:967-972(1989).
RN [5]
RP MOTAGENESIS.
RX MEDLINE=91266896; PubMed=2050107;
RA Glaser P., Munier H., Gilles A.-M., Krin E., Porumb T., Barzu O.,
RA Sarfati R., Pellequer C., Danchin A.;
RT "Functional consequences of single amino acid substitutions in
RT calmodulin-activated adenylyl cyclase of Bordetella pertussis.";
RT EMO J. 10:1683-1688(1991).
RN [6]
RP REVIEW.
RX MEDLINE=93119764; PubMed=8418825;
RA Danchin A.;
RT "Phylogeny of adenylyl cyclases.";
RT Adv. Second Messenger Phosphoprotein Res. 27:109-162(1993).
RN [7]
RP PALMITOYLATION OF LYS-983.
RX MEDLINE=95025937; PubMed=7939682;
RA Hackett M., Guo L., Shabanowitz J., Hunt D.F., Hewlett E.L.;
RT "Internal lysine palmitoylation in adenylyl cyclase toxin from
RT Bordetella pertussis.";
RT Science 266:433-435(1994).
RN [8]
RP PALMITOYLATION OF LYS-860.
RX MEDLINE=99214144; PubMed=10196151;
RA Basar T., Havlicek V., Bezoukova S., Halada P., Hackett M., Sebo P.;
RT "The conserved lysine 860 in the additional fatty-acylation site of
RT Bordetella pertussis adenylyl cyclase is crucial for toxin function
RT independently of its acylation status.";
RT J. Biol. Chem. 274:10777-10783(1999).
RN [9]
RP FUNCTION: THIS ADENYLYL CYCLASE BELONGS TO A SPECIAL CLASS OF
RP BACTERIAL TOXIN. IT CAUSES WHOOPING COUGH BY ACTING ON MAMMALIAN
RP CELLS BY ELEVATING CAMP-CONCENTRATION AND THUS DISRUPTS NORMAL
RP CELL FUNCTION.
CC -1- CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.
CC -1- ENZYME REGULATION: ACTIVATED BY HOST CALMODULIN.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY (BY SIMILARITY).
CC -1- PTM: RELEASED IN A PROCESSED FORM.
CC -1- PTM: PALMITOYLATED BY CYAC. THE TOXIN ONLY BECOMES ACTIVE WHEN
CC MODIFIED IN POSITION LYS-983.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO ADENYLYL CYCLASE
CC CLASS-2 FAMILY.
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE RTX
CC PROKARYOTIC TOXIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Y00545; CA6613.1; -
DR EMBL: X14199; CA32411.1; -
DR EMBL: A07292; CA00653.1; -
DR EMBL: A14850; CA01202.1; -
DR PIR: S00893; OYBRC.
DR PIR: S09403; S09403.
DR InterPro: IPR001343; Hemolysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR InterPro: IPR003995; RTXA.
DR Pfam: PF00353; hemolysincabind; 5.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CAMDNGRPT.
DR PRINTS: PR01488; RTXTOXINA.
DR PROSITE: PS00330; HEMOLYSIN_CALCIIUM; 5.

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2002, 04:16:55 : Search time 4960.61 Seconds
(without alignments)
11744.418 Million cell updates/sec

Title: US-09-884-696-1

Perfect score: 2784
Sequence: 1 atgtccaataataatgaat.....tttggtcccaagtgttag 2784

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pal:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Score Match Length DB ID Description

1	2784	100.0	2784	1	AF205359	AF205359 Moraxella
2	815.6	29.3	3311	6	AR104900	AR104900 Sequence
3	815.6	29.3	3311	6	I33956	I33956 Sequence 1
4	815.6	29.3	6952	1	AF314503	AF314503 Mannheiml
5	815.6	29.3	7801	1	PASAILKT	M20730 Pasteurella
6	814.6	29.3	6958	1	AF314523	AF314523 Pasteurel
7	814.6	29.3	6958	1	AF314524	AF314524 Pasteurel
8	814.4	29.3	2794	6	AR054439	AR054439 Pasteurel
9	814.4	29.3	2794	6	AR081029	AR081029 Sequence
10	814.4	29.3	2794	6	AR085997	AR085997 Sequence
11	814.4	29.3	2794	6	BD009870	BD009870 GNRH-Leuk
12	814.4	29.3	2794	6	I12257	I12257 Sequence 1
13	814.4	29.3	2794	6	I23447	I23447 Sequence 1
14	814.4	29.3	2794	6	I80029	I80029 Sequence 1
15	814.4	29.3	2794	6	I89774	I89774 Sequence 5
16	814.4	29.3	2817	6	I12265	I12265 Sequence 9
17	814.4	29.3	2817	6	I80037	I80037 Sequence 11
18	814.4	29.3	2838	6	I12264	I12264 Sequence 8
19	814.4	29.3	2838	6	I80036	I80036 Sequence 9
20	814.4	29.3	2861	6	I12266	I12266 Sequence 10
21	814.4	29.3	2861	6	I80038	I80038 Sequence 13
22	814.4	29.3	2934	6	AR054440	AR054440 Sequence
23	814.4	29.3	2934	6	AR081030	AR081030 Sequence
24	814.4	29.3	2934	6	BD009871	BD009871 GNRH-Leuk
25	814.4	29.3	2934	6	I89775	I89775 Sequence 7
26	814.4	29.3	3329	6	AR104901	AR104901 Sequence
27	814.4	29.3	3329	6	I33957	I33957 Sequence 3
28	814	29.2	2862	1	AF314504	AF314504 Mannheiml
29	814	29.2	2862	1	AF314507	AF314507 Mannheiml
30	813	29.2	6959	1	AF314525	AF314525 Pasteurel
31	812.4	29.2	2862	1	AF314505	AF314505 Mannheiml
32	812.4	29.2	6952	1	AF314506	AF314506 Mannheiml
33	811.4	29.1	6958	1	AF314526	AF314526 Pasteurel
34	811.2	29.1	6952	1	AF314514	AF314514 Mannheiml
35	808.8	28.9	6952	1	AF314512	AF314512 Mannheiml
36	803.6	28.9	6952	1	AF314519	AF314519 Mannheiml
37	802.8	28.8	7742	1	PASLKTCABD	M24197 P. haemolyti
38	801.4	28.8	6952	1	AF314508	AF314508 Mannheiml
39	801.4	28.8	6952	1	AF314520	AF314520 Mannheiml
40	800.4	28.8	2802	6	I26636	I26636 Sequence 79
41	800.4	28.8	3848	6	I26635	I26635 Sequence 1
42	800.4	28.8	6952	1	AF314522	AF314522 Mannheiml
43	800.4	28.8	7841	1	PAJLEUKOT	L12148 Pasteurella
44	799.6	28.7	3385	1	U01216	U01216 Pasteurella
45	798.8	28.7	6952	1	AF314517	AF314517 Mannheiml

ALIGNMENTS

RESULT 1	AF205359	2784 bp	DNA	linear	BCT 02-OCT-2001
LOCUS	AF205359				
DEFINITION	Moraxella bovis RTX toxin (mbxa) gene, complete cds.				
ACCESSION	AF205359				
VERSION	AF205359.1	GI:15146407			
KEYWORDS					
SOURCE					
ORGANISM	Moraxella bovis.				
	Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;				
	Moraxella.				
REFERENCE	1 (bases 1 to 2784)				
AUTHORS	Angelos,J.A., Hess,J.F. and George,L.W.				
TITLE	Cloning and Characterization of a Moraxella bovis cytotoxin gene				
JOURNAL	Am. J. Vet. Res. 62 (8), 1222-1228 (2001)				
MEDLINE	21388402				
PUBMED	11497442				
REFERENCE	2 (bases 1 to 2784)				
AUTHORS	Angelos,J.A., Hess,J.F. and George,L.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (15-NOV-1999) Veterinary Medicine/Epidemiology, University of California, Davis, 2108 Tupper Hall, Davis, CA 95616, USA				


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QY 1141 ggaattcttagaagcgtctcaaaacaggcaatgttgaagtcgtctaacccgttacaagtt 1200
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QY 1201 aaaaattcttagagctgggaaaaagcacaatgtggcgtcagaactattctgataaaggctatgt 1260
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DB 1201 aaaaatttttagagctgggaaaaagcacaatgtggcgtcagaactatttttgcattaaagcctatgtat 1260
QY 1261 tctcgttatcgtcgtctatttagcttaataacttaaaatttctcctgaagctaaataaagg 1320
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DB 1261 tctcgttatcgtcgtctatttagcttaataacttaaaatttctcctgaagctaaataaagg 1320
QY 1321 tctgaagcctgaacgctgtctatttgcataccaccaacacgtctgggataataatactctgtgag 1380
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QY 2041 tctaccgaatacttgaacacagtagaagaagaatgtgtctccaattlaatgaatgctatc 2100
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    |||
DB 2281 gatgtctatactcttcggaaaagtgatgtgtatgtactcttgatgaatgacggagcaat 2340
QY 2341 gataaattagcatttcgaatgcaaatatatacttgatatgtatgatactgaatgcaagaag 2400
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DB 2341 gataaattagcatttcgaatgcaaatatatacttgatatgtatgatactgaatgcaagaag 2400
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LOCUS ARI04900 Sequence 1 from patent US 6096320.
DEFINITION ARI04900
ACCESSION ARI04900
VERSION ARI04900.1 GI:12818497
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 3311)
AUTHORS Potter, A., Campos, M. and Hughes, H. P. A.
TITLE Vaccines with chimeric protein comprising gamma-interferon and
leukotoxin derived from pasteurella haemolytica
JOURNAL Patent: US 6096320-A 1 01-AUG-2000;
FEATURES
location/Qualifiers
source 1..3311
BASE COUNT 1113 a 592 c 699 g 907 t
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Best Local Similarity 60.1%; Pred. No. 3,8e-133;
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QY 97 ---tatgtccgcaaaaggtggtgaactttaaagtattatlaaagcgtgtatgaatt 152
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DB 591 ccaatgatgactgaacaagaatgaatggtttacagatattttagtcaaaagcggcgaaagatt 650

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Oy	214		
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Oy	273	agaaagttcttcacaaaacatctccacaatnagttagccaaaggtttagaacsgltaga	332
Oy	274		
Db	771	TGATAAATTTGCTACACAAA-----ACTTAACGACGGCCACACATTAGGTTCTGCCCA	821
Oy	333	aaatatgatcgttaaattagttagaacgaatgtaattatcatcaacatcaagctctttt	392
Oy	334		
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Oy	750	tcaagttatgtgaatgtaacaaagaacatllcttcataatglttttagacaacgltgtgc	809
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Oy	810	tgcgtgtcatcaactactcgtgctgtgtgtgttaattactaatgatgatattagtgc	869
Db	1299	ACCAAGTTTATCTTCAACTGGGGCTTGGCTGGCTGTTAATTTGCTTACGTTTCTCTTCC	1358
Oy	870	aatgctcccttggtcatltaagaatgagcagaataatcaatcaatcagtaatgctctga	929
Db	1359	GATTGAGCCATTACACTTTTGGCGGTATTTGCCGATAATTAATTCANCGAAAAGTTTGA	1418
Oy	930	tgaagttgcaaaacaattcognaaattgtgcatatgagtgagatcattatttgcgtgata	989
Db	1419	GAGTATATGCCCAAGCCTTTAAAAAATTAGCGCTATGACGGAGATAATTTATGACAGATA	1478
Oy	990	tcaagtggtgtgtgtgtactatgaaggttcaatcaactacaatagaagcagatggtgc	1049
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Db	1539	TATTGCTGTGGTGTGTCGTGCTGACGCGCGCTGGTATATGCTTACCGATTGCTCT	1598
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Qy	1350	ccaacaacgtttgggataataataatattggtgaggttagcagattatccaaatttgggtgaacg	1409
Db	1839	TCACCAACAATGGGATTAACAACATTGGTGATTTACTCTGTGATTACCGCTTTAGGTGATAA	1898
Qy	1410	cattaagaagcgaaagacttaatgacatgctcttttgaagaatgycagaagaagtltgaagctg	1469
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Qy	1762	-----gcttgcaatagcatatctttgtgttgcgaagttaaatgcaatgtga	1808
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Qy	1809	tggtgagatggaacagacgtgtctctatagtaaagacggaagattggtlaatatatc	1868
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Qy	1869	tgtagatgtgcggtgcaacaagaagcaggttaataagttacgttaatgttgaagttgtctcg	1928
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Db	2436	CGGTAAAGCACTACACGAGTAGACTTCAACCCATTCGCGATTAGTGGGCAACCGTAGA	2495
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Qy	2109	taaatcaacgacatattccatagbtgtgaaggtgatattactcogatggtgtgtcgtg	2168
Db	2613	TAACTTCAATGATGCTTTTAACGGTGTGTGTGTCGATACATTATGACGAGTAAACGACGG	2672
Qy	2169	tgaagcagcgtgtttgtgttgaagcagaagctgcacttcttgagagatgaaagcgatga	2228
Db	2673	CAATGACCGCTTATTGGTGTGTAAGGCGATGATATTTCGATGTGTGAAATGCTGATGA	2732
Qy	2229	tttaacacgtgcggtcttcgttgatgatagtataaattggtgtcgtgtaaatgatgtcta	2288
Db	2733	TTTTATTCGATGGCGGTAAAGCAACGACACTATTAAACAGGTGGCAAGGCGATGATATTTT	2792
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Db	2793	CGTTCACCGCTAAAGGCCATGGTAAATGATATATTATTCGCATTCTGACGGCAATGATAAATT	2852
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DEFINITION	133956	3311 bp	DNA		
ACCESSION	133956	Sequence 1 from patent US 5594107.			
VERSION	133956.1	GI:1824747			
KEYWORDS					
SOURCE		Unknown.			
ORGANISM		Unknown.			
REFERENCE		Unclassified.			
AUTHORS		1 (bases 1 to 3311)			
TITLE		Potter A., Campos M. and Hughes H.P.A.			
JOURNAL		Chimeric protein comprising an RFX-family cytotoxin and			
FEATURES		Interferon-2 or Interferon			
source		Patent: US 5594107-A 1 14-JAN-1997;			
		Location/Qualifiers			
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ORIGIN					

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OY	153	aggtatgctcgttttagcagaagagccaatcacactgaacagcagcaaaaaaattcgttga	212
Db	651	GGGGATTGAGGTACAAACAGAAAGCAAAATATTTCACACAGCTCAAAACGATTTAGG	710
OY	213	cacagtaatcagttctctctctcacaacaactgtagttgctattctgcagcaaaatt	272
Db	711	CACGATTCAAACCGCTATTGGCTTAACTGAGCGTGCGATTGTTATCCGCTCCACAAT	770
OY	273	agaaagttcttcaacaacaattctacaataagttagtcgaagaagttagacagttaga	332
Db	771	TGATTAATTTGCTACGAANA-----ACrTAACAGGCCAAGCATTAAGTTCTTGCCGA	821
OY	333	aaatatgatcgtlaaatltagtlaaagcaagaatgtatattatcaacatlaagctctttt	392
Db	822	AAGCTATTACAAANAATGCAANAATAAGCCAAACGTATATTCTGGCATTCATCTAATTTT	881
OY	393	gggcacatgcattagcgggtatagaacttgattcttlaacaaaaaagtgatgctgcacc	452
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[illegible]

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QY	1590	acgtttcaactatgqtaaacctcttatataaagttaaatcgcgagctglaaaaaa	1649	DEFINITION		Mannheimia haemolytica strain PH2 lktCABD operon, partial sequence.
Db	2079	ACCGGTCAAAACAGGTAAATATGATATATTACCAAGCTCAATATATACCGGTAGATAG	2138	ACCESSION		AF314503
				VERSION		AF314503.2 GI:15987890
QY	1650	ctggcaagttacagataggagagctagctctaaatagattctcctaagtattacgag	1709	KEYWORDS		Mannheimia haemolytica.
Db	2139	CTGGAAATTAACAGATGCTGACGCAAGTCTACCTTGATTGAATTAACCTGTGTGAGCG	2198	SOURCE		Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
QY	1710	tgtagccgagacagagagccagacgagattggtcctaattgtaaatgcaaaa-----	1761	ORGANISM		Mannheimia.
Db	2199	TATTGATTGAATTACACATGCTGCAATGTACTAAACCAAGAAACAAAATTAAT	2258	REFERENCE		1 (bases 1 to 6952)
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Db	2259	TGCCAACTTGTAAGGTGATGACAAACGTAATTGTTGTTCTGTCTGACGACGGAATTTGA	2318	TITLE		Sequence diversity and molecular evolution of the leukotoxin (lktA) gene in bovine and ovine strains of Mannheimia (Pasteurella) haemolytica
QY	1809	tgtgtgagatgagacagatcgtgtctctctatagtaaaagcagagatttgtaataatc	1868	JOURNAL		J. Bacteriol. 183 (4), 1394-1404 (2001)
Db	2319	TGGCGGTGAAGGTTACGACCGAGTTCACTATAG--CCGTGGAACATATGCTGCTTTAC	2375	MEDLINE		21101823
QY	1869	tgtagatgtagcagtgcaacagacagcagttatcacagttacgttaagctgtctcg	1928	PUBMED		11157953
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QY	1929	aggtgatactacacatgaagtgtggaagcgtcaagaaacaaagttgggttaacgtactga	1988	AUTHORS		Davies,R.L., Campbell,S. and Whittam,T.S.
Db	2436	CGGTAAACACTACACGAAAGGACTTCMAACCCATACCGCATTAATGTGGAACCGTGAAAG	2495	TITLE		Mosaic Structure and Molecular Evolution of the Leukotoxin Operon (lktCABD) in Mannheimia (Pasteurella) haemolytica, Mannheimia glucosida, and Pasteurella trehalosi
QY	1989	aactacagatcgtgtgattgaattaagaagttggtatgtaagttacagttacogta	2048	JOURNAL		J. Bacteriol. 184 (1), 266-277 (2002)
Db	2486	AAAAATACAAATATCTCTTACCAATTAACCAACCAACCATG---CCGTTATTTACCAACAAG	2552	REFERENCE		3 (bases 1 to 6952)
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QY	2109	taaatccaagacatatactccatagtggtggaaggtgatbattactcgtgtgtgtcgtg	2168	COMMENT		Submitted (04-OCT-2001) Institute of Biomedical and Life Sciences,
Db	2613	TAAGTTCATATGATGCCCTTTAACGGGTGATGCTGTCATTCATTTGACGGTAAACGACGG	2672	FEATURES		Division of Infection and Immunity, University of Glasgow, Joseph Black Building, University Avenue, Glasgow G12 8QQ, Scotland
QY	2169	tgaacgcgcgtgtgtgtgtgtaaaagcaacatcgactcttcctgagataagaagcgatga	2228	REMARK		Sequence update by submitter
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QY	2229	tttactcgatggcggtctctgtgatgataatgaatggtgtgtcgtgtaatgatactcta	2288	source		1. 6952
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Db	2793	CGTTACCGTTAAAGCGATGATGATATTTATTCGATTCGTGACGGCAATGATAAATT	2852	serotype="A1"		
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LOCUS	7801 bp DNA linear BCT 26-APR-1993
DEFINITION	<i>Pasteurella haemolytica A1</i> leukotoxin gene, encoding LktA, LktB, LktC and LktD proteins, complete cds.
ACCESSION	M20730.1 GI:150492
VERSION	
KEYWORDS	LkTA protein; LkTB protein; LkTC protein; LkTD protein.
SOURCE	<i>P.haemolytica</i> (serotype 1, biotype A) DNA.
ORGANISM	<i>Mannheimia haemolytica</i> <i>Bacteria</i> ; <i>Proteobacteria</i> ; gamma subdivision; <i>Pasteurellaceae</i> ; <i>Mannheimia</i> .
REFERENCE	1 (bases 1 to 7801)
AUTHORS	Lo,R., Strathdee,C.A. and Shewen,P.
TITLE	Nucleotide Sequence of the Leukotoxin Genes of <i>Pasteurella haemolytica A1</i>
JOURNAL	Infect. Immun. 55, 1987-1996 (1987)
MEDLINE	87306837
COMMENT	Submitted in computer readable form by C.Strathdee21-SEP-1988.

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CDS

BASE COUNT 2621 a 1366 c 1542 g 2272 t
ORIGIN 3 bp upstream of EcorV site.

Query Match 29.3%; Score 815.6; DB 1; Length 7801;
Best Local Similarity 60.1%; Pred. No. 3.5e-133;
Matches 1544; Conservative 0; Mismatches 964; Indels 60; Gaps 9;
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AUTHORS Davies, R.L., Whittam, T.S. and Selander, R.K.
TITLE Sequence diversity and molecular evolution of the leukotoxin (lktA) gene in bovine and ovine strains of Mannheimia (Pasteurella) haemolytica
JOURNAL J. Bacteriol. 183 (4), 1394-1404 (2001)
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AUTHORS Davies, R.L., Campbell, S. and Whittam, T.S.
TITLE Mosaic Structure and Molecular Evolution of the Leukotoxin Operon (lktCABD) in Mannheimia (Pasteurella) haemolytica, Mannheimia glucosida, and Pasteurella trehalosi
JOURNAL J. Bacteriol. 184 (1), 266-277 (2002)
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PUBMED 3 (bases 1 to 6958)
AUTHORS Davies, R.L., Whittam, T.S. and Selander, R.K.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-2000) Institute of Biomedical and Life Sciences, Division of Infection and Immunity, University of Glasgow, Joseph Black Building, University Avenue, Glasgow G12 8QQ, Scotland
REFERENCE 4 (bases 1 to 6958)
AUTHORS Davies, R.L., Whittam, T.S. and Selander, R.K.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-2001) Institute of Biomedical and Life Sciences, Division of Infection and Immunity, University of Glasgow, Joseph Black Building, University Avenue, Glasgow G12 8QQ, Scotland
REMARK Sequence update by submitter
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 Davies,R.L., Whitlam,T.S. and Selander,R.K.
 Sequence diversity and molecular evolution of the leukotoxin (lktA)
 gene in bovine and ovine strains of Mannheimia (Pasteurella)
 haemolytica
 J. Bacteriol. 183 (4), 1394-1404 (2001)
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 2 (bases 1 to 6958)
 Davies,R.L., Campbell,S. and Whitlam,T.S.
 Mosaic Structure and Molecular Evolution of the Leukotoxin Operon
 (lktCABD) in Mannheimia (Pasteurella) haemolytica, Mannheimia
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 J. Bacteriol. 184 (1), 266-277 (2002)
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 3 (bases 1 to 6958)
 Davies,R.L., Whitlam,T.S. and Selander,R.K.
 Direct Submission
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 Division of Infection and Immunity, University of Glasgow, Joseph
 Black Building, University Avenue, Glasgow G12 8QD, Scotland
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 Direct Submission
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 Sequence update by submitter
 On Oct 9, 2001 this sequence version replaced gi:11762059.
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 ACCESSION AR054439
 VERSION AR054439.1 GI:5980016
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 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2794)
 AUTHORS Potter,A.A. and Manns,J.G.
 TITLE GHRH-leukotoxin chimeras
 JOURNAL Patent: US 5837268-A 5 17-NOV-1998;
 FEATURES
 source Location/Qualifiers
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Query Match 29.3%; Score 814.4; DB 6; Length 2794;
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ACCESSION	BD009870				
VERSION	BD009870.1	GI:18638243			
KEYWORDS	JP 2001502887-A/3.				
SOURCE	unidentified.				
ORGANISM	unclassified.				
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AUTHORS	Potter,A.A. and Manns,J.G.				
TITLE	GnRH-leukotoxin chimeras.				
JOURNAL	Patent: JP 2001502887-A 3 06-MAR-2001;				
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	PF 08-AUG-1997 JP 1998509192				
PC	PI 09-AUG-1996 US 08/694865				
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	PC C12N15/16,C12N15/31,C12N15/62,C12N1/21,C07K14/285,C07K1/23, PC				
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CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 1..2778.
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BASE COUNT 930 a 487 c 599 g 778 t
ORIGIN

Query Match 29.3%: Score 814.4; DB 6; Length 2794;
Best Local Similarity 60.2%: Pred. No. 6.2e-133;
Matches 1538; Conservative 0; Mismatches 956; Indels 60; Gaps 9;

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DB 1397 AAGCTATGTCGATGCGCTTGAAGAAGCAACACATTAAGCCGATTAATTTAGTACGT 1456
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DB 1457 TGCATTTGGCAACGGATTTATTTGATGATTAATTTGCGGTGAAGCGCAAACTCAGCTA 1516
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DB 1637 ATGCTGACGCAAGTTCTTACCTTTGATTAATTAACGTTGTCAGCGTTATTTGATTTGANT 1696
QY 1724 aagcacaagaagatgcttcaatagtaagttaaa-----g 1762
DB 1697 TAGACAATGCTGGAATTTAATTAACCAAGAAACAAAATTAATTTGCCAAACTTGGTG 1736
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QY 1823 acgactgcttctctatagaataaagcgaagatttggtaatactactgtagatgtaga 1882
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DB 1874 AAGGACCGGACGAAGATGATTAACCGTAATTCGTTTCGTGAACCGGTAAGCACTAC 1933
QY 1943 atgaagtgtgaagcgtcaagaacaaagtggtgtaaacgtactgaaactatccagta 2002

Db	1934	ACGAAGTACTTCAACCCATATCCGATTTAGTGGCCAAACCGTGAAGAAAAATTAACATATC	1993
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Db	1994	GTCAATAGCAATAAACAGACACCATG---CCGGTTATTACACCAAGAAATACCTTGAAGCTG	2050
Qy	2063	tagaagaagatattggtttcatttaatgattgattatcgaatgaagttcctaattgaagaca	2122
Db	2051	TTTGAAGAAATTAATGGTACATACATTAACGATATCTTTAAAGGTAGTAGTCAATGATG	2110
Qy	2123	tattccatagtggtgaaagtgatgatattaccacgcgatctgtygtygcctggtgaacccgctgt	2182
Db	2111	CCTTTAAGAGGTGTGATGTTGTCGATACTATTGACAGGTAAAGACGACGCAATGACCGCTTAT	2170
Qy	2183	tttggtgttaaaagcgaacgaatcgaacttcttgagatgaagcgcgatgatattactgatgcg	2242
Db	2171	TTTGGTGTAAAGGCGCATGATATTCTCGATGTGTGGAATAGTGATGATTTTATCGATGGCG	2230
Qy	2243	gttcctggtgagatgattatgaatggtgtgtctggtgaatgagatgctcatalacttcgsgaaag	2302
Db	2231	GTTAAAGGCAACGACCTATTATACAGGTGGCAAGGCGGATGATATTTTCGTTACCGTTAAG	2290
Qy	2303	gtgagtgaatgatatactttgtaacgatgycgaacgggcaatgatgaattgaactgtcgaatg	2362
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Db	2408	GCAAAAAAGAGCAAAATGACACTTCAAACTGGTTCCGAGAGGCTGATTTTGCTTAAAGAG	2467
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Db	2528	AGCGATCACCTCAACAGCATTTGATGATCTTAT	2561
RESULT	12		
LOCUS	112257	2794 bp	DNA
DEFINITION	Sequence 1 from patent US 5422110.		linear
ACCESSION	112257		
VERSION	112257.1	GI:910280	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 2794)		
AUTHORS	Potter,A.A., Redmond,M.J. and Hughes,H.P.A.		
TITLE	Enhanced immunogenicity using leukotoxin chimeras		
JOURNAL	Patent: US 5422110-A 1 06-JUN-1995;		
FEATURES	Location/Qualifiers		
SOURCE	1..2794		
BASE COUNT	930 a 487 c 599 g 778 t		
ORIGIN	/organism="unknown"		

Query Match	Similarity	Score	81.4	DB	6	Length	2794
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						Gaps	9
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DB	29	CAAAAAGTGGGGCCAAAAAATATTCCTCTATATCCCAAAATATCCAAATATGACG	88				
QY	107	aaaaagctgagagctttaaattgattttatcaagcgcgcgtatgaattagatgctgcgtt	166				

Db	89	AACAGGTAATGGTTTACAGATTATGTCAAAAGCGGCCGAAGACTTGGGATTTAGGTAC	148
Qy	167	taagcaagaagcctaatacactgaaacagcaaaaaaactcgttgacaagtaactcagt	226
Db	149	AAAGAGAGAACCCCAATAATATGTCAACAGCTCAAAACCAAGTTTGGACAGATTCAAACCG	208
Qy	227	ttctctctcacacaacactgattgtcattcttccttcgcaaaaaattgaagaattctac	286
Db	209	CTATTGGCTTTAACTGACCGGTGGCATTTGTGTATCCGCTCCCAAAATTGATTAATTTGGTAC	268
Qy	287	aaaaacaattacccaataagttagccaaagggttagaacagtgtaaaaaataatgatcgta	346
Db	269	AGAAA-----ACTAAAGCAGCGCAAGCATTTGTGGTTGCCGAAAGCATTTGTCAAA	319
Qy	347	aattagttaagcaagtaatgatatatacaacttaagctcttttttgggcctcattag	406
Db	320	ATGCAAAATTAAGCCAAAACGTATATTTCGSCATTTCAAATCTATTATTAGCCATATTGG	379
Qy	407	cgggataagaacttgattcttataatcaaaaaaaggatgacgacactgattcttgcta	466
Db	380	CTGGAATGGAATTTAGATGAGGCGCTTACAGA--TAAAGCAACCAACATGCTCTTCTCTA	436
Qy	467	aagctagtaattgacttgattaatgagataactatgttaactatcagaagtctaacaaga	526
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Qy	527	ttagaagatttcttcaacttagcaagttagttctactataatcgaagctaaagct	586
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Qy	587	tctctaataaggaacaagttgcaaaacttaaat---tttctaaaaaacttggt	643
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Qy	644	tggaataaattacatggtttgctaaaggaatttcgcaagcttcttgacgataaaa	703
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Qy	824	ctactgctgctgctgctgctttaaacttaactcatcgataatgttggcaattagtccttgg	883
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Db 1934 ACCAATGTACTTCAACCCATACCGCATTTAGTGGCAACCGTGAAGAAATAATGAAATATC 1993
QY 2003 gtgaattatgaataaagaattgggtatgtatcatcagttacaccgaataatccag 2062
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RESULT 13
LOCUS 123447 2794 bp. DNA linear PAT 07-OCT-1996
DEFINITION Sequence 1 from patent US 5534256.
ACCESSION 123447
VERSION 123447.1 GI:1603317
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2794)
AUTHORS Potter, A.A. and Harland, R.J.
TITLE Haemophilus somnus outer membrane protein extract enriched with iron-regulated proteins
JOURNAL Patent: US 5534256-A 1 09-JUL-1996;
FEATURES
source 1.2794
BASE COUNT 930 a 487 c 599 g 778 t
ORIGIN

Query Match 29.3%; Score 814.4; DB 6; Length 2794;
Best Local Similarity 60.2%; Pired. No. 6.2e-133;
Matches 1538; Conservative 0; Mismatches 956; Indels 60; Gaps 9;

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Db 2528 AAGGATCACCTCAAGCAAGTTGATGATTTAT 2561

[illegible]

D	677	ATGCTTCAACAGCTAATAAAGTGGGCGGGTGGTGAATGTGCAAAACCAAGTTGTGGTA	736
Q	764	atgtacaagaagaattcttccatcatglttttagcacaacgtgtcgtcgtgtatca	823
D	737	ATATTACCAAGACCGCTTTCTTCTTCATATTTPAGCCCAACGCTTCCACACAGATTATCTT	796
Q	824	ctactgtgtcgtgtgtgtcttcaattacttcaatcgatatagtgttcgaattgctcttgg	883
D	797	CAACTGGGCGCTGGCGCTTTAATTGCTTCTTACTGTTTCTTTCGCAATTACCCATTAG	856
Q	884	catltaatgaatgcagcagataaattccatcatcgtctaagtctctgtatgagtttgcnaac	943
D	857	CATTTCGCCGATTTGCGCGATAATTAAATCAATGCAAAAAAGTTTAGAGATTATGCCGAA	916
Q	944	aattccgaaaatttgcgtatgatgtggagatcatltaattgtcgtgaataatcagcgttgcg	1003
D	917	GCTTTAAAAAATTAAGGCTATTGACGGAGATAATTATTAGCAGAAATATACGGCGGAACAG	976
Q	1004	gtactatgaagcttcaattactacacatattagtagcgcattagtgcaattctcgtctgtg	1063
D	977	GGACATTATGATGATGCATGGTTACTGCAATTAATACCGCATTTGGCCGCTATTGGCTGGTG	1036
Q	1064	ttccgctgtcgtcgtgaagatctgctgtgtgtgtgcacgcgaattgcactatagtgcagtg	1123
D	1037	TGCTCTCTGCTGCAGCGCGCTCGGTTATTGCTTCACCGATTCCTATTATGATCTGGGA	1096
Q	1124	ttacagatgtatctcttgcgaatttttgaagcgtctcaaacagcgaatgttttgaagtgttg	1183
D	1097	TTACCGGTGAATTTCTTACGATTTCTGCATAATTCTTAACACACAAATGTTTGACACGTTG	1156
Q	1184	ctaacgcgttacaagtaaaattttagagtgggaaagcaaaatgcgcgttcagaactat	1243
D	1157	CAATATAAATTTCTATACAAATAATGTGTGATGGGAAAAAATATATACCGTTAAGCACTCT	1216
Q	1244	ttataaagcgtatgttctcgtttagcgtctattttagcttaattacttaaatatttgt	1303
D	1217	TTGAAAATGGTTACGATGCCCGTTATCTTGCGAATTTACAGATTAATGAAATCTTAC	1276
Q	1304	cttagcctaaataaagagtttgcgaagctgcgaacgtgttatctgcaatccacacaacgttgc	1363
D	1277	TGAACTTTAAACAAGAGTTTACAGCGAGAACGTTGTCATGCTATTCTCAGACGCAATGG	1336
Q	1364	ataataatatgtgtgcgtttagcaggtatattaccaaatitgggtgcacgcattaaagcggaa	1422
D	1337	ATTACACAACTGGTGTGATTTTAGCGGTATTAGCCGTTTAGCTGAAAAGTCTTACTGCTA	1398
Q	1424	aagcctatgcagaatgtcttttgaagaatgcgcaagaagaagtgcgaatcgtgtccaaatctact	1483
D	1397	AAGCCTATGTGGATGTGGCTTTGAAAGAGGCAACACATTAAAGCCATTAATTAGTACAGT	1456
Q	1484	tggatgcctaaacatggtatcatatagacatagatgaattcaaatcgaatvggaaaaaacgcagcgt	1543
D	1457	TGCAATTCGGCAACCGTATTATTTGATGTAGTAATTCGGGTAAACGGAACCTCAGCATTA	1518
Q	1544	tgcatttcaacttcgcctctgtttaaagcagcagcagcgaatcaatcgaatgaatgaatgaatga	1603
D	1517	TCTTATTTCGAAGCGCATTTATTTAGCGCGGGAACAGAGCATGTGTAAAGCGGTACAAACAG	1578
Q	1604	gtataactcttcatctaaatlaagtctaaatctgcgacgtgttaaaaaactgcgcaagttacag	1663
D	1577	GTAATATATGAATATTATTACCAAGCTCAATATTAACCGTGTAGATGCTGGAATAATTACAG	1633
Q	1664	atgtagaagcgtagttcttcaaatatagatttcttctaaagtatcttaagcgtgtagccgaagca	1722
D	1637	ATGGTCCAGCAACTTCTACCTTTGATTTTAACGTAAACGTTGTTCAAGCGTATTTGGATTGAAT	1696
Q	1724	aagcgacacagcagatctgtgtcctaattgtaattgcgaaa-----g	1762
D	1697	TAAACATAGCTGGAATTTGTAACATAAACAAGAAACAAATAATTATTGCCAAACTTTGGTG	1756
Q	1763	ctggcaatgcagatattcttgtgtcgaagtgaataatgaataatgatgtgtgcgaatgagc	1822
D	1757	AAGGTATGACCAAGCTATTGTTGGTTGCTGTGATACGACGGAATTTGATGGCGGTGAAGCTT	1816

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 11, 2002, 09:01:25 ; Search time 65.81 Seconds

(without alignments)
31.544 Million cell updates/sec

Title: US-09-884-696-6
Perfect score: 57
Sequence: 1 FLSLNKLEAE 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	927	2 Q93G12	Q93G12 moraxella b
2	43	75.4	946	2 Q9EV24	Q9EV24 mannheimia
3	43	75.4	953	2 Q9ETX2	Q9ETX2 mannheimia
4	43	75.4	953	2 Q9ETG5	Q9ETG5 pasteurella
5	43	75.4	953	2 Q9EV34	Q9EV34 pasteurella
6	43	75.4	953	2 Q9EV33	Q9EV33 pasteurella
7	43	75.4	953	2 Q9EV32	Q9EV32 pasteurella
8	43	75.4	953	2 Q9EV31	Q9EV31 pasteurella
9	43	75.4	953	2 Q9EV30	Q9EV30 pasteurella
10	43	75.4	953	2 Q9EV29	Q9EV29 pasteurella
11	43	75.4	953	2 Q9EV27	Q9EV27 pasteurella
12	43	75.4	953	2 Q9EV26	Q9EV26 mannheimia
13	43	75.4	953	2 Q9EV25	Q9EV25 mannheimia
14	43	75.4	953	2 Q9EV23	Q9EV23 mannheimia
15	43	75.4	953	2 Q9EV28	Q9EV28 pasteurella
16	43	75.4	954	2 Q9EUE1	Q9EUE1 pasteurella

17	43	75.4	955	2 Q9EUD4	Q9EUD4 pasteurella
18	43	75.4	955	2 Q9EV22	Q9EV22 pasteurella
19	43	75.4	956	2 Q93NP1	Q93NP1 actinobacil
20	42	73.7	897	13 Q13098	Q13098 xenopus lae
21	42	73.7	913	13 Q13099	Q13099 xenopus lae
22	39	68.4	798	13 Q90307	Q90307 carassius a
23	38	66.7	73	9 Q9MBS7	Q9MBS7 staphylococ
24	38	66.7	73	9 Q9G032	Q9G032 bacterioph
25	38	66.7	73	16 Q932B3	Q932B3 staphylococ
26	38	66.7	211	9 Q80148	Q80148 bacterioph
27	38	66.7	222	5 Q9V3V7	Q9V3V7 drosophila
28	38	66.7	382	16 Q25891	Q25891 helicobacte
29	38	66.7	508	5 Q18051	Q18051 caenorhabd
30	38	66.7	977	4 Q75300	Q75300 homo sapien
31	38	66.7	977	4 Q9H476	Q9H476 homo sapien
32	38	66.7	993	2 Q52054	Q52054 enterococcu
33	38	66.7	1407	4 Q96S82	Q96S82 homo sapien
34	38	66.7	1586	4 Q9P2E9	Q9P2E9 homo sapien
35	37	64.9	275	11 Q63306	Q63306 rattus norv
36	37	64.9	646	11 Q63779	Q63779 rattus norv
37	37	64.9	653	2 Q9RUK0	Q9RUK0 streptomyce
38	37	64.9	899	10 Q9C895	Q9C895 aradidopsis
39	37	64.9	913	11 Q9QYX7	Q9QYX7 citriculus
40	37	64.9	1200	11 P97692	P97692 rattus norv
41	37	64.9	1534	6 Q28298	Q28298 canis famil
42	37	64.9	2779	5 Q9W4N7	Q9W4N7 drosophila
43	36	63.2	117	10 Q80380	Q80380 daucus caro
44	36	63.2	141	11 Q88651	Q88651 marmota mon
45	36	63.2	151	10 Q04767	Q04767 bolusanthus

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	927 AA.
Q93G12	Q93G12	Q93G12		
AC	Q93G12	Q93G12		
DT	01-DEC-2001 (Tremblrel. 19, Created)			
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)			
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)			
DE	RTX TOXIN.			
GN	MBXA.			
OS	Moraxella bovis.			
OC	Bacteria: Proteobacteria: gamma subdivision: Moraxellaceae: Moraxella.			
OX	NCBI_TaxID-476;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-TIFON I;			
RX	MEDLINE-21388402: PubMed-11497442;			
RA	Angelos J.A., Hess J.F., George L.W.;			
RT	"Cloning and characterization of a Moraxella bovis cytotoxin gene.";			
RL	Am. J. Vet. Res. 62:1222-1228(2001).			
DR	EMBL: AF205359; AAK84651.1; "			
SO	SEQUENCE 927 AA: 98845 MW: F4B703577E10A96D CRC64;			
Query Match	100.0%;	Score 57;	DB 2;	Length 927;
Best local similarity	100.0%;	Pred. No. 0.17;		
Matches 12;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	1 FLSLNKLEAE 12			
DB	433 FLSLNKLEAE 444			
RESULT	2			
ID	Q9EV24	PRELIMINARY;	PRT;	946 AA.
AC	Q9EV24;			
DT	01-MAR-2001 (Tremblrel. 16, Created)			
DT	01-MAR-2001 (Tremblrel. 16, Last sequence update)			
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)			

DE LEUKOTOXIN.
 GN LKTA.
 OS Mannheimia glucosida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Mannheimia.
 OX NCBI_TaxID=85401;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PH574;
 RX MEDLINE=21101823; PubMed=11157953;
 RA Davies R.L., Whitlam T.S., Selander R.K.;
 RT "Sequence Diversity and Molecular Evolution of the leukotoxin (lktA)
 RT Gene in Bovine and Ovine Strains of Mannheimia (pasteurella)
 RT haemolytica.";
 RL J. Bacteriol. 183:1394-1404(2001).
 DR EMBL; AF314521; AAG40305.1; -;
 DR InterPro: IPR001753; Enoyl_COA_hydrase.
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003355; RTX_N.
 DR Pfam; PF02382; RTX; 1.
 DR PRINTS; PR001313; CABNDNGRPT.
 DR PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN.1.
 SO SEQUENCE 946 AA; 101480 MW; 25C07858BDC76C4 CRC64;

Query Match 75.4%; Score 43; DB 2; Length 946;
 Best Local Similarity 75.0%; Pred. No. 45;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
 Db 444 FLNLNKELOAE 455

RESULT 3
 Q9ETX2 PRELIMINARY; PRT; 953 AA.
 AC Q9ETX2;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE LEUKOTOXIN.
 GN LKTA.
 OS Mannheimia glucosida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Mannheimia.
 OX NCBI_TaxID=85401;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PH498, AND PH344;
 RA Davies R.L., Whitlam T.S., Selander R.K.;
 RT "Sequence diversity and molecular evolution of the leukotoxin (lktA)
 RT gene in bovine and ovine strains of Mannheimia (pasteurella)
 RT haemolytica.";
 RL J. Bacteriol. 0:0-0(2001).
 DR EMBL; AF314518; AAG40302.1; -;
 DR EMBL; AF314517; AAG40301.1; -;
 DR InterPro: IPR001753; Enoyl_COA_hydrase.
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003355; RTX_N.
 DR Pfam; PF003353; hemolysincabind; 1.
 DR Pfam; PF02382; RTX; 1.
 DR PRINTS; PR001313; CABNDNGRPT.
 DR PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN.1.
 SO SEQUENCE 953 AA; 102135 MW; 70DB354157F5881E CRC64;

Query Match 75.4%; Score 43; DB 2; Length 953;
 Best Local Similarity 75.0%; Pred. No. 45;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12

Db 451 FLNLNKELOAE 462

RESULT 4
 Q9ETG5 PRELIMINARY; PRT; 953 AA.
 AC Q9ETG5;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE LEUKOTOXIN.
 GN LKTA.
 OS Pasteurella haemolytica.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Mannheimia.
 OX NCBI_TaxID=75985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PH284, PH388, AND PH8;
 RA Davies R.L., Whitlam T.S., Selander R.K.;
 RT "Sequence diversity and molecular evolution of the leukotoxin (lktA)
 RT gene in bovine and ovine strains of Mannheimia (pasteurella)
 RT haemolytica.";
 RL J. Bacteriol. 0:0-0(2001).
 DR EMBL; AF314507; AAG40291.1; -;
 DR EMBL; AF314504; AAG40288.1; -;
 DR EMBL; AF314506; AAG40290.1; -;
 DR InterPro: IPR001753; Enoyl_COA_hydrase.
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003355; RTX_N.
 DR Pfam; PF003353; hemolysincabind; 1.
 DR Pfam; PF02382; RTX; 1.
 DR PRINTS; PR001313; CABNDNGRPT.
 DR PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN.1.
 SO SEQUENCE 953 AA; 101997 MW; D593D6A577C3ADE9 CRC64;

Query Match 75.4%; Score 43; DB 2; Length 953;
 Best Local Similarity 75.0%; Pred. No. 45;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
 Db 451 FLNLNKELOAE 462

RESULT 5
 Q9EV34 PRELIMINARY; PRT; 953 AA.
 AC Q9EV34;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE LEUKOTOXIN.
 GN LKTA.
 OS Pasteurella haemolytica.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Mannheimia.
 OX NCBI_TaxID=75985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PH56;
 RX MEDLINE=21101823; PubMed=11157953;
 RA Davies R.L., Whitlam T.S., Selander R.K.;
 RT "Sequence Diversity and Molecular Evolution of the leukotoxin (lktA)
 RT Gene in Bovine and Ovine Strains of Mannheimia (pasteurella)
 RT haemolytica.";
 RL J. Bacteriol. 183:1394-1404(2001).
 DR EMBL; AF314505; AAG40289.1; -;
 DR InterPro: IPR001753; Enoyl_COA_hydrase.
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003355; RTX_N.

DR Pfam: PF00353; hemolysincabind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 102010 MW; DE48B28E0E0B09FB CRC64;

Query Match
Best Local Similarity 75.4%; Score 43; DB 2; Length 953;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
|| |||||:||
Db 451 FLTLNKELEQAE 462

RESULT 6
O9EV33 PRELIMINARY; PRT; 953 AA.
AC O9EV33:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE LEUKOTOXIN.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
ON NCBI_TaxID=75985;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-PH66;
RX MEDLINE-21101823; PubMed-1157953;
RA Davies R.L., Whitlam T.S., Selander R.K.;
RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
RT haemolytica.";
RL J. Bacteriol. 183:1394-1404(2001).
DR EMBL: AF314508; ANG40292.1; -;
DR InterPro: IPR001753; Enoyl_COA_hydrtse.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PF00353; hemolysincabind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 102132 MW; 4138AB5FAE2843B3 CRC64;

Query Match
Best Local Similarity 75.4%; Score 43; DB 2; Length 953;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
|| |||||:||
Db 451 FLTLNKELEQAE 462

RESULT 7
O9EV32 PRELIMINARY; PRT; 953 AA.
AC O9EV32:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE LEUKOTOXIN.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
ON NCBI_TaxID=75985;
RN (1)
RP SEQUENCE FROM N.A.

RC STRAIN-PH706;
RX MEDLINE-21101823; PubMed-1157953;
RA Davies R.L., Whitlam T.S., Selander R.K.;
RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
RT haemolytica.";
RL J. Bacteriol. 183:1394-1404(2001).
DR EMBL: AF314509; ANG40293.1; -;
DR InterPro: IPR001753; Enoyl_COA_hydrtse.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PF00353; hemolysincabind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 102078 MW; EF425243C8741EB4 CRC64;

Query Match
Best Local Similarity 75.4%; Score 43; DB 2; Length 953;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
|| |||||:||
Db 451 FLTLNKELEQAE 462

RESULT 8
O9EV31 PRELIMINARY; PRT; 953 AA.
AC O9EV31:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE LEUKOTOXIN.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
ON NCBI_TaxID=75985;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-PH588;
RX MEDLINE-21101823; PubMed-1157953;
RA Davies R.L., Whitlam T.S., Selander R.K.;
RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
RT haemolytica.";
RL J. Bacteriol. 183:1394-1404(2001).
DR EMBL: AF314510; ANG40294.1; -;
DR InterPro: IPR001753; Enoyl_COA_hydrtse.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PF00353; hemolysincabind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 102160 MW; A189BF80754A7907 CRC64;

Query Match
Best Local Similarity 75.4%; Score 43; DB 2; Length 953;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
|| |||||:||
Db 451 FLTLNKELEQAE 462

RESULT 9
O9EV30 PRELIMINARY; PRT; 953 AA.
AC O9EV30:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE LEUKOTOXIN.
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
ON NCBI_TaxID=75985;
RN (1)
RP SEQUENCE FROM N.A.

DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE LEUKOTOXIN.
 GN LKTA.
 OS Pasteurella haemolytica.
 OC Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Mannheimia.
 OX NCBI_TaxID=75985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PH196;
 RX MEDLINE=21101823; PubMed=11157953;
 RA Davies R.L., Whittam T.S., Selander R.K.;
 RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
 RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
 RT haemolytica.";
 RL J. Bacteriol. 183:1394-1404(2001).
 DR EMBL: AF314512; AAG40296.1; -;
 DR InterPro: IPR001753; Enoyl_COA_hydrtse.
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003353; RTX_N.
 DR Pfam: PF003353; hemolysinCbind; 1.
 DR PRINTS: PR00313; CABNDNGRPT.
 DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN.1.
 SQ SEQUENCE 953 AA; 102043 MW; 4E8F11490479A69A CRC64;

Query Match 75.4%; Score 43; DB 2; Length 953;
 Best Local Similarity 75.0%; Pred. No. 45;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLSELNKELEAE 12
 || |||||:
 Db 451 FLNLNKELEAE 462

RESULT 10
 Q9EV29 PRELIMINARY; PRT; 953 AA.
 AC Q9EV29;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE LEUKOTOXIN.
 GN LKTA.
 OS Pasteurella haemolytica.
 OC Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Mannheimia.
 OX NCBI_TaxID=75985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PH278;
 RX MEDLINE=21101823; PubMed=11157953;
 RA Davies R.L., Whittam T.S., Selander R.K.;
 RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
 RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
 RT haemolytica.";
 RL J. Bacteriol. 183:1394-1404(2001).
 DR EMBL: AF314514; AAG40298.1; -;
 DR InterPro: IPR001753; Enoyl_COA_hydrtse.
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003353; RTX_N.
 DR Pfam: PF003353; hemolysinCbind; 1.
 DR PRINTS: PR00313; CABNDNGRPT.
 DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN.1.
 SQ SEQUENCE 953 AA; 102147 MW; 11600FDA7849A1CA CRC64;

Query Match 75.4%; Score 43; DB 2; Length 953;
 Best Local Similarity 75.0%; Pred. No. 45;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 FLSELNKELEAE 12
 || |||||:
 Db 451 FLNLNKELEAE 462

RESULT 11
 Q9EV27 PRELIMINARY; PRT; 953 AA.
 AC Q9EV27;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE LEUKOTOXIN.
 GN LKTA.
 OS Pasteurella haemolytica.
 OC Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Mannheimia.
 OX NCBI_TaxID=75985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PH392;
 RX MEDLINE=21101823; PubMed=11157953;
 RA Davies R.L., Whittam T.S., Selander R.K.;
 RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
 RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
 RT haemolytica.";
 RL J. Bacteriol. 183:1394-1404(2001).
 DR EMBL: AF314516; AAG40300.1; -;
 DR InterPro: IPR001753; Enoyl_COA_hydrtse.
 DR InterPro: IPR001343; Hemlysn_Ca_bind.
 DR InterPro: IPR003353; RTX_N.
 DR Pfam: PF003353; hemolysinCbind; 1.
 DR PRINTS: PR00313; CABNDNGRPT.
 DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN.1.
 SQ SEQUENCE 953 AA; 102230 MW; 2B686808EB370090 CRC64;

Query Match 75.4%; Score 43; DB 2; Length 953;
 Best Local Similarity 75.0%; Pred. No. 45;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FLSELNKELEAE 12
 || |||||:
 Db 451 FLNLNKELEAE 462

RESULT 12
 Q9EV26 PRELIMINARY; PRT; 953 AA.
 AC Q9EV26;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE LEUKOTOXIN.
 GN LKTA.
 OS Mannheimia glucosida.
 OC Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Mannheimia.
 OX NCBI_TaxID=85401;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PH240;
 RX MEDLINE=21101823; PubMed=11157953;
 RA Davies R.L., Whittam T.S., Selander R.K.;
 RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
 RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
 RT haemolytica.";
 RL J. Bacteriol. 183:1394-1404(2001).
 DR EMBL: AF314519; AAG40303.1; -;
 DR InterPro: IPR001753; Enoyl_COA_hydrtse.

DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PF00353; hemolysinCbind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 102236 MW; ACS874B3B75D1C98 CRC64;

Query Match 75.4%; Score 43; DB 2; Length 953;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
DB 451 FLNLNKELOAE 462

RESULT 13

O9EV25 PRELIMINARY; PRT; 953 AA.
AC O9EV25;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LEUKOTOXIN.
GN LKTA.
OS Mannheimia glucosida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=85401;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PH496;
RX MEDLINE-21101823; PubMed-1157953;
RA Davies R.L., Whittam T.S., Selander R.K.;
RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
RT haemolytica";
RL J. Bacteriol. 183:1394-1404(2001).
DR EMBL: AF314520; AAG40304.1; -;
DR InterPro: IPR001753; Enoyl_CoA_hydrase.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PF00353; hemolysinCbind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 102138 MW; CA1D9EBC1D79951 CRC64;

Query Match 75.4%; Score 43; DB 2; Length 953;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
DB 451 FLNLNKELOAE 462

RESULT 14

O9EV23 PRELIMINARY; PRT; 953 AA.
AC O9EV23;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LEUKOTOXIN.
GN LKTA.
OS Mannheimia glucosida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=85401;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PH290;
RX MEDLINE-21101823; PubMed-1157953;
RA Davies R.L., Whittam T.S., Selander R.K.;
RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
RT haemolytica";
RL J. Bacteriol. 183:1394-1404(2001).
DR EMBL: AF314522; AAG40306.1; -;
DR InterPro: IPR001753; Enoyl_CoA_hydrase.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PF00353; hemolysinCbind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 102150 MW; D99C36DA595B1624 CRC64;

Query Match 75.4%; Score 43; DB 2; Length 953;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FLSELNKELEAE 12
DB 451 FLNLNKELOAE 462

RESULT 15

O9EV28 PRELIMINARY; PRT; 953 AA.
AC O9EV28;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LEUKOTOXIN (LKTA).
GN LKTA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PH292, AND PH296;
RX MEDLINE-21101823; PubMed-1157953;
RA Davies R.L., Whittam T.S., Selander R.K.;
RT "Sequence Diversity and Molecular Evolution of the Leukotoxin (Lkta)
RT Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
RT haemolytica";
RL J. Bacteriol. 183:1394-1404(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PH296;
RA Davies R.L., Campbell S., Whittam T.S.;
RT "Mosaic structure and molecular evolution of the leukotoxin operon
RT (lktCABD) of Mannheimia (pasteurella) haemolytica, Mannheimia
RT glucosida and Pasteurella trehalosi";
RL J. Bacteriol. 0:0-0(2001).
DR EMBL: AF314515; AAG40299.1; -;
DR EMBL: AF414141; AAL13281.1; -;
DR InterPro: IPR001753; Enoyl_CoA_hydrase.
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR InterPro: IPR003355; RTX_N.
DR Pfam: PF00353; hemolysinCbind; 1.
DR Pfam: PF02382; RTX; 1.
DR PRINTS: PR00313; CABNDNGRPT.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SQ SEQUENCE 953 AA; 102218 MW; 04AB1715B819E571 CRC64;

Query Match 75.4%; Score 43; DB 2; Length 953;
Best Local Similarity 75.0%; Pred. No. 45;

Matches	9;	Conservative	1;	Mismatches	2;	Indels	0;	Gaps	0;
QY	1	FLSEINKELAE	12						
Db	451	FLNINKELQAE	462						

Search completed: September 11, 2002, 09:01:26
 Job time: 284 sec

ALIGNMENTS

68029

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RESULT 1
AAF57290
ID AAF57290 standard; DNA; 3231 BP.
XX AAF57290;
AC
XX
DT 29-MAY-2001 (first entry)
XX
DE M. bovis Dalton 2d RTX toxin A subunit encoding DNA.
XX
KW Moraxella; antigen; immune response; infection; RTX toxin; vaccine;
XX antibacterial; ds.
XX
OS Moraxella bovis.
XX
EH location/Qualifiers
FT 232..3015
FT /*tag- a
FT /product- "RTX toxin A subunit"
FT 1..195
FT /*tag- b
FT /note- "partial coding region of RTX toxin C subunit"
FT 3080..3250
FT /*tag- c
FT /note- "partial coding region of RTX toxin B subunit"
XX
XX WO200116172-A1.
XX PN
XX 08-MAR-2001.
XX PD
XX 31-AUG-2000; 2000WO-AU01048.
XX PF
XX

```

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68217

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RESULT 1
AAB62110
ID AAB62110 standard: Protein: 927 AA.
XX
AC AAB62110:
XX
DT 29-MAY-2001 (first entry)
XX
DE M. bovis Dalton 2d RTX toxin A subunit.
XX
KW Moraxella: antigen; immune response; infection; RTX toxin; vaccine;
XX antibacterial; A subunit.
XX
OS Moraxella bovis.
XX
PN MO200116172-A1.
XX
PD 08-MAR-2001.
XX
PF 31-AUG-2000; 2000MO-AU01048.
XX
PR 31-AUG-1999; 99AU-0002571.
XX
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX (UYME ) UNIV MELBOURNE.
XX
PI Farn J, Strugnelli R, Tennent J;
XX
XX WPI: 2001-235092/24.
XX DR N-PSDB: AAF57290.
XX
XX Novel Moraxella bovis antigen useful in compositions for raising immune
XX response in an animal, has protease, lipase or hemolysin activity
XX
PS Claim 26: Fig 5; 60pp; English.
XX
XX The invention relates to new Moraxella bovis antigens and nucleic acid
XX sequences encoding these antigenic polypeptides. The antigenic
XX polypeptides and polynucleotides are useful for raising an immune
XX response in an animal directed against Moraxella, preferably against
XX M. bovis or M. catarrhalis, and for treating Moraxella infections. The
XX present sequence represents the amino acid sequence of the A subunit of
XX the RTX toxin from M. bovis Dalton 2d.
XX
XX Sequence 927 AA:
XX
QY 1 FNDIFHSGEGDDL 14
Db 705 fndifhsgegd11 718

Query Match 100.0%; Score 77; DB 22; Length 927;
Best Local Similarity 100.0%; Pred. No. 7,4e-05; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;
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ALIGNMENTS

RESULT 1

AAB62110

ID AAB62110 standard; Protein; 927 AA.

XX

AC AAB62110;

XX

DT 29-MAY-2001 (first entry)

XX

DE M. bovis Dalton 2d RTX toxin A subunit.

XX

KW Moraxella; antigen; immune response; infection; RTX toxin; v
KW antibacterial; A subunit.

XX

OS Moraxella bovis.

XX

PN WO200116172-A1.

XX

PD 08-MAR-2001.

XX

PF 31-AUG-2000; 2000WO-AU01048.

XX

PR 31-AUG-1999; 99AU-0002571.

XX

PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

PA (UYME) UNIV MELBOURNE.

XX

PI Farn J, Strugnell R, Tennent J;

XX

DR WPI; 2001-235092/24.

DR N-PSDB; AAF57290.

XX

PT Novel Moraxella bovis antigen useful in compositions for raising immune
PT response in an animal, has protease, lipase or hemolysin activity

XX

PS Claim 26; Fig 5; 60pp; English.

XX

CC The invention relates to new Moraxella bovis antigens and nucleic acid
 CC sequences encoding these antigenic polypeptides. The antigenic
 CC polypeptides and polynucleotides are useful for raising an immune
 CC response in an animal directed against Moraxella, preferably against
 CC M. bovis or M. catarrhalis, and for treating Moraxella infections. The
 CC present sequence represents the amino acid sequence of the A subunit of
 CC the RTX toxin from M. bovis Dalton 2d.

XX

SQ Sequence 927 AA;

Query Match 100.0%; Score 57; DB 22; Length 927;

Best Local Similarity 100.0%; Pred. No. 0.2;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLSELNKELEAE 12

|||||||

Db 433 flselnkeleae 444

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530 13

RESULT 5
 AAR86998
 ID AAR86998 standard; Protein; 758 AA.
 XX
 AC AAR86998;
 XX
 DT 04-JUL-1996 (first entry)
 XX
 DE Enterohaemorrhagic E.coli hlyA gene product.
 XX
 KW Enterohaemorrhagic Escherichia coli; virulent; EHEC; O157:H7 serotype;
 KW detection; probe; primer; hlyA gene; enterohaemorrhagic colitis;
 KW haemolytic uremic syndrome; mesenteric adenitis.
 XX
 OS Escherichia coli (enterohaemorrhagic).
 XX
 PN US5475098-A.
 XX
 PD 12-DEC-1995.
 XX
 PF 14-JUN-1994; 94US-0258188.
 XX
 PR 14-JUN-1994; 94US-0258188.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Hall RH, Xu JG;
 XX
 DR WPI; 1996-048546/05.
 DR N-PSDB; AAT08098.
 XX
 PT Enterohaemorrhagic E. coli (EHEC) nucleic acid sequences - useful
 PT for probe and primer design for sensitive and specific detection of
 PT EHEC
 XX
 PS Claim 1; Columns 37-42; 32pp; English.
 XX
 CC Enterohaemorrhagic E.coli (EHEC) associated with enterohaemorrhagic
 CC colitis, haemolytic uremic syndrome and mesenteric adenitis have
 CC been found to carry a hlyA gene and a hlyB gene, separated by an
 CC intergenic region. The hly genes and the intergenic region are
 CC absent from bacteria not associated with these diseases and so
 CC provide a useful target for detecting EHEC pathogens, esp. O157:H7
 CC serotype E.coli. The present sequence is that of the protein
 CC encoded by the EHEC hlyA gene.
 XX
 SQ Sequence 758 AA;

Query Match 67.5%; Score 52; DB 17; Length 758;
 Best Local Similarity 57.1%; Pred. No. 1.4;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FNDIFHSGE GDDL 14
 ||||| :|:|:
 Db 480 fndifhgadgndyi 493

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RESULT 2

AAW22159

ID AAW22159 standard; Protein; 1049 AA.

XX

AC AAW22159;

XX

DT 16-FEB-1998 (first entry)

XX

DE ApxIIIB protein.

XX

KW RTX toxin; apxICA gene; apxIBD gene; apxIIAB'C gene; apxIIIABCD gene;
KW repeat in toxins toxin; cell-associated RTX toxin; vaccine production;
KW therapy; A. pleuropneumoniae infection; swine pleuropneumonia.

XX

OS Actinobacillus pleuropneumoniae.

XX

PN CA2170839-A.

XX

PD 02-SEP-1996.

XX

PF 01-MAR-1996; 96CA-2170839.

XX

PR 01-MAR-1995; 95US-0396244.

XX

PA (UYGU-) UNIV GUELPH.

XX

PI MacInnes J, Mallard B, Ricciatti P, Rosendal S;

XX

DR WPI; 1997-245536/23.

DR

N-PSDB; AAT73220.

XX

PT Preparations of microorganisms producing cell-associated RTX toxins
PT - especially for production of vaccines against swine
PT pleuro-pneumonia

XX

PS Disclosure; Pages 107-110; 151pp; English.

XX

CC AAW22151-W22161 represent A. pleuropneumoniae RTX (repeat in toxins)
CC toxins. These sequence are encoded by the apxICA, apxIBD, apxIIAB'C, and
CC apxIIIABCD genes (see AAT73217-T73220), and can be expressed by
CC microorganisms used in the preparations of the invention. The
CC preparations are bacterial preparations comprising one or more isolated
CC and purified strains of a microorganism that produces one or more RTX
CC toxins, where the strains have at least one cell-associated RTX toxin.
CC The preparations are used for production of vaccines for the prophylaxis
CC and treatment of infectious diseases caused by microorganisms that
CC produce RTX toxins, where the strains have been attenuated or
CC inactivated. The vaccines are preferably against Actinobacillus
CC pleuropneumoniae infection (swine pleuropneumonia). It has been found
CC that A. pleuropneumonia produces significant quantities of
CC cell-associated RTX toxins when cultured under certain conditions, and

CC that the whole-cell protein composition of the cultures corresponds to
CC the whole-cell protein profiles obtained from cells recovered at
CC necropsy from the pleural fluid of infected swine. Vaccination with a
CC bacterin prepared from heat-inactivated cultures having significant
CC quantities of cell-associated RTX toxins give significant protection of
CC swine against challenge with homologous strains.

XX

SQ Sequence 1049 AA;

Query Match 75.3%; Score 58; DB 18; Length 1049;
Best Local Similarity 71.4%; Pred. No. 0.18;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FNDIFHSGEGDDL 14
| | | | | : | | | | |
Db 747 frdifhgadgddl 760

580 13

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us-09-884-

us-09-884-696-1.rng

on Sep 16 16:43:25 2002

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 |||| | | ||| |||| | || |
 Db 2528 tcactcaaaagcaagtgtgatcttat 2555

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RESULT 2

AAQ10727

ID: AAQ10727 standard; DNA; 2788 BP.

XX

AC AAQ10727;

XX

DT 11-APR-1991 (first entry)

XX

DE Leukotoxin 352 gene in plasmid PAA352.

XX

KW LKT; vaccine; antigen; respiratory disease; shipping fever pneumonia;

KW

ds.

XX

OS Pasteurella haemolytica A1 strain B122.

XX

PN CA2014033-A.

XX

PD 07-OCT-1990.

XX

PF 06-APR-1990; 90CA-2014033.

XX

PR 07-APR-1989; 89US-0335018.

XX

PA (UYSA-) UNIV SASKATCHEWAN.

XX

PI Acres SD, Babiuk LA, Potter AA, Lawman MJP;

XX

DR WPI; 1991-000097/01.

DR

P-PSDB; AAR10889.

XX

PT Pasteurella haemolytica proteins and genes - used for producing
PT vaccines to protect animals esp. cattle from respiratory diseases
PT e.g. pneumonia.

XX

PS Claim 13; Fig 5; 87pp; English.

XX

CC Plasmid PAA352 is derived from pAA114, a clone isolated from a
CC genomic library of P. haemolytica. The protein encoded by the
CC plasmid, "new leukotoxin" or "LKT 352" is 98% homologous to
CC authentic leukotoxin. LKT 352 and pref. antigenic fragments of it,
CC can be used in vaccines to protect cattle from respiratory diseases.
CC They can also be used to produce antibodies for immunoaffinity
CC purification of further proteins. [Fig. contg. sequence v. poor]
CC See also AAR10890, AAR20909, AAR10910 and AAQ10783.

XX

SQ Sequence 2788 BP; 928 A; 487 C; 597 G; 776 T; 0 other;

Query Match 29.4%; Score 817.6; DB 12; Length 2788;
 Best Local Similarity 60.0%; Pred. No. 3.5e-171;
 Matches 1530; Conservative 0; Mismatches 964; Indels 54; Gaps 8;

Qy 53 caaagctcggattaaaaaatctttacttggctattccaaagattatgatccgcaaaaag 112
 Db 29 caaaaactggggcaaaaaaattatcctctatattcccaaaattaccaatatgatactg 88
 Qy 113 gtgggacttttaaatgattttattaaagctgctgatgaattaggtattgctcgtttagcag 172
 Db 89 aacaaggtttacaggatttagtcaaagcggccgaagagttggggattgaggtacaaagag 148
 Qy 173 aagagcctaatacactgaaacagcaaaaaaatctgttgacacagtaaatcagtttctct 232
 Db 149 aagaacgcaataatattgcaacagctcaaaccagtttaggcacgattcaaaccgctattg 208
 Qy 233 ctctcacacaaactggtattgctatttctgcaacaaaattagaaaagttcttacaaaaac 292
 Db 209 gcttaactgagcgtggcattgtgttatccgctccacaattgataaattgctacagaaa- 267
 Qy 293 attctaccaataagtttagccaaagggttagacagtgtagaaaaattgatcgtaaatag 352
 Db 268 -----actaaagcaggccaagcattaggttctgcccgaagcattgtacaaaatgcaa 319
 Qy 353 gtaaagcaagtaattgtattatcaacattaagctcttttttgggcactgcattagcgggta 412

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RESULT 9

AAR10889

ID AAR10889 standard; Protein; 924 AA.

XX

AC AAR10889;

XX

DT 11-APR-1991 (first entry)

XX

DE Leukotoxin 352 encoded by plasmid pAA352.

XX

KW LKT; vaccine; antigen; respiratory disease; shipping fever pneumonia.

XX

OS Pasteurella haemolytica A1 strain B122.

XX

PN CA2014033-A.

XX

PD 07-OCT-1990.

XX

06-APR-1990; 90CA-2014033.

07-APR-1989; 89US-0335018.

UUSA-) UNIV SASKATCHEWAN.

Acres SD, Babiuk LA, Potter AA, Lawman MJP;

DR WPI; 1991-000097/01.

DR N-PSDB; AAQ10272.

XX

PT Pasteurella haemolytica proteins and genes - used for producing
PT vaccines to protect animals esp. cattle from respiratory diseases
PT e.g. pneumonia.

XX

PS Claim 13; Fig 5; 87pp; English.

XX

CC Plasmid pAA352 is derived from pAA114, a clone isolated from a
CC genomic library of P. haemolytica. The protein, designated "new
CC leukotoxin" or "LKT 352" is 98% homologous to authentic leukotoxin.
CC LKT 352 and pref. antigenic fragments of it, can be used in
CC vaccines to protect cattle from respiratory diseases. They can also
CC be used to produce antibodies for immunoaffinity purification of
CC further proteins. [Fig. contg. sequence v. poor].
CC See also AAR10890, AAR10909, AAR10910 and AAQ10783.

XX

SQ Sequence 924 AA;

Query Match 63.6%; Score 49; DB 12; Length 924;
Best Local Similarity 58.3%; Pred. NO. 5.7;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDIFHSGEGDDL 13
||: | | :|||:
Db 745 ndllhggkgddi 756

58213

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RESULT 1
B30169
leukotoxin A - Pasteurella haemolytica (serotype 1)
N:Alternate names: lktA protein
C:Species: Pasteurella haemolytica
C>Date: 12-Oct-1989 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999
C:Accession: B30169; C32051; S29516
R:Highlander, S.K.; Chidambaram, M.; Engler, M.J.; Weinstock, G.M.
DNA 8, 15-28, 1989
A>Title: DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster.
A:Reference number: A30169; MUID:89210283
A:Accession: B30169
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-953 <HIG>
R:Strathdee, C.A.; Lo, R.Y.C.
J. Bacteriol. 171, 916-928, 1989
A>Title: Cloning, nucleotide sequence, and characterization of genes encoding the
A:Reference number: A32051; MUID:89123172
A:Accession: C32051
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 947-953 <STR>
R:Lo, R.Y.C.; Strathdee, C.A.; Shewen, P.E.
Infect. Immun. 55, 1987-1996, 1987
A>Title: Nucleotide sequence of the leukotoxin genes of Pasteurella haemolytica A1
A:Reference number: S29515; MUID:87306837
A:Accession: S29516
A:Molecule type: DNA
A:Residues: 1-741, 'D', 743-953 <LOR>
A:Cross-references: EMBL:M20730; NID:g150492; PIDN:AAA25529.1; PID:g150494
C:Comment: This organism causes bovine pneumonic pasteurellosis (shipping fever).
C:Genetics:
A:Gene: lktA
C:Function:
A:Description: lyses leukocytes
C:Superfamily: hemolysin A; hemolysin A homology
C:Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem ;
F:238-784/Domain: hemolysin A homology <HLVA>
F:716-807/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
F:554/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match 50.0%; Score 2325; DB 1; Length 953;
Best Local Similarity 49.9%; Pred. No. 1.6e-111;
Matches 464; Conservative 175; Mismatches 264; Indels 26; Gaps 13;

QY 8 KSNIQAGLNSTKSGKLNLYLAIPKD--YDPQGGTLDNFIKADELGIARLAEEPNNHTET 65
Db 28 QSLTQAG-SSLKTGAKIILYIPQNYQYDTEQGNGLQDLVKAEEELGIEVQREERNNIAT 86
QY 66 AKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLKASNVLS 125
Db 87 AQTSLGTIQTAIGLTERGIVLSAPQIDKLLQK---TKAGQALGSAESIVQNANKAKTVLS 143
QY 126 TLSSFLGTALAGIELDSLIIKGDAAAPDALAKASIDLINEIIGNLSQSTOTIEAFSSQLAK 185
Db 144 GIQSLGSLVLAGMDLDEAL-QNNSNOHALAKAGLELTNSLIENIANSVKTLDDEFGEQISQ 202
QY 186 LGSTISQAKGFSNIGNKLQNL-NFSKTNLGLLEIITGLLSGISAGFALADKNASTGKKVAA 244
Db 203 FGSKLQNIKGLGLTGLDKLKNIGGLDKAGLGLDVISGLLSGATAALVLADKNASTAKKVA 262
QY 245 GFELSNQVIGNVTKAISSYVLAQVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFN 304
Db 263 GFELANQVVGNTKAVSSYILAQVAAGLSTTGVAALIASTVSLAISPLAFAGIADKFN 322
QY 305 HANALDEFKQFRKFGYDGDHLLAEYQRCVGTIEASLTITISTALGAVSAGVSAAGVSAV 364
Db 323 HAKSLESYAERFKKLGVDGDNLLAEYQRCGTGTIDASVTAINALAAIAGGVSAAGSVI 382
QY 365 GAPIALLVAGVTGLISGILEASKQAMPESVANRLQGKILEWEKQNGQNYFDKGYDSRYA 424
Db 383 ASPIALLVSGITGVISTILQYSKQAMFEHVANKIHKNKIVEWEKNNHGKNYPENGVDARYL 442
QY 425 AYLANNLKFSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDG 484
Db 443 ANLQDNMKFLLNLNKLQAERVIAITQQQWDNNIGDLAGISRLGKVLSGKAYVDAFEEG 502
QY 485 KKVEAGSNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLK 544
Db 503 KHAKADKLVLQDSANGIIDVSNNGKAKTQHILFRTPLLTGTEHRERVOTGKYEYITKLN 562
QY 545 FGRVKNQVTDGEASSKLDPSKVIQRV-----AETEGTDEIGLIVNAKAGNDDIFVGO 597
Db 563 INRVDSWKITDGAASSTFDLTNNVQRIEGLDNAGNVTKTKETKIIAKLGEGDDNVFVGS 622
QY 598 GKMNIDGGDGHDRVFSYKDGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETK 657
Db 623 GTTEIDGEGGYDRVHYSR-GNYGALTIDATKETEQQSYTVNRVETGKALHEVTSTHTAL 681
QY 658 VGKRTETIQYRDYELRKVGYGQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEQDDL 717
Db 682 VGNREEKIEYR-HSNNQHAGYYTKDTLKAVEEIIIGTSHNDIFKGSKFNDAFNGGDDVDT 740
QY 718 LDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDDNDTLTDG 777
Db 741 IYGNDDNDRLFGGKGDDILDGGNGDDFIDGGKGNLHGGKGDDIFVHRKGDGNDIITDS 800
QY 778 TGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTD 833
Db 801 DGNKLSFSDSNLKDLTTFEKVKNLVI-TNSKKEKVTIQNWFEADFAKEVPNYKATK-D 858
QY 834 HKIEQLIGKDGSIYTSQDIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNK 893
Db 859 EKIEEIQNGERITSKQVDDLI--AKGNKQITQDELSKVVDNYELLKHS-KNVTNSLOK 915

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